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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on:      May 13, 2001, 07:05:25 ; Search time 5997.24 Seconds
              (without alignments)
              241.810 Million cell updates/sec

Title:      US-09-451-527-88
Perfect score: 166
Sequence:    1 ctcagcttaggccagcctac.....caaccctcaaggagctcatt 166

Scoring table:  IDENTITY_NUC
                  Gapop 10.0 , Gapext 1.0

Searched:      9623517 seqs, 4368049070 residues

Total number of hits satisfying chosen parameters:      19247034

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

Database :
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match %	Length	DB	ID	Description
C	1	57.4	34.6	581	219	AZ305110	AZ305110 1M0005P05
	2	37.6	22.7	1996	170	BF867977	BF867977 963095D02
	3	37.2	22.4	918	170	BF868214	BF868214 963104H02
	4	37	22.3	225	130	BB300252	BB300252 BB300252
	5	37	22.3	830	231	CNS04M4J	AL296956 Tetraodon
	6	36.8	22.2	719	143	BF033106	BF033106 601454522
	7	36.6	22.0	782	227	B21994	B21994 F23G15-Sp6
C	8	35.6	21.4	1979	144	BF131613	BF131613 601820420
	9	35.4	21.3	247	133	BB435254	BB435254 BB435254
	10	35.4	21.3	860	231	CNS041Q7	AL270520 Tetraodon
	11	35.2	21.2	639	171	BF967613	BF967613 602287495
C	12	35.2	21.2	1756	141	BE897251	BE897251 601437224
C	13	35	21.1	844	229	CNS0052P	AL056652 Drosophil
	14	35	21.1	919	229	CNS006S5	AL065856 Drosophil
	15	35	21.1	1018	168	BF718319	BF718319 EST92 mic
C	16	35	21.1	1101	229	CNS017RP	AL108415 Drosophil
C	17	35	21.1	1236	170	BF868213	BF868213 963104G06
C	18	35	21.1	1409	146	BF257317	BF257317 HVSMEF001



C 19	C 35	21.1	1690	171	BF975197	BF975197
C 20	34.8	21.0	543	161	BE031946	BE031946
C 21	34.8	21.0	777	143	BF034619	BF034619
C 22	34.8	21.0	839	229	CNS004NB	AL054280
C 23	34.8	21.0	902	146	BF317377	BF317377
C 24	34.6	20.8	949	173	BG106666	BG106666
C 25	34.6	20.8	1872	146	BF310467	BF310467
C 26	34.4	20.7	1225	173	BG115260	BG115260
C 27	34.2	20.6	335	148	BF4211354	BF4211354
C 28	34.2	20.6	494	172	BG052316	BG052316
C 29	34.2	20.6	608	214	AQ947792	AQ947792
C 30	34	20.5	213	169	BF840572	BF840572
C 31	34	20.5	505	30	AV603278	AV603278
C 32	34	20.5	911	217	AZ197129	AZ197129
C 33	34	20.5	997	229	CNS005TE	AL060767
C 34	34	20.5	1081	144	BF139436	BF139436
C 35	34	20.5	1405	145	BF204710	BF204710
C 36	34	20.5	1498	144	BF137829	BF137829
C 37	34	20.5	1517	145	BF206910	BF206910
C 38	33.8	20.4	279	132	BB399409	BB399409
C 39	33.8	20.4	280	126	BB152910	BB152910
C 40	33.8	20.4	300	131	BB346864	BB346864
C 41	33.6	20.2	543	220	AZ387482	AZ387482
C 42	33.6	20.2	836	229	CNS017XZ	AL108641
C 43	33.6	20.2	1186	145	BF256669	BF256669
C 44	33.6	20.2	1653	146	BF338185	BF338185
C 45	33.4	20.1	491	102	AI819748	AI819748

ALIGNMENTS

RESULT 1	
AZ305110	AZ305110
LOCUS	1M0005P05R Mouse 10kb plasmid UUGCLM library Mus musculus genomic
DEFINITION	clone UUGCLM0005P05 R, DNA sequence.
ACCESSION	AZ305110
VERSION	AZ305110.1 GI:10341800
KEYWORDS	GSS.
SOURCE	house mouse.
ORGANISM	Mus musculus

REFERENCE  
AUTHORS  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly  
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.  
and Wright,D.,Weiss,R.  
TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL  
COMMENT  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0005 row: P column: 05  
Seq primer: CACACAGGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 581.

FEATURES  
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Location/Qualifiers  
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/organism="Mus musculus"  
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/clone="UUGCLM0005P05"  
/clone\_lib="Mouse 10kb plasmid UUGCLM library"  
/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PWD42 (gi4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

BASE COUNT 169 a 139 c 153 g 120 t  
ORIGIN  
Query Match 34.6%; Score 57.4; DB 219; Length 581;  
Best Local Similarity 76.9%; Pred. No. 6.5e-05;  
Matches 70; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

Qy	46	tctgcattggtctggtccatggcgctctggtgactgtggtcattgctcacctg	105
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Qy	106	cctcggtggccttgcctcccgagccctgtg	136
Db	551	CCTTGGTGGTCTCGCCGCCAGGCCGGTG	581

RESULT 2  
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DEFINITION  
BF867977 1996 bp mRNA EST 19-JAN-2001  
963095D02.x1 C. reinhardtii CC-1690, Stress condition I, normalized  
, Lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA sequence.  
ACCESSION  
VERSION  
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SOURCE  
ORGANISM  
BF867977  
BF867977.1 GI:12258121  
EST.  
Chlamydomonas reinhardtii.  
Chlamydomonas reinhardtii  
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;  
Chlamydomonadaceae; Chlamydomonas.  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
1 (bases 1 to 1996)  
Grossman,A., Davies,J., Federspiel,N., Harris,E., Hauser,C.,  
Lefebvre,P., McDermott,J.P., Shrager,J., Silflow,C. and Stern,D.  
Analyses of the Chlamydomonas reinhardtii Genome: A Model,  
Unicellular System for Analyzing Gene Function and Regulation in  
Vascular Plants; project phase 3  
Unpublished (2000)  
Contact: Charles Hauser  
DCMB Box 91000  
Duke University  
Durham, NC 27708-1000  
Tel: 919 613 8159  
Fax: 919 613 8177  
Email: chauser@duke.edu.  
Location/Qualifiers  
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/note="Vector: pBluescript II SK-; Site\_1: EcoRI; Site\_2:  
XhoI; This library, constructed by John Davies and Jeffrey  
McDermott, combines cDNAs from CC-1690 cells grown to









QY 24 ctgcctgctcttcctccctcctcctgcattggctctgtgggtccatcgcgctctgtgtga 83  
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QY 144 ccccaacct 153  
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RESULT 9  
BB435254  
LOCUS BB435254 247 bp mRNA EST 01-AUG-2000  
DEFINITION BB435254 RIKEN full-length enriched, adult pancreas Islet cells Mus  
musculus cDNA clone C820012M21 3' similar to dbj:AF026124 Mus  
musculus schwannoma-associated protein (SAM9) mRNA, mRNA sequence.  
BB435254  
BB435254.1 GI:9274981  
EST.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 247)  
AUTHORS Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T., Carninci  
, P., Endo,T., Fukuda,S., Fukunishii,Y., Hara,A., Hayatsu,N.,  
Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M.,  
Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N.,  
Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C., Kusakabe,M.,  
, Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y.,  
, Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K., Shibata,K., Shibata  
, Y., Shigemoto,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Sugahara,Y.,  
, Suzuki,H., Suzuki,H., Tagawa,A., Takahashi,F., Tominaga,N., Toya  
, T., Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yamanaka,I.,  
, Yano,R., Yasunishi,A., Yokota,T., Yoshida,K., Yoshiki,A., Yoshino  
, M., Muramatsu,M. and Hayashizaki,Y.  
RIKEN Mouse ESTs (Konno,H., et al.)  
Unpublished (2000)  
COMMENT Contact: Yoshihide Hayashizaki  
Genome Exploration Research Group, Life Science Tsukuba Center,  
Genome Science Laboratory  
The Institute of Physical and Chemical Research (RIKEN), Genomic  
Sciences Center  
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan  
Tel: +81-298-36-9013  
Fax: +81-298-36-9098  
Email: genome-res@rtc.riken.go.jp,  
URL:http://genome.rtc.riken.go.jp/  
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki  
, N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.  
Thermotabilization and thermoactivation of thermostabile enzymes by  
trehalose and its application for the synthesis of full length  
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)  
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,  
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki  
, Y. and Hayashizaki,Y.  
Automated filtration-based high-throughput plasmid preparation  
system. Genome Res. 9 (5), 463-470 (1999)  
Carninci,P. and Hayashizaki,Y.  
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,  
19-44 (1999)  
Please visit our web site (<http://genome.rtc.riken.go.jp>) for  
further details.  
Location/Qualifiers  
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Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in  
RIKEN. Division of Experimental Animal Research in Riken  
contributed to prepare mouse tissues. 1st strand cDNA was  
primed with a primer [5'  
GAGAGAGAAGGATCCAAGAGCTCTTTTCTTTTCTTTTCTTTT 3'], cDNA was  
prepared by using trehalose thermo-activated reverse  
transcriptase and subsequently enriched for full-length by  
cap-trapper. Second strand cDNA was prepared with the  
primer adapter of sequence [5'  
GAGAGAGAGATTCGAGTTAATTAAATTAATCCCCCCCCCC 3'], cDNA  
was cleaved with XhoI and BamHI. Vector: a modified  
pBluescript KS(+) after bulk excision from Lambda FLC  
I.-Islet cells were provided by Hiroo Iwata, Institute for  
Frontier Medical Sciences, Kyoto University, Sakyo-ku,  
Kyoto, 606-8507 Japan, whose assistance we gratefully  
acknowledge."  
BASE COUNT 46 a 96 c 43 g 62 t  
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Query Match 21.3%; Score 35.4; DB 133; Length 247;  
Best Local Similarity 55.2%; Pred. No. 23;  
Matches 69; Conservative 0; Mismatches 56; Indels 0; Gaps 0;  
  
QY 33 cttccctgcctcctcctgcattggctctgggtccatcgctgtgactgtgtgta 92  
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QY 153 tcaag 157  
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Db 206 CCAAG 210  
  
RESULT 10  
CNS041Q7  
LOCUS CNS041Q7 860 bp DNA GSS 18-MAY-2000  
DEFINITION Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone  
074N24 of library G from Tetraodon nigroviridis, genomic survey  
sequence.  
AL270520  
AL270520.1 GI:7992444  
GSS: genome survey sequence.  
Tetraodon nigroviridis.  
Tetraodon nigroviridis  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
Eurypterygii; Ctenosquamata; Acanthomorpha; Euacanthomorpha;  
Holacanthopterygii; Acanthopterygii; Percomorpha;  
Tetraodontiformes; Tetraodontidae; Tetraodontidae; Tetraodon.  
1 (bases 1 to 860)  
Roest-Crolius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,  
Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and  
Weissenbach,J.  
Charaterization and repeat analysis of the compact genome of the  
freshwater pufferfish Tetraodon nigroviridis  
Unpublished  
2 (bases 1 to 860)  
Roest-Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,  
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,  
Saurin,W. and Weissenbach,J.  
Human gene number estimate provided by genome wide analysis using  
Tetraodon nigroviridis DNA sequence







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S81230.NIH-2 3', mRNA sequence.
ACCESSION   BF718319
VERSION     BF718319.1  GI:12017418
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1018)
AUTHORS    Darling,T.N., Koh,B.B and Yancey,K.B.
TITLE      Delineation of Genes Expressed in Human Epidermis by Large-Scale
            Sequencing of a cDNA Library from Laser Capture Microdissected Skin
JOURNAL    J. Invest. Dermatol. 112 (4), 673 (1999)
COMMENT     Contact: Yancey, K.B.
            Dermatology Branch
            National Cancer Institute
            Building 10, Room 12N238, 10 Center Drive MSC 1908, Bethesda, MD
            20892-1908, USA
            Tel: 301 402 1863
            Fax: 301 496 5370
            Seq primer: M13R
            High quality sequence stop: 132.

FEATURES             Location/Qualifiers
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                     /sex="Male"
                     /tissue_type="epidermis"
                     /dev_stage="adult"
                     /note="Organ: skin; Vector: pAMPl; Epidermis from 20
                     cryostat skin sections (8 um thick) was selectively
                     isolated using laser capture microdissection. Total RNA
                     was extracted, reverse transcribed, and directionally
                     cloned using uracyl DNA glycosylase (Krizman protocol 2,
                     see http://www.ncbi.nlm.nih.gov/CGAP/info/libconst.cgi#Protocol2)."
BASE COUNT      27 a   332 c   41 g   504 t   114 others
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Query Match      21.1%; Score 35; DB 168; Length 1018;
Best Local Similarity 54.2%; Pred. NO. 34;
Matches 71; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

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Job time: 16448 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 13, 2001, 14:16:04 ; Search time 9342.78 Seconds  
(without alignments)  
429.360 Million cell updates/sec

Title: US-09-451-527-89  
Perfect score: 272  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1283235 seqs, 7373929652 residues

Total number of hits satisfying chosen parameters: 2566470

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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4: gb\_in1:\*

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8: gb\_ov:\*

9: gb\_pat1:\*

10: gb\_pat2:\*

11: gb\_ph:\*

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13: gb\_pl2:\*

14: gb\_pl3:\*

15: gb\_pl4:\*

16: em\_bal:\*

17: em\_ba2:\*

18: em\_fun:\*

19: em\_htgo\_hum:\*

20: em\_htgo\_inv:\*

21: em\_htgo\_rod:\*

22: em\_htg\_hum1:\*

23: em\_htg\_hum2:\*

24: em\_htg\_hum3:\*

25: em\_htg\_hum4:\*

26: em\_htg\_hum5:\*

27: em\_htg\_hum6:\*

28: em\_htg\_hum7:\*

29: em\_htg\_hum8:\*

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31: em\_htg\_inv2:\*

32: em\_htg\_other:\*

33: em\_htg\_rod:\*

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83: gb\_htg24:\*

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93: gb\_pr9:\*

94: gb\_rol:\*

95: gb\_ro2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	176.4	64.9	1270	93	HUMIL13A	L06801 Homo sapien
3	176.4	64.9	1282	92	HSNC30	X69079 H.sapiens 1
4	176.4	64.9	1290	10	I34548	I34548 Sequence 1
5	174.8	64.3	417	88	AF043334	AF043334 Homo sapi
6	174.8	64.3	1297	9	A29948	A29948 Coding sequ
7	174.8	64.3	1297	10	I58488	I58488 Sequence 15
8	174.2	64.0	343	7	AF072807	AF072807 Bos tauru
9	165.8	61.0	384	9	A29950	A29950 Nucleic aci
10	165.8	61.0	384	10	I58489	I58489 Sequence 17
11	165.2	60.7	336	9	A29931	A29931 Sequence co



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Db 210 ATCAACCTGACAGCTGGCATGTACTGTGCAGCCCTGGAATCCCTGATCAACGTGTGAGGC 269
Qy 179 tgcagcgccatccaaaggaccagaggatgctgaaagcactgtgctctcaaaagcccgcg 238
Db 270 TGCAGTGCCATCGAGAGACCCAGAGGATGCTGAGCGGATTCTGCCCGCACAAAGGTCTCA 329
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Db 330 GCTGGCAGTTTTCCAGCTTGCAATGTCAGGAGACA 363

RESULT 3
HSNC30
LOCUS
DEFINITION H.sapiens interleukin-13 mRNA. PRI 17-FEB-1997
ACCESSION X69079
VERSION X69079.1 GI:297787
KEYWORDS lymphokine.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1282)
AUTHORS Minty,A.J.
DIRECT SUBMISSION
SUBMITTED (02-NOV-1992) A.J. Minty, Sanofi-Elf Bio Recherches,
Labège Innopole, Voie 1, BP 137, 31676 Labège Cedex, FRANCE
REFERENCE 2 (bases 1 to 1282)
AUTHORS Minty,A.J., Chalon,P., Derocq,J.M., Dumont,X., Guillemot,J.C.,
Kaghad,M., Labit,C., Leplatois,P., Liauzun,P., Miloux,B., Minty,C.,
Casellas,P., Loison,G., Lupker,J., Shire,D., Ferrara,P. and
Caput,D.
TITLE Interleukin-13 is a new human lymphokine regulating inflammatory
and immune responses
JOURNAL Nature 362 (6417), 248-250 (1993)
MEDLINE 93211479
FEATURES
source Location/Qualifiers
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/db\_xref="taxon:9606"
/chromosome="5q 23-31"
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15..455
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Matches 220; Conservative 0; Mismatches 51; Indels 3; Gaps 1;

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Db 162 CTGGTCAACATCACCCAGAACCAAGAGGCTCCGCTCTGCAATGGCAGCATGGTATGGAGC 221
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Db 282 TGCAGTGCCATCGAGAGACCCAGAGGATGCTGAGCGGATTCTGCCCGCACAAAGGTCTCA 341
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RESULT 4
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LOCUS
DEFINITION Sequence 1 from patent US 5596072. PAT 06-FEB-1997
ACCESSION I34548
VERSION I34548.1 GI:1825339
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1290)
AUTHORS Culpepper,J., McKenzie,A., Dang,W. and Zurawski,G.
TITLE Method of refolding human IL-13
JOURNAL Patent: US 5596072-A 1 21-JAN-1997;
FEATURES Location/Qualifiers
1..1290
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BASE COUNT 308 a 335 c 336 g 311 t
ORIGIN







SOURCE synthetic construct.  
ORGANISM synthetic construct  
REFERENCE artificial sequence.  
AUTHORS 1 (bases 1 to 384)  
Caput,D., Ferrara,P., Guillemot,J.C., Kaghad,M., Labit-le  
Bouteiller,C., Leplatols,P., Magazin,M. and Minty,A.  
TITLE Protein having cytokin type activity, recombinant DNA coding for  
this protein, transformed cells and microorganisms  
JOURNAL Patent: EP 0506574-A 23 30-SEP-1992;  
ELF SANOFI  
FEATURES Location/Qualifiers  
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DEFINITION Sequence 17 from patent US 5652123.  
ACCESSION I58489  
VERSION I58489.1 GI:2477727  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
AUTHORS 1 (bases 1 to 384)  
Caput,D., Ferrara,P., Guillemot,J., Kaghad,M., Labit-Le  
Bouteiller,C., Leplatols,P., Magazin,M. and Minty,A.  
TITLE Protein having interleukin 13 activity, recombinant DNA coding for  
this protein, transformed cells and microorganisms  
JOURNAL Patent: US 5652123-A 17 29-JUL-1997;  
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A29931  
LOCUS A29931 336 bp DNA PAT 23-JUN-1995  
DEFINITION Sequence coding for the mature cytokine like protein.  
ACCESSION A29931  
VERSION A29931.1 GI:1249019  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct  
REFERENCE artificial sequence.  
REFERENCE 1 (bases 1 to 336)  
AUTHORS Caput,D., Ferrara,P., Guillemot,J.C., Kaghad,M., Labit-le  
Bouteiller,C., Leplatols,P., Magazin,M. and Minty,A.  
TITLE Protein having cytokin type activity, recombinant DNA coding for  
this protein, transformed cells and microorganisms  
JOURNAL Patent: EP 0506574-A 3 30-SEP-1992;  
ELF SANOFI  
FEATURES Location/Qualifiers  
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DEFINITION Sequence 24 from patent US 5652123.  
ACCESSION I58494



VERSION I58494.1 GI:2477732  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 336)  
AUTHORS Caput,D., Ferrara,P., Guillemot,J., Kaghad,M., Labit-Le Bouteiller,C., Leplatols,P., Magazin,M. and Minty,A.  
TITLE Protein having interleukin 13 activity, recombinant DNA coding for this protein, transformed cells and microorganisms  
JOURNAL Patent: US 5652123-A 24 29-JUL-1997;  
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DEFINITION Sequence 4 from patent US 5856142.  
ACCESSION AR027065  
VERSION AR027065.1 GI:5937905  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 425)  
AUTHORS Legoux,R., Maldonado,P. and Salome,M.  
TITLE Method for the extraction of periplasmic proteins from prokaryotic microorganisms in the presence of arginine  
JOURNAL Patent: US 5856142-A 4 05-JAN-1999;  
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Best Local Similarity 78.4%; Pred. No. 9.6e-31;  
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QY 245 cagatttccagtgaaacgcagccgagaca 272  
Db 295 CAGTTTCCAGCTTGCATGTCCGAGACA 322

RESULT 14  
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LOCUS I86198 425 bp DNA PAT 10-JUN-1998  
DEFINITION Sequence 4 from patent US 5700665.  
ACCESSION I86198  
VERSION I86198.1 GI:3205916  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 425)  
AUTHORS Legoux,R., Maldonado,P. and Salome,M.  
TITLE Method for the extraction of periplasmic proteins from prokaryotic microorganisms in the presence of arginine  
JOURNAL Patent: US 5700665-A 4 23-DEC-1997;  
FEATURES Location/Qualifiers  
source 1..425  
/organism="unknown"  
BASE COUNT 100 a 116 c 110 g 99 t  
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Best Local Similarity 78.4%; Pred. No. 9.6e-31;  
Matches 210; Conservative 0; Mismatches 55; Indels 3; Gaps 1;

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Db 55 GCCTTCGCTGGCCCTGTGCCTCCCAGTACTGCCCTCAGGGAGCTCATTGAGGAGCTGGTC 114  
QY 68 aacatcacccagaatc---aggcatccctctgcaaacgagcagcatggtgtggagcgtcaac 124  
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QY 125 ctgaccgcccggcatgtactgcgcagctctagaatctctgatcaatgtctccgactgcagc 184  
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QY 185 gccatcaaaagaccagagagatgctgaaagcacgtgctctcaaaaagccgcgaggg 244  
Db 235 GCCATCGAGAAGACCCAGAGGATGCTGAGCGGATTCTGCCCGCACAAAGGTCTCAGCTGGG 294  
QY 245 cagatttccagtgaaacgcagccgagaca 272  
Db 295 CAGTTTTCAGCTTGCATGTCCGAGACA 322

RESULT 15  
A52326  
LOCUS A52326 4410 bp DNA PAT 12-DEC-1997  
DEFINITION Sequence 1 from Patent EP0725140.  
ACCESSION A52326  
VERSION A52326.1 GI:2851987  
KEYWORDS  
SOURCE unidentified.  
ORGANISM unidentified

unclassified.  
REFERENCE 1 (bases 1 to 4410)  
AUTHORS Legoux,R., Maldonado,P. and Salome,M.  
TITLE Process of extraction of periplasmic proteins from prokaryotic  
microorganisms in the presence of arginine  
JOURNAL Patent: EP 0725140-A 1 07-AUG-1996;  
SANOFI SA (FR)  
COMMENT Other publication SK 10696 960904  
Other publication CZ 9600290 960814  
Other publication JP 8242879 960924  
Other publication FI 960427 960801  
Other publication PL 312543 960805  
Other publication NO 960396 960801  
Other publication FR 2729972 960802  
Other publication CA 2168382 960801  
Other publication AU 4224496 960808.  
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misc\_RNA 338. .762  
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terminator 763. .812  
terminator 813. .1012  
/note="TERMINATEUR DU GENE 10 DU PHAGE T7"  
terminator 1013. .1253  
/note="TERMINATEUR DU PHAGE FD"  
misc\_RNA 1254. .2505  
/note="GENE CODANT POUR LE REPRESSEUR DE L'OPERON LACTOSE"  
misc\_RNA 2506. .4410  
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Best Local Similarity 78.4%; Pred. No. 7e-31;  
Matches 210; Conservative 0; Mismatches 55; Indels 3; Gaps 1;  
  
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QY 125 ctgaccgccggcatgtactgcgcagctctagaatctctgatcaatgtctccgactgcagc 184  
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QY 185 gccatccaaaggaccagaggatgctgaaagcactgtgctctcaaaagcccgcgagg 244  
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Db 572 GCCATCGAGAAGACCCAGAGGATGCTGAGCGGATTCTGCCCGCACAAAGGTC TCAGCTGGG 631  
  
QY 245 cagatttccagtgaaacgagccgagaca 272  
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Db 632 CAGTTTTCAGCTTGCATGTC CGGAGACA 659

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.  
OM nucleic - nucleic search, using sw model  
Run on: May 13, 2001, 09:02:00 ; Search time 9342.78 Seconds  
(without alignments)  
262.036 Million cell updates/sec

Title: US-09-451-527-88  
Perfect score: 166  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1283235 seqs, 7373929652 residues

Total number of hits satisfying chosen parameters: 2566470

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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5: gb\_in2:\*  
6: gb\_in3:\*  
7: gb\_om:\*  
8: gb\_ov:\*  
9: gb\_pat1:\*  
10: gb\_pat2:\*  
11: gb\_ph:\*  
12: gb\_pl1:\*  
13: gb\_pl2:\*  
14: gb\_pl3:\*  
15: gb\_pl4:\*  
16: em\_ba1:\*  
17: em\_ba2:\*  
18: em\_fun:\*  
19: em\_htgo\_hum:\*  
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21: em\_htgo\_rod:\*  
22: em\_htg\_hum1:\*  
23: em\_htg\_hum2:\*  
24: em\_htg\_hum3:\*  
25: em\_htg\_hum4:\*  
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27: em\_htg\_hum6:\*  
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54: gb\_sts2:\*  
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56: gb\_sy:\*  
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86: gb\_pr2:\*  
87: gb\_pr3:\*  
88: gb\_pr4:\*  
89: gb\_pr5:\*  
90: gb\_pr6:\*  
91: gb\_pr7:\*  
92: gb\_pr8:\*  
93: gb\_pr9:\*  
94: gb\_rol:\*  
95: gb\_ro2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES						
Result No.	Score	Query Match %	Length	DB ID	Description	
c	1	166	100.0	213343	78	AF276990 Canis fam
	2	150	90.4	1302	7	AF244915 Canis fam
	3	88.4	53.3	1270	93	HUMIL13A L06801 Homo sapien
	4	88.4	53.3	1282	92	HSNC30 X69079 H.sapiens 1
	5	88.4	53.3	1290	10	I34548 I34548 Sequen
	6	88.4	53.3	1297	9	A29948 A29948 Coding sequ
c	7	88.4	53.3	1297	10	I58488 I58488 Sequen
	8	88.4	53.3	3714	93	HUMIL13B L42080 Homo sapien
	9	88.4	53.3	4600	93	HUMIL13B L13029 Human inter
	10	88.4	53.3	4740	93	HSU10307 U10307 Human inter
	11	88.4	53.3	5670	93	HSU31120 U31120 Human inter

c	12	88.4	53.3	50282	85	AC004039	AC004039 Homo sapi
c	13	88.4	53.3	78469	75	AC074127	AC074127 Homo sapi
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	15	78.4	47.2	3520	7	BTA132441	AJ132441 Bos tauru
	16	74.4	44.8	417	88	AF043334	AF043334 Homo sapi
	17	68.6	41.3	343	7	AF072807	AF072807 Bos tauru
	18	59.6	35.9	102	9	A29939	A29939 Sequence co
	19	59.6	35.9	102	10	I58483	I58483 Sequence 10
	20	57.8	34.8	447	10	I58495	I58495 Sequence 26
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	22	57.8	34.8	1212	10	I34549	I34549 Sequence 3
	23	57.8	34.8	4376	94	MUSIL13A	L13028 Mouse inter
c	24	57.8	34.8	142732	88	AC084392	AC084392 Homo sapi
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	26	57.8	34.8	237823	66	AC020886	AC020886 Mus muscu
	27	54.6	32.9	96	9	A29938	A29938 Sequence co
	28	54.6	32.9	96	10	I58482	I58482 Sequence 9
	29	47	28.3	443	94	RATIL13A	L26913 Rattus Norv
	30	44.6	26.9	60	9	A29941	A29941 Oligonucleo
	31	44.6	26.9	60	10	I58485	I58485 Sequence 12
	32	39.6	23.9	54	9	A29940	A29940 Sequence co
	33	39.6	23.9	54	10	I58484	I58484 Sequence 11
	34	39.6	23.9	7218	10	I66494	I66494 Sequence 14
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	36	36.8	22.2	81061	67	AC021867	AC021867 Homo sapi
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	41	35.2	21.2	163157	66	AC020779	AC020779 Homo sapi
	42	35	21.1	10851	65	AC018342	AC018342 Drosophil
	43	35	21.1	83333	65	AC018484	AC018484 Drosophil
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ALIGNMENTS

RESULT 1  
AF276990/c  
LOCUS  
DEFINITION  
Canis familiaris chromosome 4 clone RPCI-81 390C13, \*\*\* SEQUENCING  
IN PROGRESS \*\*\*, 25 ordered pieces.  
AF276990  
AF276990.1 GI:9964079  
HTG: HTGS\_PHASE2.  
dog.  
ORGANISM  
Canis familiaris  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
Dubchak, I., Brudno, M., Loots, G.G., Pachter, L., Mayor, C., Rubin, E.M.  
and Frazer, K.A.  
Active conservation of noncoding sequences revealed by three-way  
species comparisons  
Genome Res. 10 (9), 1304-1306 (2000)  
20442524  
10984448  
2 (bases 1 to 213343)  
Blankespoor, C.M., Dean, W.B. and Lewis, K.D.  
Direct Submission  
Submitted (10-JUN-2000) Genome Sciences Department, Lawrence  
Berkeley National Laboratory, 1 Cyclotron Road, Berkeley, CA 94720,  
USA

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
PUBMED  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

COMMENT  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 25 contigs. Gaps between the contigs  
\* are represented as runs of N. The order of the pieces  
\* is believed to be correct as given, however the sizes  
\* of the gaps between them are based on estimates that have  
\* provided by the submittor.  
\* This sequence will be replaced  
\* by the finished sequence as soon as it is available and

\* the accession number will be preserved.  
\* 1 16269: contig of 16269 bp in length  
\* gap of unknown length  
\* 16270 24613: contig of 8344 bp in length  
\* gap of unknown length  
\* 24614 28694: contig of 4081 bp in length  
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\* 28695 31694: contig of 3000 bp in length  
\* gap of unknown length  
\* 31695 32391: contig of 697 bp in length  
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\* 32392 36538: contig of 4147 bp in length  
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\* 36539 39567: contig of 3029 bp in length  
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\* 39568 41164: contig of 1597 bp in length  
\* gap of unknown length  
\* 41165 56023: contig of 14859 bp in length  
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\* 56024 69825: contig of 13802 bp in length  
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\* 69826 71104: contig of 1279 bp in length  
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\* 96588 105542: contig of 8955 bp in length  
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\* 105543 108418: contig of 2876 bp in length  
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\* 113669 116446: contig of 2778 bp in length  
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Best Local Similarity 100.0%; Pred. No. 2e-34;  
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QY 1 ctcagcttagccagccttacgacctgcctgctctctccctcgctcctcctgcattggctct 60  
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Db 114456 GGGCTCCATGGCGCTCTGGTTGACTGTGGTCAATTGCTCTCACCTGCCTCGGTGGCTTGC 114397  
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Db 26 CCTCAATCCTCTCCTGTGGCACTGGGCGCTCATGGCGCTTTGTTGACCAACGGTCATTGC 85

QY 97 tctcacctgcctcgtggccttgccctcccgagccctgtgactccctcccaaccctcaa 156
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QY 157 ggagctcatt 166
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Db 146 GGAGCTCATT 155

RESULT 5
LOCUS I34548 1290 bp DNA PAT 06-FEB-1997
DEFINITION Sequence 1 from patent US 5596072.
ACCESSION I34548

  Query Match 53.3%; Score 88.4; DB 9; Length 1297;
  Best Local Similarity 80.0%; Pred. No. 1.3e-13;
  Matches 104; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

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VERSION I34548.1 GI:1825339
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1290)
AUTHORS Culpepper,J., McKenzie,A., Dang,W. and Zurawski,G.
TITLE Method of refolding human IL-13
JOURNAL Patent: US 5596072-A 1 21-JAN-1997;
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QY 157 ggagctcatt 166
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RESULT 6
LOCUS A29948 1297 bp DNA PAT 23-JUN-1995
DEFINITION Coding sequence for protein with cytokine like activity.
ACCESSION A29948
VERSION A29948.1 GI:1249028
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
  artificial sequence.
REFERENCE 1 (bases 1 to 1297)
AUTHORS Caput,D., Ferrara,P., Guilleminot,J.C., Kaghad,M., Labit-le
  Bouteiller,C., Leplatois,P., Magazin,M. and Minty,A.
TITLE Protein having cytokin type activity, recombinant DNA coding for
  this protein, transformed cells and microorganisms
JOURNAL Patent: EP 0506574-A 21 30-SEP-1992;
  ELF SANOFI
FEATURES
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QY 37 cctcgctcctcctgcatgtggtctgtggctccatggcgctctgtggtgactgtggtcattgc 96
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QY	97	tctcacctgcctcgtggccttgccctcccgagccctgtgactccctccccaacctcaa	156
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RESULT	7		
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DEFINITION	Sequence 15 from patent US 5652123.	PAT	07-OCT-1997
ACCESSION	I58488		
VERSION	I58488.1	GI:2477726	
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 1297)		
AUTHORS	Caput,D., Ferrara,P., Guillemot,J., Kaghad,M., Labit-Le Bouteiller,C., Leplatois,P., Magazin,M. and Minty,A.		
TITLE	Protein having interleukin 13 activity, recombinant DNA coding for this protein, transformed cells and microorganisms		
JOURNAL	Patent: US 5652123-A 15 29-JUL-1997;		
FEATURES	Location/Qualifiers		
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DEFINITION	Homo sapiens (subclone 3_f2 from P1 H11) DNA sequence.	PRI	10-MAY-1995
ACCESSION	L42080		
VERSION	L42080.1	GI:804720	
KEYWORDS	Interleukin growth hormone cluster on chromosome 5 (5q31).		
SOURCE	Homo sapiens (tissue library: Subclones in Homo sapiens from P1 clone H11) DNA.		
ORGANISM	Homo sapiens		
REFERENCE	1 (bases 1 to 3714)		
AUTHORS	Martin,C.H., Bondoc,M.M., Chiang,A., Cloutier,T., Davis,C.A., Erlesson,C.L., Jaklevic,M.A., Kim,R.J., Lee,M.T., Li,M., Mayeda,C.A., Steiert-El Kheir,A. and Palazzolo,M.J.		
TITLE	Sequencing of the interleukin growth hormone cluster on chromosome 5 (5q31) of homo sapiens		
JOURNAL	Unpublished (1995)		
COMMENT	Sequence submitted by: Human Genome Center and Drosophila Genome Center		

Lawrence Berkeley Laboratory Berkeley, CA 94720 e-mail: seq@genome.lbl.gov This subclone overlaps H11 8_al. The P1, from which this subclone is derived, is adjacent to P1 (none).	Location/Qualifiers		
source	1..3714		
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LOCUS	HUMIL13B	4600 bp	DNA
DEFINITION	Human interleukin-13 gene sequence with four exons.	PRI	27-JUL-1993
ACCESSION	L13029		
VERSION	L13029.1	GI:307044	
KEYWORDS	interleukin 13.		
SOURCE	Homo sapiens (library: EMBL-3 SP6/T7) female placenta DNA.		
ORGANISM	Homo sapiens		
REFERENCE	1 (bases 1 to 4600)		
AUTHORS	Mckenzie,A.N.J., Li,X., Largaespada,D.A., Sato,A., Kaneda,A., Zurawski,S.M., Doyle,E.L., Milatovich,A., Francke,U., Copeland,N.G., Jenkins,N.A. and Zurawski,G.		
TITLE	Structural comparison and chromosomal localization of the human and mouse IL-13 genes		
JOURNAL	J. Immunol.	150,	5436-5444 (1993)
MEDLINE	93294299		
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LOCUS	HSU10307	4740 bp	DNA			PRI	21-DEC-1995		
DEFINITION	Human interleukin 13 (IL13) gene, complete cds.								
ACCESSION	U10307								
VERSION	U10307.1	GI:505626							
KEYWORDS		human.							
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ORGANISM		Homo sapiens							
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.							
AUTHORS	1	(bases 1 to 4740)							
TITLE	Smirnov,D.V., Smirnova,M.G., Korobko,V.G. and Frolova,E.I. Tandem arrangement of human genes for interleukin-4 and interleukin-13: resemblance in their organization								
JOURNAL	Gene	155 (2), 277-281 (1995)							
MEDLINE	95237624								
REFERENCE	2	(bases 1 to 4740)							
AUTHORS	Smirnov,D.V.								
TITLE	Direct Submission								
JOURNAL	Submitted (02-JUN-1994) Dmitry V. Smirnov, Shemyakin and Ovchinnikov Institute of Bioorganic Chemistry, ul.Miklukho-Maklaya 16/10, Moscow V-437, 117871 GSP7, Russia								
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ACCESSION	U31120								
VERSION	U31120.1	GI:1045451							
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SOURCE		human.							
ORGANISM		Homo sapiens							
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.							
AUTHORS	1	(bases 1 to 5670)							
TITLE	Dolganov,G., Bort,S., Lovett,M., Burr,J., Schubert,L., Short,D., McGurn,M., Gibson,C. and Lewis,D.B. Coexpression of the interleukin-13 and interleukin-4 genes correlates with their physical linkage in the cytokine gene cluster on human chromosome 5q23-31								
JOURNAL	Blood	87 (8), 3316-3326 (1996)							
MEDLINE	96184791								
REFERENCE	2	(bases 1 to 5670)							
AUTHORS	Dolganov,G.M.								
TITLE	Direct Submission								
JOURNAL	Submitted (06-JUL-1995) Gregory M. Dolganov, Human Genetics, Genelabs, Inc., 505 Penobscot, Redwood City, CA 94063, USA								
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SEQUENCE, 19 unordered pieces.  
AC074127  
ACCESSION AC074127.1 GI:9211237  
VERSION AC074127.1 GI:9211237  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 78469)  
AUTHORS DOE Joint Genome Institute.  
TITLE Sequencing of Human Chromosome 5  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 78469)  
AUTHORS DOE Joint Genome Institute.  
TITLE Direct Submission  
JOURNAL Submitted (15-JUL-2000) Production Sequencing Facility, DOE Joint  
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA  
COMMENT  
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Center: Joint Genome Institute  
Center Code: JGI  
Web site: http://www.jgi.doe.gov  
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Project Information  
Center Project Name: 637386  
Center clone name: CITB-HI\_2025J21  
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Consensus quality: 73718 bases at least Q20  
Estimated insert size: 137500; agarose-fp estimation  
Quality coverage: 7.05 in Q20 bases; agarose-fp estimation  
Quality coverage: 12.65 in Q20 bases; agarose-fp estimation  
Quality coverage: 12.65 in Q20 bases; sum-of-contigs estimation.  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 19 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.









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OM nucleic - nucleic search, using sw model

Run on: May 13, 2001, 14:28:50 ; Search time 472.02 Seconds  
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Title: US-09-451-527-89  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 678276 seqs, 291890651 residues

Total number of hits satisfying chosen parameters: 1356552

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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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14	234	86.0	278	21	255554 Canine interleukin
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25	165.2	60.7	336	13	Q28944 Gly41-Cytokine cod
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37	35.2	12.9	3192	18	T72106 Myceliophthora the
38	35.2	12.9	3192	18	T63318 Myceliophthora the
39	35.2	12.9	3192	21	Z24236 M. thermophila lac
40	34	12.5	479	21	C38383 Zea mays DNA fragm
41	34	12.5	1896	21	Z48297 S. coelicolor Yesw
42	33.6	12.4	772	19	V48405 Dominant-negative
43	33.2	12.2	2712	20	Z06825 Streptomyces albid
44	33.2	12.2	77536	21	A14651 Nucleotide sequenc
45	32.4	11.9	717	21	A93373 Enhanced green flu

ALIGNMENTS

RESULT 1  
255553  
ID Z55553 standard; cDNA; 272 BP.  
XX  
AC Z55553;  
XX  
DT 14-MAR-2000 (first entry)  
XX  
DE Canine interleukin-13 (IL-13) cDNA fragment nCaIL13-272.  
XX  
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;  
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.  
XX  
OS Canis familiaris.  
XX  
PN WO9961618-A2.  
XX  
PD 02-DEC-1999.  
XX  
PF 28-MAY-1999; 99WO-US11942.  
XX  
PR 29-MAY-1998; 98US-0087306.  
XX  
PA (HESK-) HESKA CORP.  
XX  
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;  
XX  
DR WPI; 2000-072623/06.  
XX  
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
PT useful for treating or preventing e.g. tumors or autoimmune disease  
XX  
PS Claim 1i; Page 228; 264pp; English.  
XX





```
OS Canis familiaris.
XX
PN WO9961618-A2.
XX
PD 02-DEC-1999.
XX
PF 28-MAY-1999; 99WO-US11942.
XX
PR 29-MAY-1998; 98US-0087306.
XX
PA (HESK-) HESKA CORP.
XX
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;
XX
DR WPI; 2000-072623/06.
DR P-PSDB; Y58221.
XX
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,
PT useful for treating or preventing e.g. tumors or autoimmune disease
XX
PS Claim 1i; Page 233; 264pp; English.
XX
CC Sequences 255552-255560 and 255561-255566 represent cDNA
CC sequences encoding canine interleukin-13 (IL-13) clones 80
CC and 78 respectively. The invention relates to canine
CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these
CC immunoregulatory proteins. The proteins, their associated
CC nucleic acids, specific antibodies and inhibitors may be used as
CC vaccines for therapeutic or prophylactic regulation of an immune
CC response in animals (particularly cats, dogs, horses and humans).
CC They may be used to treat autoimmune or infectious diseases including
CC allergies, tumours, inflammation and graft rejection, and to increase
CC the response from a co-administered antigen. The nucleotide sequences
CC can also be used for the recombinant production of a protein, while
CC nucleotide fragments are useful as probes, as amplification primers and
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
CC The proteins may be used to raise antibodies and to screen for
CC modulators of activity, while the antibodies may be used in detection,
CC and in drug targetting.
XX
SQ Sequence 393 BP; 82 A; 100 C; 118 G; 93 T; 0 other;

Query Match 100.0%; Score 272; DB 21; Length 393;
Best Local Similarity 100.0%; Pred. No. 5.3e-67;
Matches 272; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tggccttgctccccgagccctgtgactccctcccccacccctcaaggagctcattgagga 60
Db TGGCCTTGCTCCCCGAGCCCTGTGACTCCCTCCCCAACCCCTCAAGGAGGCTCATTTGAGGA 290

QY 61 gctgggtcaacatcacccagaaatcaggcatccctctgcaacgagcagcatggtgtggagcgt 120
Db GTGGTCAACATCACCCAGAAATCAGGCATCCCTCTGCAACGGCAGCATGGTGTGGAGCGT 230

QY 121 caactgaccgcgcggcatgtactgcgagctctagaaatctctgatcaaatgtctccgactg 180
Db CAACCTGACCGCCGCGCATGTACTGCGCAGCTCTAGAAATCTCTGATCAATGCTCTCCGACTG 170

QY 181 cagcgccatccaaaggaccagaggatgctgaaagcactgtgctctcctcaaaaagcccgccg 240
Db CAGCGCCATCCAAAGGACCCAGAGGATGCTGAAAGCACTGTGCTCTCTCAAAAGCCCGCGGC 110

QY 241 agggcagatttcagtgaaacgacgacccagagaca 272
Db AGGCAGATTTCAGTGAACGCAGCCGAGACA 78

RESULT 4
25555
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ID OS
XX Canis familiaris.
AC WO9961618-A2.
XX
DT 14-MAR-2000 (first entry)
XX
DE Canine interleukin-13 (IL-13) clone 80 cDNA.
XX
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
XX
OS Canis familiaris.
XX
FH Key Location/Qualifiers
CDS 52..447
FT /*tag= a
FT /product= "Canine IL-13 clone 80"
XX
PN WO9961618-A2.
XX
PD 02-DEC-1999.
XX
PF 28-MAY-1999; 99WO-US11942.
XX
PR 29-MAY-1998; 98US-0087306.
XX
PA (HESK-) HESKA CORP.
XX
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;
XX
DR WPI; 2000-072623/06.
DR P-PSDB; Y58221.
XX
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,
PT useful for treating or preventing e.g. tumors or autoimmune disease
XX
PS Claim 1i; Page 229-230; 264pp; English.
XX
CC Sequences 255552-255560 and 255561-255566 represent cDNA
CC sequences encoding canine interleukin-13 (IL-13) clones 80
CC and 78 respectively. The invention relates to canine
CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these
CC immunoregulatory proteins. The proteins, their associated
CC nucleic acids, specific antibodies and inhibitors may be used as
CC vaccines for therapeutic or prophylactic regulation of an immune
CC response in animals (particularly cats, dogs, horses and humans).
CC They may be used to treat autoimmune or infectious diseases including
CC allergies, tumours, inflammation and graft rejection, and to increase
CC the response from a co-administered antigen. The nucleotide sequences
CC can also be used for the recombinant production of a protein, while
CC nucleotide fragments are useful as probes, as amplification primers and
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
CC The proteins may be used to raise antibodies and to screen for
CC modulators of activity, while the antibodies may be used in detection,
CC and in drug targetting.
XX
SQ Sequence 1302 BP; 337 A; 318 C; 340 G; 307 T; 0 other;

Query Match 100.0%; Score 272; DB 21; Length 1302;
Best Local Similarity 100.0%; Pred. No. 7.3e-67;
Matches 272; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tggccttgctccccgagccctgtgactccctcccccacccctcaaggagctcattgagga 60
Db tggccttgctccccgagccctgtgactccctcccccacccctcaaggagctcattgagga 155

QY 61 gctgggtcaacatcacccagaaatcaggcatccctctgcaacgagcagcatggtgtggagcgt 120
Db gctgggtcaacatcacccagaaatcaggcatccctctgcaacgagcagcatggtgtggagcgt 215
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Qy 121 caacctgaccgcggcatgtactgcgcagctctagaatctctgatcaatgtctccgactg 180  
|||||  
Db 216 caacctgaccgcggcatgtactgcgcagctctagaatctctgatcaatgtctccgactg 275  
|||||  
Qy 181 cagcgccatcaaaaggacccagaggtgctgaaagcactgtgctctcaaaagcccgggc 240  
|||||  
Db 276 cagcgccatcaaaaggacccagaggtgctgaaagcactgtgctctcaaaagcccgggc 335  
|||||  
Qy 241 agggcagatttcagtgaaacgcagccgagaca 272  
|||||  
Db 336 agggcagatttcagtgaaacgcagccgagaca 367  
|||||  
RESULT 5  
255556/c  
ID 255556 standard; cDNA; 1302 BP.  
XX  
AC 255556;  
XX  
DT 14-MAR-2000 (first entry)  
XX  
DE Canine interleukin-13 (IL-13) clone 80 cDNA complement.  
XX  
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;  
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.  
XX  
OS Canis familiaris.  
XX  
FH Key Location/Qualifiers  
FT CDS complement (856..1251)  
FT /\*tag= a  
FT /product= "Canine IL-13 clone 80"  
XX  
PN WO9961618-A2.  
XX  
PD 02-DEC-1999.  
XX  
PF 28-MAY-1999; 99WO-US11942.  
XX  
PR 29-MAY-1998; 98US-0087306.  
XX  
PA (HESK-) HESKA CORP.  
XX  
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;  
XX  
DR WPI; 2000-072623/06.  
DR P-PSDB; Y58221.  
XX  
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
PT useful for treating or preventing e.g. tumors or autoimmune disease  
XX  
PS Claim 1i; Page 231-232; 264pp; English.  
XX  
CC Sequences 255552-255560 and 255561-255566 represent cDNA  
CC sequences encoding canine interleukin-13 (IL-13) clones 80  
CC and 78 respectively. The invention relates to canine  
CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or  
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline  
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage  
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these  
CC nucleic acids, specific antibodies and inhibitors may be used as  
CC vaccines for therapeutic or prophylactic regulation of an immune  
CC response in animals (particularly cats, dogs, horses and humans).  
CC They may be used to treat autoimmune or infectious diseases including  
CC allergies, tumours, inflammation and graft rejection, and to increase  
CC the response from a co-administered antigen. The nucleotide sequences  
CC can also be used for the recombinant production of a protein, while  
CC nucleotide fragments are useful as probes, as amplification primers and  
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
CC The proteins may be used to raise antibodies and to screen for  
CC modulators of activity, while the antibodies may be used in detection,

CC and in drug targetting.  
XX  
SQ Sequence 1302 BP; 307 A; 340 C; 318 G; 337 T; 0 other;  
  
Query Match 100.0%; Score 272; DB 21; Length 1302;  
Best Local Similarity 100.0%; Pred. No. 7.3e-67;  
Matches 272; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 tggccttgccctcccgagccctgtgactccctcccaacccctcaaggagctcattgagga 60  
|||||  
Db 1207 TGGCCTTGCCCTCCCGAGCCCTGTGACTCCCTCCCAACCCCTCAAGGAGCTCATTGAGGA 1148  
|||||  
Qy 61 gctggtcaacatcacccagaaatcaggcatccctctgcaacggcagcatggtgtggagcgt 120  
|||||  
Db 1147 GCTGGTCAACATCACCCAGAATCAGGCATCCCTCTGCAACGGCAGCATGGTGTGGAGCGT 1088  
|||||  
Qy 121 caacctgaccgcggcatgtactgcgcagctctagaatctctgatcaatgtctccgactg 180  
|||||  
Db 1087 CAACCTGACCGCGGCATGTACTGCCGAGCTCTAGAATCTCTGATCAATGTCTCCGACTG 1028  
|||||  
Qy 181 cagcgccatcaaaaggacccagaggtgctgaaagcactgtgctctcaaaagcccgggc 240  
|||||  
Db 1027 CAGCGCATCCAAAGGACCCAGAGGATGCTGAAAGCACTGTGCTCTCAAAAGCCCGCGGC 968  
|||||  
Qy 241 agggcagatttcagtgaaacgcagccgagaca 272  
|||||  
Db 967 AGGGCAGATTTCAGTGAACGCAGCCGAGACA 936  
|||||  
RESULT 6  
255559  
ID 255559 standard; cDNA; 333 BP.  
XX  
AC 255559;  
XX  
DT 14-MAR-2000 (first entry)  
XX  
DE Canine mature interleukin-13 (IL-13) clone 80 cDNA.  
XX  
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;  
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.  
XX  
OS Canis familiaris.  
XX  
PN WO9961618-A2.  
XX  
PD 02-DEC-1999.  
XX  
PF 28-MAY-1999; 99WO-US11942.  
XX  
PR 29-MAY-1998; 98US-0087306.  
XX  
PA (HESK-) HESKA CORP.  
XX  
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;  
XX  
DR WPI; 2000-072623/06.  
DR P-PSDB; Y58222.  
XX  
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
PT useful for treating or preventing e.g. tumors or autoimmune disease  
XX  
PS Claim 1i; Page 233-234; 264pp; English.  
XX  
CC Sequences 255552-255560 and 255561-255566 represent cDNA  
CC sequences encoding canine interleukin-13 (IL-13) clones 80  
CC and 78 respectively. The invention relates to canine  
CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or  
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline  
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage  
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these  
CC immunoregulatory proteins. The proteins, their associated

CC nucleic acids, specific antibodies and inhibitors may be used as  
CC vaccines for therapeutic or prophylactic regulation of an immune  
CC response in animals (particularly cats, dogs, horses and humans).  
CC They may be used to treat autoimmune or infectious diseases including  
CC allergies, tumours, inflammation and graft rejection, and to increase  
CC the response from a co-administered antigen. The nucleotide sequences  
CC can also be used for the recombinant production of a protein, while  
CC nucleotide fragments are useful as probes, as amplification primers and  
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
CC The proteins may be used to raise antibodies and to screen for  
CC modulators of activity, while the antibodies may be used in detection,  
CC and in drug targeting.  
XX  
SQ Sequence 333 BP; 89 A; 97 C; 83 G; 64 T; 0 other;

Query Match 94.1%; Score 256; DB 21; Length 333;  
Best Local Similarity 100.0%; Pred. No. 1.5e-62;  
Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 agcctgtgactccctcccaaccctcaaggagctcattgaggagctggtcaacatcacc 76  
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Db 1 agcctgtgactccctcccaaccctcaaggagctcattgaggagctggtcaacatcacc 60  
  
QY 77 cagaatcaggcatccctctgcaacggcagcatggtgtggagcgtcaacctgaccgccggc 136  
|||||  
Db 61 cagaatcaggcatccctctgcaacggcagcatggtgtggagcgtcaacctgaccgccggc 120  
  
QY 137 atgtactgagcagctctagaatctctgatcaatgtctccgactgcagcgccatccaaagg 196  
|||||  
Db 121 atgtactgagcagctctagaatctctgatcaatgtctccgactgcagcgccatccaaagg 180  
  
QY 197 acccagaggatgctgaaagcactgtgctctcaaaagcccgccgagggcagatttcagg 256  
|||||  
Db 181 acccagaggatgctgaaagcactgtgctctcaaaagcccgccgagggcagatttcagg 240  
  
QY 257 gaacgcagccgagaca 272  
|||||  
Db 241 gaacgcagccgagaca 256

RESULT 7  
255560/c  
ID 255560 standard; cDNA; 333 BP.  
XX  
AC 255560;  
XX  
DT 14-MAR-2000 (first entry)  
XX  
DE Canine mature interleukin-13 (IL-13) clone 80 cDNA complement.  
XX  
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;  
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.  
XX  
OS Canis familiaris.  
XX  
PN WO9961618-A2.  
XX  
PD 02-DEC-1999.  
XX  
PF 28-MAY-1999; 99WO-US11942.  
XX  
PR 29-MAY-1998; 98US-0087306.  
XX  
PA (HESK-) HESKA CORP.  
XX  
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;  
XX  
DR WPI; 2000-072623/06.  
DR P-PSDB; Y58222.  
XX  
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
PT useful for treating or preventing e.g. tumors or autoimmune disease

XX  
PS  
XX  
CC Sequences Z55552-Z55560 and Z55561-255566 represent cDNA  
CC sequences encoding canine interleukin-13 (IL-13) clones 80  
CC and 78 respectively. The invention relates to canine  
CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or  
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline  
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage  
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these  
CC immunoregulatory proteins. The proteins, and inhibitors associated  
CC nucleic acids, specific antibodies and inhibitors may be used as  
CC vaccines for therapeutic or prophylactic regulation of an immune  
CC response in animals (particularly cats, dogs, horses and humans).  
CC They may be used to treat autoimmune or infectious diseases including  
CC allergies, tumours, inflammation and graft rejection, and to increase  
CC the response from a co-administered antigen. The nucleotide sequences  
CC can also be used for the recombinant production of a protein, while  
CC nucleotide fragments are useful as probes, as amplification primers and  
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
CC The proteins may be used to raise antibodies and to screen for  
CC modulators of activity, while the antibodies may be used in detection,  
CC and in drug targeting.  
XX  
SQ Sequence 333 BP; 64 A; 83 C; 97 G; 89 T; 0 other;

Query Match 94.1%; Score 256; DB 21; Length 333;  
Best Local Similarity 100.0%; Pred. No. 1.5e-62;  
Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 agcctgtgactccctcccaaccctcaaggagctcattgaggagctggtcaacatcacc 76  
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Db 333 AGCCTGTGACTCCCTCCCAACCTCAAGGAGCTCATTTGAGGAGCTGGTCAACATCACC 274  
  
QY 77 cagaatcaggcatccctctgcaacggcagcatggtgtggagcgtcaacctgaccgccggc 136  
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Db 273 CAGAATCAGGCATCCCTCTGCAACGGCAGCATGGTGTGGAGCGTCAACCTGACCGCCGGC 214  
  
QY 137 atgtactgagcagctctagaatctctgatcaatgtctccgactgcagcgccatccaaagg 196  
|||||  
Db 213 ATGTACTGCGCAGCTCTAGAAATCTCTGATCAATGTCTCCGACTGACGCGCATCCAAAGG 154  
  
QY 197 acccagaggatgctgaaagcactgtgctctcaaaagcccgccgagggcagatttcagg 256  
|||||  
Db 153 ACCCAGAGGATGCTGAAAGCAGCTGTGCTCTCAAAAGCCCGGCGAGGCGAGATTTCAGT 94  
  
QY 257 gaacgcagccgagaca 272  
|||||  
Db 93 GAACGCAGCCGAGACA 78

RESULT 8  
255563  
ID Z55563 standard; cDNA; 390 BP.  
XX  
AC Z55563;  
XX  
DT 14-MAR-2000 (first entry)  
XX  
DE Canine interleukin-13 (IL-13) clone 78 cDNA coding region.  
XX  
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;  
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.  
XX  
OS Canis familiaris.  
XX  
PN WO9961618-A2.  
XX  
PD 02-DEC-1999.  
XX  
PF 28-MAY-1999; 99WO-US11942.  
XX





RESULT 10  
Z55561  
ID Z55561 standard; cDNA; 1269 BP.  
XX  
AC Z55561;  
XX  
DT 14-MAR-2000 (first entry)  
XX  
DE Canine interleukin-13 (IL-13) clone 78 cDNA.  
XX  
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;  
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.  
XX  
OS Canis familiaris.  
XX  
FH Key Location/Qualifiers  
FT CDS 57..449  
FT /\*tag= a  
FT /product= "Canine IL-13 clone 78"  
XX  
PN WO9961618-A2.  
XX  
PD 02-DEC-1999.  
XX  
PF 28-MAY-1999; 99WO-US11942.  
XX  
PR 29-MAY-1998; 98US-0087306.  
XX  
PA (HESK-) HESKA CORP.  
XX  
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;  
XX  
DR WPI; 2000-072623/06.  
DR P-PSDB; Y58223.  
XX  
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
PT useful for treating or preventing e.g. tumors or autoimmune disease -  
XX  
PS Claim 1i; Page 235-236; 264pp; English.  
XX  
CC Sequences Z55552-Z55560 and Z55561-Z55566 represent cDNA  
CC sequences encoding canine interleukin-13 (IL-13) clones 80  
CC and 78 respectively. The invention relates to canine  
CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or  
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline  
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage  
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these  
CC immunoregulatory proteins. The proteins, their associated  
CC nucleic acids, specific antibodies and inhibitors may be used as  
CC vaccines for therapeutic or prophylactic regulation of an immune  
CC response in animals (particularly cats, dogs, horses and humans).  
CC They may be used to treat autoimmune or infectious diseases including  
CC allergies, tumours, inflammation and graft rejection, and to increase  
CC the response from a co-administered antigen. The nucleotide sequences  
CC can also be used for the recombinant production of a protein, while  
CC nucleotide fragments are useful as probes, as amplification primers and  
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
CC The proteins may be used to raise antibodies and to screen for  
CC modulators of activity, while the antibodies may be used in detection,  
CC and in drug targeting.  
XX  
SQ Sequence 1269 BP; 302 A; 320 C; 340 G; 307 T; 0 other;

Query Match 94.1%; Score 256; DB 21; Length 1269;  
Best Local Similarity 98.9%; Pred. No. 2.1e-62;  
Matches 269; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 1 tggccttgccctcccgagccctgtgactccctcccccacccctcaaggagctcattgagga 60  
|||||  
DB 101 tggccttgccctcccgagccctgtgactccctcccccacccctcaaggagctcattgagga 160  
|||||

QY 61 gctgggtcaacatcacccagatcaggcatccctctgcaacggcagcatggtgtgagcgt 120  
|||||  
Db 161 gctgggtcaacatcacccagatcaggcatccctctgcaacggcagcatggtgtgagcgt 220  
|||||  
QY 121 caacctgaccgcccgcgtactgctgagctctgagaaatctctgatcaatgtctccgactg 180  
|||||  
Db 221 caacctgaccgcccgcgtactgctgagctctgagaaatctctgatcaatgtctccgactg 280  
|||||  
QY 181 cagcgccatccaaaggaccagaggatgctgaaagcactgtctctcaaaagcccgcgc 240  
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Db 281 cagcgccatccaaaggaccagaggatgctgaaagcactgtctctcaaaagcccgcgc 340  
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QY 241 agggcagatttccagtgaaacgagccgagaca 272  
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Db 341 agg---gatttccagtgaaacgagccgagaca 369  
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RESULT 11  
Z55562/C  
ID Z55562 standard; cDNA; 1269 BP.  
XX  
AC Z55562;  
XX  
DT 14-MAR-2000 (first entry)  
XX  
DE Canine interleukin-13 (IL-13) clone 78 cDNA complement.  
XX  
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;  
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.  
XX  
OS Canis familiaris.  
XX  
FH Key Location/Qualifiers  
FT CDS complement (821..1213)  
FT /\*tag= a  
FT /product= "Canine IL-13 clone 78"  
XX  
PN WO9961618-A2.  
XX  
PD 02-DEC-1999.  
XX  
PF 28-MAY-1999; 99WO-US11942.  
XX  
PR 29-MAY-1998; 98US-0087306.  
XX  
PA (HESK-) HESKA CORP.  
XX  
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;  
XX  
DR WPI; 2000-072623/06.  
DR P-PSDB; Y58223.  
XX  
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
PT useful for treating or preventing e.g. tumors or autoimmune disease -  
XX  
PS Claim 1i; Page 237-238; 264pp; English.  
XX  
CC Sequences Z55552-Z55560 and Z55561-Z55566 represent cDNA  
CC sequences encoding canine interleukin-13 (IL-13) clones 80  
CC and 78 respectively. The invention relates to canine  
CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or  
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline  
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage  
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these  
CC immunoregulatory proteins. The proteins, their associated  
CC nucleic acids, specific antibodies and inhibitors may be used as  
CC vaccines for therapeutic or prophylactic regulation of an immune  
CC response in animals (particularly cats, dogs, horses and humans).  
CC They may be used to treat autoimmune or infectious diseases including  
CC allergies, tumours, inflammation and graft rejection, and to increase  
CC the response from a co-administered antigen. The nucleotide sequences  
CC can also be used for the recombinant production of a protein, while  
CC nucleotide fragments are useful as probes, as amplification primers and

CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
CC The proteins may be used to raise antibodies and to screen for  
CC modulators of activity, while the antibodies may be used in detection,  
CC and in drug targeting.

XX Sequence 1269 BP; 307 A; 340 C; 320 G; 302 T; 0 other;

Query Match 94.1%; Score 256; DB 21; Length 1269;  
Best Local Similarity 98.9%; Pred. No. 2.1e-62;  
Matches 269; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

Qy 1 tggccttgccctcccgagccctgtgactccctcccccacccctcaaggagctcattgagga 60  
|||||  
Db 1169 TGGCCTTGCCCTCCCGAGCCCTGTGACTCCCTCCCCAACCCCTCAAGGAGCTCATTTGAGGA 1110  
|||||

Qy 61 gctggtcaacatcacccagaatcaggcagcatccctctgcaacggcagcatggtgtgagcgt 120  
|||||  
Db 1109 GCTGGTCAACATCACCCAGAATCAGGCATCCCTCTGCAACGGCAGCATGGTGTGGAGCGT 1050  
|||||

Qy 121 caacctgaccgcccgtactgctgcgagctctagatctctgatcaatgtctccgactg 180  
|||||  
Db 1049 CAACCTGACCGCCGCGATGTAAGCTCTGAGATCTCTGATCAATGTCTCCGACTG 990  
|||||

Qy 181 cagcgccatccaaaggacccagagatgctgaaagcactgtgctctcaaaagcccgggc 240  
|||||  
Db 989 CAGCGCCATCCAAAGGACCCAGAGGATGCTGAAAGCACTGTGCTCTCAAAAGCCCCGGGC 930  
|||||

Qy 241 agggcagatttccagtgaacgcagccgagaca 272  
|||  
Db 929 AGG---GATTTCCAGTGAACGCAGCCGAGACA 901  
|||

RESULT 12  
Z55565  
ID Z55565 standard; cDNA; 330 BP.  
XX  
AC Z55565;  
XX

DT 14-MAR-2000 (first entry)  
XX  
XX Canine mature interleukin-13 (IL-13) clone 78 cDNA.  
DE  
XX

KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;  
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.  
XX

OS Canis familiaris.

PN WO9961618-A2.

XX  
PD 02-DEC-1999.

PF 28-MAY-1999; 99WO-US11942.

XX  
PR 29-MAY-1998; 98US-0087306.

XX  
PA (HESK-) HESKA CORP.

XX  
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;

XX  
XX WPI; 2000-072623/06.

DR P-PSDB; Y58224.

XX  
XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
PT useful for treating or preventing e.g. tumors or autoimmune disease

XX  
PS Claim 1i; Page 239-240; 264pp; English.

XX  
XX Sequences Z55552-Z55560 and Z55561-Z55566 represent cDNA  
CC sequences encoding canine interleukin-13 (IL-13) clones 80  
CC and 78 respectively. The invention relates to canine  
CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or  
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline

CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage  
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these  
CC immunoregulatory proteins. The proteins, their associated  
CC nucleic acids, specific antibodies and inhibitors may be used as  
CC vaccines for therapeutic or prophylactic regulation of an immune  
CC response in animals (particularly cats, dogs, horses and humans).  
CC They may be used to treat autoimmune or infectious diseases including  
CC allergies, tumours, inflammation and graft rejection, and to increase  
CC the response from a co-administered antigen. The nucleotide sequences  
CC can also be used for the recombinant production of a protein, while  
CC nucleotide fragments are useful as probes, as amplification primers and  
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
CC The proteins may be used to raise antibodies and to screen for  
CC modulators of activity, while the antibodies may be used in detection,  
CC and in drug targeting.

XX  
SQ Sequence 330 BP; 88 A; 96 C; 82 G; 64 T; 0 other;

Query Match 88.2%; Score 240; DB 21; Length 330;  
Best Local Similarity 98.8%; Pred. No. 4.3e-58;  
Matches 253; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

Qy 17 agccctgtgactccctcccccacccctcaaggagctcattgaggagctggtcaacatcacc 76  
|||||  
Db 1 agccctgtgactccctcccccacccctcaaggagctcattgaggagctggtcaacatcacc 60  
|||||

Qy 77 cagaatcaggcatccctctgcaacggcagcatggtgtgagcgtcaacctgaccgcccgc 136  
|||||  
Db 61 cagaatcaggcatccctctgcaacggcagcatggtgtgagcgtcaacctgaccgcccgc 120  
|||||

Qy 137 atgtactgcgagctctagaatctctgatcaatgtctccgactgcagcgccatccaaagg 196  
|||||  
Db 121 atgtactgcgagctctagaatctctgatcaatgtctccgactgcagcgccatccaaagg 180  
|||||

Qy 197 acccagaggatgctgaaagcactgtgtctctcaaaagcccgaggcagatttccagt 256  
|||||  
Db 181 acccagaggatgctgaaagcactgtgtctctcaaaagcccgaggcagatttccagt 237  
|||||

Qy 257 gaacgcagccgagaca 272  
|||||  
Db 238 gaacgcagccgagaca 253  
|||||

RESULT 13  
Z55566/c  
ID Z55566 standard; cDNA; 330 BP.  
XX  
AC Z55566;

XX  
DT 14-MAR-2000 (first entry)

XX  
DE Canine mature interleukin-13 (IL-13) clone 78 cDNA complement.

XX  
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;  
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.

XX  
OS Canis familiaris.

XX  
PN WO9961618-A2.

XX  
PD 02-DEC-1999.

XX  
PF 28-MAY-1999; 99WO-US11942.

XX  
PR 29-MAY-1998; 98US-0087306.

XX  
PA (HESK-) HESKA CORP.

XX  
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;

XX  
XX WPI; 2000-072623/06.

DR P-PSDB; Y58224.



XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
PT useful for treating or preventing e.g. tumors or autoimmune disease  
XX  
XX  
PS Claim 11; Page 241; 264pp; English.  
XX  
CC Sequences Z55552-Z55560 and Z55561-Z55566 represent cDNA  
CC sequences encoding canine interleukin-13 (IL-13) clones 80  
CC and 78 respectively. The invention relates to canine  
CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or  
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline  
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage  
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these  
CC immunoregulatory proteins. The proteins, their associated  
CC nucleic acids, specific antibodies and inhibitors may be used as  
CC vaccines for therapeutic or prophylactic regulation of an immune  
CC response in animals (particularly cats, dogs, horses and humans).  
CC They may be used to treat autoimmune or infectious diseases including  
CC allergies, tumours, inflammation and graft rejection, and to increase  
CC the response from a co-administered antigen. The nucleotide sequences  
CC can also be used for the recombinant production of a protein, while  
CC nucleotide fragments are useful as probes, as amplification primers and  
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
CC The proteins may be used to raise antibodies and to screen for  
CC modulators of activity, while the antibodies may be used in detection,  
CC and in drug targeting.  
XX Sequence 330 BP; 64 A; 82 C; 96 G; 88 T; 0 other;  
SQ  
  
Query Match 88.2%; Score 240; DB 21; Length 330;  
Best Local Similarity 98.8%; Pred. No. 4.3e-58;  
Matches 253; Conservative 0; Mismatches 0; Indels 3; Gaps 1;  
  
QY 17 agccctgtgactccctcccccacccctcaaggagctcattgaggagctggtcaacatcacc 76  
Db 330 AGCCCTGTGACTCCCTCCCCAACCCCTCAAGGAGCTCATTTGAGGAGCTGGTCAACATCACC 271  
  
QY 77 cagaatcaggcatccctctgcaacggcagcatggtgtggagcgtcaacctgaccgcccgc 136  
Db 270 CAGAATCAGGCATCCCTCTGCAACGGCAGCATGGTGTGGAGCGTCAACCTGACCGCCGGC 211  
  
QY 137 atgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgccatccaaagg 196  
Db 210 ATGTACTGCGCAGCTCTAGAAATCTCTGATCAATGTCTCCGACTGCAGCGCATCCAAAGG 151  
  
QY 197 acccagaggatgctgaaagcactgtgtctctcaaaagcccgcggcaggcgagattccagt 256  
Db 150 ACCCAGAGGATGCTGAAAGCACTGTGTCTCTCAAAAGCCCGCGGCAGG---GATTTCAGT 94  
  
QY 257 gaacgcagccgagaca 272  
Db 93 GAACCGACCGGAGACA 78  
  
RESULT 14  
Z55554  
ID Z55554 standard; cDNA; 278 BP.  
XX  
AC Z55554;  
XX  
DT 14-MAR-2000 (first entry)  
XX  
DE Canine interleukin-13 (IL-13) cDNA probe.  
XX  
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;  
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.  
XX  
OS Canis familiaris.  
XX  
PN WO9961618-A2.  
XX  
PD 02-DEC-1999.

XX 28-MAY-1999; 99WO-US11942.  
XX  
PR 29-MAY-1998; 98US-0087306.  
XX  
PA (HESK-) HESKA CORP.  
XX  
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;  
XX  
DR WPI; 2000-072623/06.  
XX  
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
PT useful for treating or preventing e.g. tumors or autoimmune disease  
XX  
XX Claim 11; Page 229; 264pp; English.  
XX  
CC Sequences Z55552-Z55560 and Z55561-Z55566 represent cDNA  
CC sequences encoding canine interleukin-13 (IL-13) clones 80  
CC and 78 respectively. The invention relates to canine  
CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or  
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline  
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage  
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these  
CC immunoregulatory proteins. The proteins, their associated  
CC nucleic acids, specific antibodies and inhibitors may be used as  
CC vaccines for therapeutic or prophylactic regulation of an immune  
CC response in animals (particularly cats, dogs, horses and humans).  
CC They may be used to treat autoimmune or infectious diseases including  
CC allergies, tumours, inflammation and graft rejection, and to increase  
CC the response from a co-administered antigen. The nucleotide sequences  
CC can also be used for the recombinant production of a protein, while  
CC nucleotide fragments are useful as probes, as amplification primers and  
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
CC The proteins may be used to raise antibodies and to screen for  
CC modulators of activity, while the antibodies may be used in detection,  
CC and in drug targeting.  
XX Sequence 278 BP; 58 A; 93 C; 69 G; 58 T; 0 other;  
SQ  
  
Query Match 86.0%; Score 234; DB 21; Length 278;  
Best Local Similarity 100.0%; Pred. No. 1.9e-56;  
Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 tggccttgctcccccagccctgtgactccctcccccacccctcaaggagctcattgagga 60  
Db 45 tggccttgctcccccagccctgtgactccctcccccacccctcaaggagctcattgagga 104  
  
QY 61 gctggtcaacatcaccacagaatcaggcatccctctgcaacggcagcatggtgtggagcgt 120  
Db 105 gctggtcaacatcaccacagaatcaggcatccctctgcaacggcagcatggtgtggagcgt 164  
  
QY 121 caactgaccgcccggcatgtactgcagctctagaatctctgataatgtctccgactg 180  
Db 165 caactgaccgcccggcatgtactgcagctctagaatctctgataatgtctccgactg 224  
  
QY 181 cagcgccatccaaaggaccagagatgctgaaagcactgtgctctcaaaagcc 234  
Db 225 cagcgccatccaaaggaccagagatgctgaaagcactgtgctctcaaaagcc 278  
  
RESULT 15  
F21334  
ID F21334 standard; DNA; 1270 BP.  
XX  
AC F21334;  
XX  
DT 14-MAR-2001 (first entry)  
XX  
DE Human low adenosine antisense oligonucleotide related sequence #2901.  
XX  
KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;  
KW human; airway disorder; bronchoconstriction; lung inflammation;



KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;  
 KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;  
 KW respiratory obstruction; pulmonary obstruction; impeded respiration;  
 KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;  
 KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;  
 KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;  
 KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;  
 KW cancer; ss.

OS Homo sapiens.

PN WO200062736-A2.

PD 26-OCT-2000.

24-MAR-2000; 2000WO-US08020.

PR 06-APR-1999; 99US-0127958.

PA (UYEC-) UNIV EAST CAROLINA.

PA (NYCE/) NYCE J W.

PT. Nyce JW;

DR WPI; 2000-679539/66.

Low adenosine (A) content antisense oligonucleotides which do not trigger adenosine receptors during metabolism, useful e.g. for treating cancers and respiratory obstructions -

PS Disclosure; Page 1336; 1592pp; English.

The present invention describes low adenosine (A) content antisense oligonucleotides and compositions (I) comprising them. In the antisense oligonucleotides the A is replaced by a 'Universal' or alternative base. (I) can have respiratory, bronchodilator, antiinflammatory, analgesic, immunosuppressive, antialsthmatic, hypotensive and cytostatic activities. The antisense oligonucleotides and (I) can be used to down-regulate the expression and or activity of target polypeptides associated with lung/respiratory disorders and malignancies, such as stimulating and activating peptide factors and transmitters, transcription factors, immunoglobulins and antibodies, antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific enzymes, binding proteins, adhesion molecules and their receptors, cytokine and chemokine receptors, adenosine receptors, bradykinin receptors, central nervous system (CNS) and peripheral nervous and non-nervous system receptors, CNS and peripheral nervous and non-nervous system transmitters, defensins, growth factors, vasoactive peptides and receptors, binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (especially pulmonary obstruction and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or surfactant hypoproduction which are associated with a disease or condition selected from pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, bronchitis, and/or cancer. F18434 to F21543 represent human polynucleotide fragments and antisense oligonucleotides used in the exemplification of the present invention.

Sequence 1270 BP; 288 A; 335 C; 336 G; 311 T; 0 other;

Query Match	64.9%;	Score 176.4;	DB 21;	Length 1270;
Best Local Similarity	80.3%;	Pred. NO. 3.5e-40;		
Matches 220;	Conservative	0;	Mismatches 51;	Indels 3;
				Gaps 1;

Qy 2 ggcttgctccccgagccctgtgactcctcccaacctcaaggagctcattgaggag 61

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835  
836  
837  
838  
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84

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 13, 2001, 14:20:45 ; Search time 226.02 Seconds  
(without alignments)  
210.123 Million cell updates/sec

Title: US-09-451-527-89  
Perfect score: 272  
Sequence: 1 tggccttgccctcccgagcc.....cagtgaacgcagccgagaca 272

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 302621 seqs, 87301344 residues

Total number of hits satisfying chosen parameters: 605242

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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6: /cgnl\_7/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	176.4	64.9	1290	5 PCT-US93-07645A-1	Sequence 1, Appl
3	176.4	64.9	1290	5 PCT-US93-07645-1	Sequence 1, Appl
4	174.8	64.3	1297	1 US-08-371-121-15	Sequence 15, Appl
5	165.8	61.0	384	1 US-08-371-121-17	Sequence 17, Appl
6	165.2	60.7	336	1 US-08-371-121-24	Sequence 24, Appl
7	164	60.3	425	1 US-08-594-469-4	Sequence 4, Appl
8	164	60.3	425	2 US-08-906-957-4	Sequence 4, Appl
9	164	60.3	4410	1 US-08-594-469-1	Sequence 1, Appl
10	164	60.3	4410	2 US-08-906-957-1	Sequence 1, Appl
11	163.6	60.1	336	1 US-08-371-121-2	Sequence 2, Appl
12	128	47.1	447	1 US-08-371-121-26	Sequence 26, Appl
13	128	47.1	1212	1 US-08-012-543-3	Sequence 3, Appl
14	128	47.1	1212	5 PCT-US93-07645A-3	Sequence 3, Appl
15	128	47.1	1212	5 PCT-US93-07645-3	Sequence 3, Appl
16	35.2	12.9	2249	3 US-08-814-052-19	Sequence 19, Appl
17	35.2	12.9	2300	3 US-08-814-052-18	Sequence 18, Appl
18	35.2	12.9	3183	2 US-08-939-218A-1	Sequence 1, Appl
19	35.2	12.9	3187	5 PCT-US95-06815-1	Sequence 1, Appl
20	35.2	12.9	3192	1 US-08-706-037-26	Sequence 26, Appl
21	35.2	12.9	3192	1 US-08-940-661A-1	Sequence 1, Appl
22	35.2	12.9	3192	2 US-09-083-485-1	Sequence 1, Appl
23	35.2	12.9	3192	2 US-09-005-397-26	Sequence 26, Appl
24	33.6	12.4	1322	4 US-09-128-450-27	Sequence 27, Appl
25	33.2	12.2	2712	3 US-09-025-691-4	Sequence 4, Appl
26	32.4	11.9	720	4 US-09-094-359-3	Sequence 3, Appl
27	32.4	11.9	720	4 US-09-094-359-7	Sequence 7, Appl

28	32.4	11.9	720	4 US-09-172-063-11	Sequence 11, Appl
29	32.4	11.9	720	4 US-09-172-063-13	Sequence 13, Appl
30	32.4	11.9	762	1 US-08-532-390-40	Sequence 40, Appl
31	32.4	11.9	762	4 US-08-717-294-40	Sequence 40, Appl
32	32.4	11.9	768	4 US-09-094-359-11	Sequence 11, Appl
33	32.4	11.9	850	4 US-09-062-102-2	Sequence 2, Appl
34	32.4	11.9	972	4 US-09-172-063-27	Sequence 27, Appl
35	32.4	11.9	972	4 US-09-172-063-29	Sequence 29, Appl
36	32.4	11.9	1095	4 US-09-085-305-5	Sequence 5, Appl
37	32.4	11.9	1929	2 US-08-818-253-1	Sequence 1, Appl
38	32.4	11.9	1929	2 US-08-818-253-5	Sequence 5, Appl
39	32.4	11.9	1929	4 US-08-818-252-1	Sequence 1, Appl
40	32.4	11.9	1929	4 US-08-818-252-5	Sequence 5, Appl
41	32.4	11.9	1959	2 US-08-818-253-3	Sequence 3, Appl
42	32.4	11.9	1959	4 US-08-818-252-3	Sequence 3, Appl
43	32.4	11.9	1971	2 US-08-818-253-7	Sequence 7, Appl
44	32.4	11.9	1971	4 US-08-818-252-7	Sequence 7, Appl
45	32.4	11.9	7938	4 US-09-331-581-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1  
US-08-012-543-1  
; Sequence 1, Application US/08012543  
; Patent No. 5596072  
; GENERAL INFORMATION:  
; APPLICANT: Culpepper, Janice  
; APPLICANT: McKenzie, Andrew  
; APPLICANT: Dang, Warren  
; APPLICANT: de Waal Malefyt, Rene  
; APPLICANT: Heath, Andrew  
; APPLICANT: Aversa, Gregorio  
; APPLICANT: Briere, Francine  
; APPLICANT: Banchereau, Jacques  
; APPLICANT: de Vries, Jan  
; APPLICANT: Zurawski, Gerard  
; TITLE OF INVENTION: Human Interleukin-13  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/012,543  
; FILING DATE: 01-FEB-1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/933,416  
; FILING DATE: 21-AUG-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0302K1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-852-9196  
; TELEFAX: 415-496-1200  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1290 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA







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; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 384 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-371-121-17

Query Match          61.0%; Score 165.8; DB 1; Length 384;
Best Local Similarity 79.2%; Pred. No. 1e-41;
Matches 210; Conservative 0; Mismatches 52; Indels 3; Gaps 1;

QY 11 tccccgagccctgtgactccctcccccacccctcaaggagctcattgaggagctggtcaac 70
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 16 TCCCCAGGCCCTGTGCCTCCCTCTACGGCCCTCAGGGAGCTCATTGAGGAGCTGGTCAAC 75

QY 71 atcaccagaatc---aggcatccctctgcaacggcagcatggtgtggagctcaacctg 127
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 76 ATCACCAGAACCCAGAGGCTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAACCTG 135

QY 128 accgcggcatgtactgcgcagctctagaaatctctgatcaatgtctccagctcagcgcc 187
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Db 136 ACAGCTGACATGTACTGTGCAGCCCTGGAATCCCTGATCAACGTGTGAGGCTGCAGTGCC 195

QY 188 atccaaagaccagaggtgctgaaagcactgtgctctcaaaaagcccgaggcgag 247
    || || || || || || || || || || || || || || || || || || || || ||
Db 196 ATCGAGAGACCCAGAGGATGTGAGCGGATTTGCCCCGCACAAAGTCTCAGCTGGGCAG 255

QY 248 atttccagtgaacgcagccgagaca 272
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Db 256 TTTTCCAGCTGCATGTCGAGACA 280

RESULT 6
US-08-371-121-24
; Sequence 24, Application US/08371121
; Patent No. 5652123
; GENERAL INFORMATION:
; APPLICANT: CAPUT, Daniel
; APPLICANT: FERRARA, Pascual
; APPLICANT: GUILLEMOT, Jean-Claude
; APPLICANT: LEPLATOIS, Pascal
; APPLICANT: MINTY, Adrian
; APPLICANT: LABIT-LE BOUTEILLER, Christine
; APPLICANT: MAGAZIN, Marilyn
; TITLE OF INVENTION: Protein having a cytokine type
; TITLE OF INVENTION: activity, recombinant DNA coding for this protein,
; TITLE OF INVENTION: transfected cells and microorganisms.
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/371.121
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/938,161
; FILING DATE: 30-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR92/00280
; FILING DATE: 27-MAR-1992

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91 00137
; FILING DATE: 08-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91 03904
; FILING DATE: 29-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 16781/383
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 336 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-371-121-24

Query Match          60.7%; Score 165.2; DB 1; Length 336;
Best Local Similarity 80.2%; Pred. No. 1.5e-41;
Matches 207; Conservative 0; Mismatches 48; Indels 3; Gaps 1;

QY 18 gccctgtgactccctcccccacccctcaaggagctcattgaggagctggtcaacatcaccc 77
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QY 78 agaatc---aggcatccctctgcaacggcagcatggtgtggagctcaacctgaccg 134
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 62 AGAACCAAGAGGCTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAACCTGACAGCTG 121

QY 135 gcatgtactgcgcagctctagaaatctctgatcaatgtctccgactgcagccatccaaa 194
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 122 GCATGTACTGTGCAGCCCTGGAATCCCTGATCAACGTGTGAGGCTGCAGTGCATCGAGA 181

QY 195 ggaaccagaggtgctgaaagcactgtgctctcaaaaagcccgaggcgagatttcca 254
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 182 AGACCCAGAGGATGCTGAGCGGATTTGCCCCGCACAAAGTCTCAGCTGGGCAGTTTCCA 241

QY 255 gtgaacgcagccgagaca 272
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Db 242 GCTTGCATGTCGAGACA 259

RESULT 7
US-08-594-469-4
; Sequence 4, Application US/08594469
; Patent No. 5700665
; GENERAL INFORMATION:
; APPLICANT: LEGOUX, Richard
; APPLICANT: MALDONADO, Paul
; APPLICANT: SALOME, Marc
; TITLE OF INVENTION: Method for the extraction of
; TITLE OF INVENTION: periplasmic proteins of prokaryotic microorganisms in the
; TITLE OF INVENTION: presence of arginine
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bacon & Thomas
; STREET: 625 Slaters Lane - Fourth Floor
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

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OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/594,469  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 95 01083  
FILING DATE: 31-JAN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: FICHTER, Richard E  
REGISTRATION NUMBER: 26,382  
REFERENCE/DOCKET NUMBER: REF/LEGOUX  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 683-0500  
TELEFAX: (703) 683-1080  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4410 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-594-469-1

Query Match 60.3%; Score 164; DB 1; Length 4410;  
Best Local Similarity 78.4%; Pred. No. 7.8e-41;  
Matches 210; Conservative 0; Mismatches 55; Indels 3; Gaps 1;  
  
QY 8 gcctccccgagccctgtgactccctcccccaaccctcaaggagctcattgaggagctggtc 67  
Db 392 GCCTTCGCTGGCCCTGTGCCCTCCAGTACTGCCCTCAGGGAGCTCATTGAGGAGCTGGTC 451  
  
QY 68 aacatcacccagaatc---aggcatccctctgcaacggcgagcatggtgtggagctcaac 124  
Db 452 AACATCACCCAGAACAGAGGCTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAAC 511  
  
QY 125 ctgaccgcccggactgtactgcgagctctagaatctctgatcaatgtctccgactgcagc 184  
Db 512 CTGACAGCTGGCATGTACTGTGCAGCCCTGGAATCCCTGTATCAACGTGTCAGGCTGCAGT 571  
  
QY 185 gccatccaaaggaccagagatgctgaaagactgtgtctctctcaaaagcccgcgaggg 244  
Db 572 GCCATCGAGAAAGACCCAGAGGATGCTGAGCGGATTCTGCCCGCACAAAGGTCTCAGCTGGG 631  
  
QY 245 cagatttccagtgaacgcagccgagaca 272  
Db 632 CAGTTTTCAGCTTGCATGTCCGAGACA 659

RESULT 10  
US-08-906-957-1  
Sequence 1, Application US/08906957  
Patent No. 5856142  
GENERAL INFORMATION:  
APPLICANT: LEGOUX, Richard  
APPLICANT: MALDONADO, Paul  
APPLICANT: SALOME, Marc  
TITLE OF INVENTION: Method for the extraction of  
periplasmic proteins of prokaryotic microorganisms in the  
presence of arginine  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Bacon & Thomas  
STREET: 625 Slaters Lane - Fourth Floor  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: USA  
ZIP: 22314  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/906,957  
FILING DATE: 06-AUG-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/594,469  
FILING DATE:  
APPLICATION NUMBER: FR 95 01083  
FILING DATE: 31-JAN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: FICHTER, Richard E  
REGISTRATION NUMBER: 26,382  
REFERENCE/DOCKET NUMBER: REF/LEGOUX  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 683-0500  
TELEFAX: (703) 683-1080  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4410 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-906-957-1

Query Match 60.3%; Score 164; DB 2; Length 4410;  
Best Local Similarity 78.4%; Pred. No. 7.8e-41;  
Matches 210; Conservative 0; Mismatches 55; Indels 3; Gaps 1;  
  
QY 8 gcctccccgagccctgtgactccctcccccaaccctcaaggagctcattgaggagctggtc 67  
Db 392 GCCTTCGCTGGCCCTGTGCCCTCCAGTACTGCCCTCAGGGAGCTCATTGAGGAGCTGGTC 451  
  
QY 68 aacatcacccagaatc---aggcatccctctgcaacggcgagcatggtgtggagctcaac 124  
Db 452 AACATCACCCAGAACAGAGGCTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAAC 511  
  
QY 125 ctgaccgcccggactgtactgcgagctctagaatctctgatcaatgtctccgactgcagc 184  
Db 512 CTGACAGCTGGCATGTACTGTGCAGCCCTGGAATCCCTGTATCAACGTGTCAGGCTGCAGT 571  
  
QY 185 gccatccaaaggaccagagatgctgaaagactgtgtctctctcaaaagcccgcgaggg 244  
Db 572 GCCATCGAGAAAGACCCAGAGGATGCTGAGCGGATTCTGCCCGCACAAAGGTCTCAGCTGGG 631  
  
QY 245 cagatttccagtgaacgcagccgagaca 272  
Db 632 CAGTTTTCAGCTTGCATGTCCGAGACA 659

RESULT 11  
US-08-371-121-2  
Sequence 2, Application US/08371121  
Patent No. 5652123  
GENERAL INFORMATION:  
APPLICANT: CAPUT, Daniel  
APPLICANT: FERRARA, Pascual  
APPLICANT: GUILLEMOT, Jean-Claude  
APPLICANT: LEPLATOIS, Pascal  
APPLICANT: MINTY, Adrian  
APPLICANT: KAGHAD, Mourad  
APPLICANT: LABIT-LE BOUTEILLER, Christine  
APPLICANT: MAGAZIN, Marilyn  
TITLE OF INVENTION: Protein having a cytokine type  
activity, recombinant DNA coding for this protein,  
transformed cells and microorganisms.  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FOLEY & LARDNER  
STREET: 3000 K Street, N.W., Suite 500







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; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07645
; FILING DATE: 19930818
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/012543
; FILING DATE: 01-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/010977
; FILING DATE: 29-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/933416
; FILING DATE: 21-AUG-1992
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1212 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
PCT-US93-07645-3
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Query Match 47.1%; Score 128; DB 5; Length 1212;
Best Local Similarity 73.2%; Pred. No. 4.5e-30;
Matches 164; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 14 ccgagccctgtgactccctcccaacccctcaaggagctcattgaggagctggtcaacatc 73
Db 139 CCAAGATCTGTGTCTCTCCCTCTGACCCCTTAAGGAGCTTATTGAGGAGCTGAGCAACATC 198

QY 74 acccagaatcaggcatccctctgcaacggcagcatggtgtggagcgtaacctgaccgcc 133
Db 199 ACACAAGACCAGACTCCCTGTGCAACGGCAGCATGGTATGGAGTGTGGACCTGGCCGCT 258

QY 134 ggcattgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgccatccaa 193
Db 259 GGCGGGTTCTGTGTAGCCCTGGATTCCCTGACCAACATCTCCAATTGCAATGCCATCTAC 318

QY 194 aggaccagaggatgctgaaagcactgtgctctctcaaaagcccg 237
Db 319 AGGACCCAGAGGATATTGCATGGCCTCTGTAAACCGCAAGGCCCC 362
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Job time: 17800 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 13, 2001, 11:39:33 ; Search time 5997.24 Seconds  
(without alignments)  
396.219 Million cell updates/sec

Title: US-09-451-527-89  
Perfect score: 272  
Sequence: 1 tggccttgccctcccgagcc.....cagtgaacgcagccgagaca 272

Scoring table: IDENTITY\_NUC  
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Searched: 9623517 seqs, 4368049070 residues

Total number of hits satisfying chosen parameters: 19247034

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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84:	em_estrol3:*
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87:	em_estrol6:*
88:	em_estrol7:*
89:	em_estrol8:*
90:	em_estrol9:*
91:	em_estrol10:*
92:	em_estrol11:*
93:	em_estrol12:*
94:	em_estrol13:*
95:	em_estrol14:*
96:	em_estrol15:*
97:	em_estrol16:*
98:	em_estrol17:*
99:	em_estrol18:*
100:	em_estrol19:*
101:	em_estrol20:*
102:	gb_est25:*
103:	gb_est26:*
104:	gb_est27:*
105:	gb_est28:*
106:	gb_est29:*
107:	gb_est30:*
108:	gb_est31:*
109:	gb_est32:*
110:	gb_est41:*
111:	gb_est42:*
112:	gb_est43:*
113:	gb_est44:*
114:	gb_est45:*
115:	gb_est46:*
116:	gb_est47:*

117: gb\_est48:\*  
118: gb\_est49:\*  
119: gb\_est50:\*  
120: gb\_est51:\*  
121: gb\_est52:\*  
122: gb\_est53:\*  
123: gb\_est54:\*  
124: gb\_est55:\*  
125: gb\_est56:\*  
126: gb\_est57:\*  
127: gb\_est58:\*  
128: gb\_est59:\*  
129: gb\_est60:\*  
130: gb\_est61:\*  
131: gb\_est62:\*  
132: gb\_est63:\*  
133: gb\_est64:\*  
134: gb\_est65:\*  
135: gb\_est66:\*  
136: gb\_est75:\*  
137: gb\_est76:\*  
138: gb\_est77:\*  
139: gb\_est78:\*  
140: gb\_est79:\*  
141: gb\_est80:\*  
142: gb\_est81:\*  
143: gb\_est82:\*  
144: gb\_est83:\*  
145: gb\_est84:\*  
146: gb\_est85:\*  
147: gb\_est86:\*  
148: gb\_est87:\*  
149: gb\_est88:\*  
150: gb\_est89:\*  
151: gb\_est90:\*  
152: gb\_est99:\*  
153: gb\_est100:\*  
154: gb\_est101:\*  
155: gb\_est102:\*  
156: gb\_est103:\*  
157: gb\_est104:\*  
158: gb\_est105:\*  
159: gb\_est106:\*  
160: gb\_est67:\*  
161: gb\_est68:\*  
162: gb\_est69:\*  
163: gb\_est70:\*  
164: gb\_est71:\*  
165: gb\_est72:\*  
166: gb\_est73:\*  
167: gb\_est74:\*  
168: gb\_est91:\*  
169: gb\_est92:\*  
170: gb\_est93:\*  
171: gb\_est94:\*  
172: gb\_est95:\*  
173: gb\_est96:\*  
174: gb\_est97:\*  
175: gb\_est98:\*  
176: em\_gss\_fun:\*  
177: em\_gss\_hum1:\*  
178: em\_gss\_hum2:\*  
179: em\_gss\_hum3:\*  
180: em\_gss\_hum4:\*  
181: em\_gss\_hum5:\*  
182: em\_gss\_hum6:\*  
183: em\_gss\_hum7:\*  
184: em\_gss\_hum8:\*  
185: em\_gss\_hum9:\*  
186: em\_gss\_inv1:\*  
187: em\_gss\_inv2:\*  
188: em\_gss\_inv3:\*  
189: em\_gss\_other:\*

190: em\_gss\_pln1:\*  
191: em\_gss\_pln2:\*  
192: em\_gss\_pro:\*  
193: em\_gss\_rod1:\*  
194: em\_gss\_rod2:\*  
195: em\_gss\_rod3:\*  
196: em\_gss\_rod4:\*  
197: em\_gss\_rod5:\*  
198: em\_gss\_vrt1:\*  
199: em\_gss\_vrt2:\*  
200: em\_gss\_vrt3:\*  
201: gb\_gss1:\*  
202: gb\_gss2:\*  
203: gb\_gss3:\*  
204: gb\_gss4:\*  
205: gb\_gss5:\*  
206: gb\_gss6:\*  
207: gb\_gss7:\*  
208: gb\_gss8:\*  
209: gb\_gss9:\*  
210: gb\_gss10:\*  
211: gb\_gss11:\*  
212: gb\_gss12:\*  
213: gb\_gss13:\*  
214: gb\_gss14:\*  
215: gb\_gss15:\*  
216: gb\_gss16:\*  
217: gb\_gss17:\*  
218: gb\_gss18:\*  
219: gb\_gss19:\*  
220: gb\_gss20:\*  
221: gb\_gss21:\*  
222: gb\_gss22:\*  
223: gb\_gss23:\*  
224: gb\_gss24:\*  
225: gb\_gss25:\*  
226: gb\_gss26:\*  
227: gb\_gss27:\*  
228: gb\_gss28:\*  
229: gb\_gss29:\*  
230: gb\_gss30:\*  
231: gb\_gss31:\*  
232: gb\_gss32:\*  
233: gb\_gss33:\*  
234: gb\_gss34:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match %	Score	Length	DB	ID	Description
1	13.4	36.4	277	137	BE593226	BE593226 WS1_99_B0
2	13.4	36.4	537	166	BE357229	BE357229 DGL_147_B
3	13.2	36	462	143	BF039993	BF039993 BP250023B
C 4	13.1	35.6	537	29	AV387571	AV387571 AV387571
C 5	13.1	35.6	1070	136	BE536034	BE536034 601062471
6	13.0	35.4	498	150	BF606532	BF606532 273595 MA
7	12.8	34.8	507	138	BE705147	BE705147 SC02_08f0
8	12.7	34.6	576	141	BE907816	BE907816 601501924
C 9	12.7	34.6	965	217	AZ201624	AZ201624 SP_0053_A
10	12.6	34.4	570	24	AI746678	AI746678 ul06b05.y
11	12.6	34.2	535	161	BE032541	BE032541 131940 MA
12	12.6	34.2	546	161	BE032543	BE032543 131942 MA
13	12.5	34	341	163	BE127683	BE127683 DEPA1432
14	12.5	34	370	166	BE363650	BE363650 WS1_64_G1
15	12.5	34	562	166	BE361027	BE361027 DGL_69_A0
C 16	12.5	34	925	229	CNS0091P	AL053013 Drosophil
C 17	12.4	33.6	177	103	AI909438	AI909438 IL-BT208-
18	12.4	33.6	544	13	AA880435	AA880435 vw89f07.r



19	33.6	12.4	577	166	BE402120	BE402120 CSB004F06
20	33.6	12.4	700	113	AW318852	un08d12.y
21	33.6	12.4	712	115	AW475303	un64b04.y
22	33.6	12.4	714	166	BE414190	SCU007.C0
23	33.6	12.4	727	164	BE216356	HV_CEB001
24	33.6	12.4	891	151	BF685554	602140603
25	33.6	12.4	1016	230	CNS024F6	AL180699 Tetraodon
26	33.6	12.4	1056	144	BF143984	601791238
27	33.4	12.3	1122	141	BE889888	601512140
28	33.2	12.2	462	164	BE228410	98AS2556
29	33.2	12.2	463	24	AI712497	UI-R-AF1-
30	33.2	12.2	487	22	AI598187	tn14f06.x
31	33.2	12.2	616	15	AI062250	GH01393.5
32	33.2	12.2	621	175	C97983	C97983 C97983 Rice
33	33.2	12.2	683	15	AI064071	GH04331.5
34	33.2	12.2	712	107	AU092344	AU092344 AU092344
35	33	12.1	505	166	BE400019	AWB010.B0
36	33	12.1	546	120	AW786287	119229 MA
37	33	12.1	600	146	BF312933	601896391
38	33	12.1	902	106	AL522415	AL522415
39	33	12.1	1946	119	AW729623	GA_Ea002
40	32.8	12.1	553	106	AU075583	AU075583 AU075583
41	32.8	12.1	698	150	BF620318	HVSMEC001
42	32.6	12.0	285	6	AA360834	EST70082
43	32.6	12.0	335	6	AA361196	EST70439
44	32.6	12.0	343	106	AU064144	AU064144
45	32.6	12.0	452	158	W80370	zh50f02.s1

ALIGNMENTS

RESULT 1  
BE593226  
LOCUS  
DEFINITION W51\_99\_B03.g1\_A002 Water-stressed 1 (WS1) Sorghum bicolor cDNA, mRNA sequence.  
ACCESSION BE593226  
VERSION BE593226.1 GI:9848299  
KEYWORDS EST.  
SOURCE sorghum.  
ORGANISM Sorghum bicolor  
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Sorghum.  
REFERENCE 1 (bases 1 to 277)  
AUTHORS Cordonnier-Pratt,M.-M., Gingle,A., Marsala,C., Sudman,M. and Pratt ,L.H.  
TITLE An EST database from Sorghum: water-stressed plants  
JOURNAL Unpublished (2000)  
COMMENT Contact: Cordonnier-Pratt MM  
Department of Botany  
The University of Georgia  
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA  
Tel: 706 542 1860  
Fax: 706 542 1805  
Email: mmpratt@uga.edu  
Sequences have been trimmed to exclude PolyA, vector and regions below Phred quality 16. The threshold for highest quality sequence is 20.

Seq primer: PolyTMix  
High quality sequence start: 5  
High quality sequence stop: 246  
POLYA=No.

FEATURES  
source Location/Qualifiers  
1..277  
/organism="Sorghum bicolor"  
/db\_xref="taxon:4558"  
/clone\_lib="Water-stressed 1 (WS1)"  
/note="Organ: Mix of 5-week old plants on days 7 & 8 after water was withheld; Vector: Lambda Zap; Site\_1: XhoI; Site\_2: EcoRI; The library was made from poly-A RNA in the cloning vector lambda ZAP II. Clones to be sequenced were

BASE COUNT 47 a prepared by mass excision."  
ORIGIN 81 c 78 g 71 t  
Query Match 13.4%; Score 36.4; DB 137; Length 277;  
Best Local Similarity 53.5%; Pred. No. 6.3;  
Matches 76; Conservative 0; Mismatches 66; Indels 0; Gaps 0;  
QY 40 cctcaaggagctcattgaggagctggtcaacatcacccagaatcaggcatccctctgcaa 99  
||| ||||| | ||||| | ||||| | ||||| | ||||| | ||||| | ||||| |  
Db 22 CCCCATGGAGAGGCTCGGGAGCCCGCGGACATCGCGCGGTTCCTCTGCAC 81  
QY 100 cggcagcatggtgtgagcgtcaacacctgacccggtgctactgcgcagctctagaatc 159  
||| | | ||||| | | ||| | | ||| | ||| | ||| | ||| | ||| |  
Db 82 CGACGCCCGGAGTGGGTCAACGGCCAGGTTCATCCGCCCAACGGCGGTACGTGTGATG 141  
QY 160 tctgatcaatgtctccgactgc 181  
||||||| | ||| |||||  
Db 142 TCTGATCTTTAGTCTTACAGC 163  
RESULT 2  
BE357229 537 bp mRNA EST 20-JUL-2000  
LOCUS DGL\_147\_B02.g1\_A002 Dark Grown 1 (DGL) Sorghum bicolor cDNA, mRNA  
DEFINITION sequence.  
ACCESSION BE357229  
VERSION BE357229.1 GI:9298786  
KEYWORDS EST.  
SOURCE sorghum.  
ORGANISM Sorghum bicolor  
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Sorghum.  
REFERENCE 1 (bases 1 to 537)  
AUTHORS Cordonnier-Pratt,M.-M., Gingle,A., Marsala,C., Sudman,M. and Pratt ,L.H.  
TITLE An EST database from Sorghum: dark-grown seedlings  
JOURNAL Unpublished (2000)  
COMMENT Contact: Cordonnier-Pratt MM  
Department of Botany  
The University of Georgia  
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA  
Tel: 706 542 1860  
Fax: 706 542 1805  
Email: mmpratt@uga.edu  
Sequences have been trimmed to exclude PolyA, vector and regions below Phred quality 16. The threshold for highest quality sequence is 20.  
Seq primer: PolyTMix  
High quality sequence start: 31  
High quality sequence stop: 514  
POLYA=No.  
FEATURES Location/Qualifiers  
source 1..537  
/organism="Sorghum bicolor"  
/db\_xref="taxon:4558"  
/clone\_lib="Dark Grown 1 (DGL)"  
/note="Organ: 5-day-old dark-grown seedlings; Vector: Lambda Zap; Site\_1: XhoI; Site\_2: EcoRI; The library was made from poly-A RNA in the cloning vector lambda ZAP II. Clones to be sequenced were prepared by mass excision."  
BASE COUNT 89 a 160 c 176 g 112 t  
ORIGIN  
Query Match 13.4%; Score 36.4; DB 166; Length 537;  
Best Local Similarity 53.5%; Pred. No. 7.3;  
Matches 76; Conservative 0; Mismatches 66; Indels 0; Gaps 0;  
QY 40 cctcaaggagctcattgaggagctggtcaacatcacccagaatcaggcatccctctgcaa 99  
||| ||||| | ||||| | ||||| | ||||| | ||||| | ||||| | ||||| |













AUTHORS	Cordonnier-Pratt,M.-M., Gingle,A., Marsala,C., Sudman,M. and Pratt,L.H.
TITLE	An EST database from Sorghum: water-stressed plants
JOURNAL	Unpublished (2000)
COMMENT	Contact: Cordonnier-Pratt MM Department of Botany The University of Georgia Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA Tel: 706 542 1860 Fax: 706 542 1805 Email: mmpratt@uga.edu Sequences have been trimmed to exclude PolyA, vector and regions below Phred quality 16. The threshold for highest quality sequence is 20.

Seq primer: PolyTMix  
High quality sequence start: 32  
High quality sequence stop: 368  
POLYA=Yes.

```

FEATURES
source
Location/Qualifiers
1. 370
/organism="Sorghum bicolor"
/db_xref="taxon:4558"
/clone_lib="Water-stressed 1 (WS1)"
/note="Organ: Mix of 5-week old plants on days 7 & 8 after
water was withheld; Vector: Lambda Zap; Site_1: XhoI;
Site_2: EcoRI; The library was made from poly-A RNA in the
cloning vector lambda Zap II. Clones to be sequenced were
prepared by mass excision."
76 a 110 c 130 g 54 t
BASE COUNT
ORIGIN

```

Query Match	12.5%;	Score 34;	DB 166;	Length 370;
Best Local Similarity	56.1%;	Pred. No. 31;		
Matches 64;	Conservative	0;	Mismatches 50;	Indels 0;
				Gaps 0;

QY	29	ccctccccaacccctcaaggagctcattgaggagctggtcaacatcacccagaatcaggca	88
Db	54	CCCTTCGGCGAGTCAAGGACGTCAAGACGCCGCTGGACCACTCCACGACGAAGCACCGC	113
QY	89	tcctctctgcaaggcagcatgggtgtggagcgtcaacctgacccgcggcatgtac	142
db	114	TCCTTCGGCTTCGTCACTTCCTTGAGCGCGAGGACGCCGCCGCTGCCATGGAC	167

RESULT	15			
BE361027				
LOCUS		562 bp	mRNA	EST
DEFINITION		DG1_69_A02.bl_A002	Dark Grown 1	(DG1) Sorghum bicolor cDNA, mRNA
				sequence.
ACCESSION		BE361027		
VERSION		BE361027.1	GI:9302584	
KEYWORDS		EST.		
SOURCE		sorghum.		
ORGANISM		Sorghum bicolor		
		Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;		
		Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae		
		; Andropogoneae; Sorghum.		
REFERENCE		1	(bases 1 to 562)	

**TITLE** An EST database from Sorghum: dark-grown seedlings  
**JOURNAL** Unpublished (2000)  
**COMMENT** Contact: Cordonnier-Pratt MM  
Department of Botany  
The University of Georgia  
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA  
Tel: 706 542 1860  
Fax: 706 542 1805  
Email: mmpratt@uga.edu  
Sequences have been trimmed to exclude PolyA, vector and regions  
below Phred quality 16. The threshold for highest quality sequence  
is 20.

```

Seq primer: JEN REV
High quality sequence stop: 560
POLYA=NO.

FEATURES
    source
        Location/Qualifiers
            1..562
                /organism="Sorghum bicolor"
                /db_xref="taxon:4558"
                /clone_lib="Dark Grown 1 (DGl)"
                /note="Organ: 5-day-old dark-grown seedlings; Vector:
                Lambda Zap; Site_1: XhoI; Site_2: EcoRI; The library was
                made from poly-A RNA in the cloning vector lambda ZAP II.
                Clones to be sequenced were prepared by mass excision."
            130 a      174 c      187 g      71 t

BASE COUNT
ORIGIN

```

	Query Match	12.5%;	Score 34;	DB 166;	Length 562;
	Best Local Similarity	56.1%;	Pred. NO. 34;		
	Matches 64; Conservative	0;	Mismatches 50;	Indels 0;	Gaps 0;
QY	29 cccctccccaccctcaaggagcgtcattgaggcggtgaacatcaccccagaatacaggcca 	88			
Dd	171 CCCTTCGGCGAGGTTCAAGGACGTCAAGACGCCGTGGACCAGTCCACGCAGAAGCACCGC	230			
QY	89 tcaccttgacaacgggcagcatgggtgtgagcgtcaaacctgacccgccggcatgtac 	142			
Dd	231 TCCTTCGGCTTCGTCAACCTTCCTTGAGCGCGAAGACGCCGCCGTGCCATGGAC	284			

Search completed: May 13, 2001, 11:39:46  
Job time: 16461 sec





GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 13, 2001, 14:16:09 ; Search time 9342.78 Seconds  
(without alignments)  
438.831 Million cell updates/sec

Title: US-09-451-527-90  
Perfect score: 278  
Sequence: 1 atggcgctctgtgtgactgt.....gcactgtgctctcaaaagcc 278

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1283235 seqs, 7373929652 residues

Total number of hits satisfying chosen parameters: 2566470

Minimum DB seq length: 0  
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:\*  
1: gb\_bal:\*  
2: gb\_ba2:\*  
3: gb\_ba3:\*  
4: gb\_in1:\*  
5: gb\_in2:\*  
6: gb\_in3:\*  
7: gb\_om:\*  
8: gb\_ov:\*  
9: gb\_pat1:\*  
10: gb\_pat2:\*  
11: gb\_ph:\*  
12: gb\_pl1:\*  
13: gb\_pl2:\*  
14: gb\_pl3:\*  
15: gb\_pl4:\*  
16: em\_bal:\*  
17: em\_ba2:\*  
18: em\_fun:\*  
19: em\_htgo\_hum:\*  
20: em\_htgo\_inv:\*  
21: em\_htgo\_rod:\*  
22: em\_htg\_hum1:\*  
23: em\_htg\_hum2:\*  
24: em\_htg\_hum3:\*  
25: em\_htg\_hum4:\*  
26: em\_htg\_hum5:\*  
27: em\_htg\_hum6:\*  
28: em\_htg\_hum7:\*  
29: em\_htg\_hum8:\*  
30: em\_htg\_inv1:\*  
31: em\_htg\_inv2:\*  
32: em\_htg\_other:\*  
33: em\_htg\_rod:\*  
34: em\_hum1:\*  
35: em\_hum2:\*  
36: em\_hum3:\*  
37: em\_hum4:\*  
38: em\_hum5:\*  
39: em\_hum6:\*  
40: em\_hum7:\*  
41: em\_in:\*  
42: em\_om:\*  
43: em\_or:\*

44: em\_ov:\*  
45: em\_pat:\*  
46: em\_ph:\*  
47: em\_pl:\*  
48: em\_ro:\*  
49: em\_sts:\*  
50: em\_sy:\*  
51: em\_un:\*  
52: em\_vi:\*  
53: gb\_sts1:\*  
54: gb\_sts2:\*  
55: gb\_sts3:\*  
56: gb\_sy:\*  
57: gb\_un:\*  
58: gb\_vil:\*  
59: gb\_vil2:\*  
60: gb\_htg1:\*  
61: gb\_htg2:\*  
62: gb\_htg3:\*  
63: gb\_htg4:\*  
64: gb\_htg5:\*  
65: gb\_htg6:\*  
66: gb\_htg7:\*  
67: gb\_htg8:\*  
68: gb\_htg9:\*  
69: gb\_htg10:\*  
70: gb\_htg11:\*  
71: gb\_htg12:\*  
72: gb\_htg13:\*  
73: gb\_htg14:\*  
74: gb\_htg15:\*  
75: gb\_htg16:\*  
76: gb\_htg17:\*  
77: gb\_htg18:\*  
78: gb\_htg19:\*  
79: gb\_htg20:\*  
80: gb\_htg21:\*  
81: gb\_htg22:\*  
82: gb\_htg23:\*  
83: gb\_htg24:\*  
84: gb\_htg25:\*  
85: gb\_prl:\*  
86: gb\_pr2:\*  
87: gb\_pr3:\*  
88: gb\_pr4:\*  
89: gb\_pr5:\*  
90: gb\_pr6:\*  
91: gb\_pr7:\*  
92: gb\_pr8:\*  
93: gb\_pr9:\*  
94: gb\_rol:\*  
95: gb\_ro2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	278	100.0	1302	7	AF244915
2	191	68.7	1270	93	AF244915 Canis fam
3	191	68.7	1282	92	L06801 Homo sapien
4	191	68.7	1290	10	X69079 H.sapiens i
5	189.4	68.1	417	88	I34548 Sequence 1
6	189.4	68.1	1297	9	AF043334 Homo sapi
7	189.4	68.1	1297	10	A29948 Coding sequ
8	183.4	66.0	343	7	I58488 Sequence 15
9	148.2	53.3	384	9	AF072807 Bos tauru
10	148.2	53.3	384	10	A29950 Nucleic aci
11	147.6	53.1	336	9	I58489 Sequence 17
					A29931 Sequence co

12	147.6	53.1	336	10	I58494	I58494 Sequence 24
13	146.4	52.7	425	9	AR027065	AR027065 Sequence
14	146.4	52.7	425	10	I86198	I86198 Sequence 4
15	146.4	52.7	4410	9	A52326	A52326 Sequence 1
16	146.4	52.7	4410	9	AR027062	AR027062 Sequence
17	146.4	52.7	4410	10	I86195	I86195 Sequence 1
18	146	52.5	336	9	A29930	A29930 Sequence co
19	146	52.5	336	10	I58481	I58481 Sequence 2
20	142.4	51.2	447	10	I58495	I58495 Sequence 26
21	142.4	51.2	1207	94	MUSSTCPE	M23504 Mus musculus
22	142.4	51.2	1212	10	I34549	I34549 Sequence 3
23	135.8	48.8	443	94	RATIL13A	L26913 Rattus Norv
C 24	130.8	47.1	213343	78	AF276990	AF276990 Canis fam
C 25	101.8	36.6	3714	93	HUM11DC99Z	L42080 Homo sapien
26	101.8	36.6	4600	93	HUM1113B	L13029 Human inter
27	101.8	36.6	4740	93	HSU10307	U10307 Human inter
28	101.8	36.6	5670	93	HSU31120	U31120 Human inter
C 29	101.8	36.6	50282	85	AC004039	AC004039 Homo sapi
30	101.8	36.6	78469	75	AC074127	AC074127 Homo sapi
C 31	101.8	36.6	78469	75	AC074127	AC074127 Homo sapi
32	92.2	33.2	3520	7	BTA132441	AJ132441 Bos tauru
C 33	66.6	24.0	3395	93	HUM11DC98Z	L42079 Homo sapien
34	61.6	22.2	4376	94	MUS1113A	L13028 Mouse inter
C 35	61.6	22.2	142732	88	AC084392	AC084392 Homo sapi
C 36	61.6	22.2	159500	94	AC005742	AC005742 Mus muscu
37	61.6	22.2	237823	66	AC020886	AC020886 Mus muscu
38	44.6	16.0	60	9	A29941	A29941 Oligonucleo
39	44.6	16.0	60	10	I58485	I58485 Sequence 12
40	44.6	16.0	102	9	A29939	A29939 Sequence co
41	44.6	16.0	102	10	I58483	I58483 Sequence 10
42	40.8	14.7	1008	94	RATNACHRR5	M33952 Rat neurona
43	40.8	14.7	2461	95	RNU42976	U42976 Rattus norv
C 44	40.8	14.7	38390	3	SC2H12	AL359215 Streptomy
45	39.6	14.2	54	9	A29940	A29940 Sequence co

ALIGNMENTS

RESULT	1
AF244915	
LOCUS	AF244915 1302 bp mRNA MAM 16-OCT-2000
DEFINITION	Canis familiaris interleukin-13 mRNA, complete cds.
ACCESSION	AF244915
VERSION	AF244915.1 GI:7528273
KEYWORDS	dog.
SOURCE	Canis familiaris
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE	1 (bases 1 to 1302)
AUTHORS	Yang,S., Boroughs,K.L. and McDermott,M.J.
TITLE	Canine interleukin-13: molecular cloning of full-length cDNA and expression of biologically active recombinant protein
JOURNAL	J. Interferon Cytokine Res. 20 (9), 779-785 (2000)
MEDLINE	20485146
PUBMED	11032397
FEATURES	2 (bases 1 to 1302)
AUTHORS	Yang,S.
TITLE	Direct Submission
JOURNAL	Submitted (13-MAR-2000) Allergy and Immunology, Heska Corporation, 1613 Prospect Parkway, Fort Collins, CO 80525, USA
polyA_site	1270
BASE COUNT	288 a 335 c 336 g 311 t
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source	1. .1302
/organism="Canis familiaris"	
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1. .51	
52. .447	
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/protein_id="AAF63204.1"	
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ORIGIN					
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Best Local Similarity	100.0%;	Pred. No. 6.4e-57;			
Matches 278;	Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	atggcgctctgttgactgtggtcattgtctcattgcctcacctgcctcggtggtgccttgccctccccg	60		
Db	52	ATGGCGCTCTGTTGACTGTGGTCAATTGCTCTCACCTGCCTCGGTGGCCTTGCCCTCCCG	111		
QY	61	agccctgtgactccctcccccacccctcaaggagctcattgaggagctggtcaacatcacc	120		
Db	112	AGCCCTGTGACTCCCTCCCCAACCCCTCAAGGAGCTCATTGAGGAGCTGGTCAACATCACC	171		
QY	121	cagaatcaggcatccctctgcacgcgcagcatggtgtggagcgtcaacctgaccgcggc	180		
Db	172	CAGAATCAGGCATCCCTCTGCAACGGCAGCATGGTGTGGAGCGTCAACCTGACCGCCCGGC	231		
QY	181	atgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgccatccaaagg	240		
Db	232	ATGTACTGGCAGCTCTAGAATCTCTGATCAATGTCTCCGACTGCAGCGCCATCCAAAGG	291		
QY	241	accagaggatgctgaaagcactgtgctctcaaaagcc	278		
Db	292	ACCCAGAGGATGCTGAAAGCACTGTGCTCTCAAAAGCC	329		
RESULT	2				
HUMIL13A					
LOCUS	HUMIL13A	1270 bp	mRNA	PRI	22-JUL-1993
DEFINITION	Homo sapiens interleukin 13 mRNA, complete cds.				
ACCESSION	L06801				
VERSION	L06801.1 GI:186275				
KEYWORDS	cytokine; growth factor; interleukin 13; regulatory protein.				
SOURCE	Homo sapiens cDNA to mRNA.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	1 (bases 1 to 1270) McKenzie,A.N.J., Culpepper,J.A., de Waal Malefyt,R., Briere,F., Punnonen,J., Aversa,G., Sato,A., Dang,W., Cocks,B.G., Menon,S., de Vries,J.E., Banchereau,J. and Zurawski,G.R.				
TITLE	Interleukin-13, a T cell-derived cytokine that regulates human monocyte and B cell function				
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 90, 3735-3739 (1993)				
MEDLINE	93234572				
FEATURES	Location/Qualifiers				
source	1. .1270 /organism="Homo sapiens" /db_xref="taxon:9606" 45. .443 /codon_start=1 /product="interleukin 13" /protein_id="AAA36107.1" /db_xref="GI:186275" /translation="MALLLTIVIALTCLGGFASPGVPVPVPPVADRELIEELVNITQNK APLNGSMVWSINLTAGMYCAALESLINVSGCSAIEKTMRLSGFCPHKVSAGQFSL HVRDTKIEVAQFVKDLLLHLKLLFREGFRN"				
polyA_site	1270				
BASE COUNT	288 a	335 c	336 g	311 t	
ORIGIN					
Query Match	68.7%;	Score 191;	DB 93;	Length 1270;	
Best Local Similarity	82.8%;	Pred. No. 4.7e-36;			
Matches 231;	Conservative	0;	Mismatches 45;	Indels 3;	Gaps 1;
QY	1	atggcgctctgttgactgtggtcattgtctcattgcctcacctgcctcggtggtgccttgccctccccg	60		

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45 ATGGCGCTTTGTTGACACCGTCAATTGCTCTCACTTGCCTTGGCGGCTTGCCTCCCCA 104
QY 61 agccctgtgactccctcccaaccctcaaggagctcattgaggagctggtcaacatcacc 120
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Db 105 GGCCCTGTGCCTCCCTACAGCCCTCAGGAGCTCATTTGAGAGCTGGTCAACATCACC 164
QY 121 cagaatc---aggcatccctctgcaacgycagcatggtgtgagctcaacctgaccgcc 177
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Db 165 CAGAACACAGAGGCTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAACCTGACAGCT 224
QY 178 ggcattgactgcgcagctctagaatctctgatcaatgtctcgactgcagcccatccaa 237
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Db 225 GGCATGTACTGTGCAGCCCTGGAATCCCTGATCAACGTGTGAGGCTGCAGTGCCATCGAG 284
QY 238 aggaccagaggtgctgaaagcactgtgctctcaaaaag 276
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Db 285 AAGACCCAGAGGATGCTGACCGGATTCTGCCCGCACAAAG 323
RESULT 3
HSNC30 1282 bp mRNA PRI 17-FEB-1997
LOCUS H.sapiens interleukin-13 mRNA.
DEFINITION H.sapiens interleukin-13 mRNA.
ACCESSION X69079
VERSION X69079.1 GI:297787
KEYWORDS lymphokine.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1282)
AUTHORS Minty,A.J.
TITLE Direct Submission
JOURNAL Submitted (02-NOV-1992) A.J. Minty, Sanofi-Elf Bio Recherches,
Labège Innopole, Voie 1, BP 137, 31676 Labège Cedex, FRANCE
REFERENCE 2 (bases 1 to 1282)
AUTHORS Minty,A.J., Chalon,P., Derocq,J.M., Dumont,X., Guillemot,J.C.,
Kaghad,M., Labit,C., Leplatois,P., Liauzun,P., Miloux,B., Minty,C.,
Casellas,P., Loison,G., Lupker,J., Shire,D., Ferrara,P. and
Caput,D.
TITLE Interleukin-13 is a new human lymphokine regulating inflammatory
and immune responses
JOURNAL Nature 362 (6417), 248-250 (1993)
MEDLINE 93211479
FEATURES
source Location/Qualifiers
1. .1282
/organism="Homo sapiens"
/db\_xref="taxon:9606"
/chromosome="5q 23-31"
/cell\_type="peripheral blood lymphocytes"
15. .455
/gene="NC30"
15. .116
/gene="NC30"
/product="NC30; alternative"
15. .455
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/evidence=experimental
/protein\_id="CAA48823.1"
/db\_xref="GI:580330"
/db\_xref="SWISS-PROT:P35225"
/translation="MHPLNPLLLALGLMALLTVTIALTCLGGFASPGVPVPPSTALR
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57. .455
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/codon\_start=1

/evidence=experimental
/protein\_id="CAA48824.1"
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APLCNGSMVWSINLTAGMYCAALESLINVSGCSAIEKQRMLSGFCPHKVSAGQFSSL
HVRDTKIEVAQFVKDLLLHLKLFREGFN"
57. .116
/gene="NC30"
/product="NC30; alternative"
117. .452
/gene="NC30"
/evidence=experimental
238
/gene="NC30"
/replace="a"
856. .860
/note="ATTTA motif"
873. .877
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1264. .1269
polyA\_signal 293 a 341 c 337 g 311 t
BASE COUNT 293 a 341 c 337 g 311 t
ORIGIN
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Best Local Similarity 82.8%; Pred. No. 4.7e-36;
Matches 231; Conservative 0; Mismatches 45; Indels 3; Gaps 1;
QY 1 atggcgctctggtgactgtggtcattgctctcacctgcctcggtggtgcctccccc 60
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Db 57 ATGGCGCTTTGTTGACACCGTCAATTGCTCTCACTTGCCTTGGCGGCTTGCCTCCCCA 116
QY 61 agccctgtgactccctcccaaccctcaaggagctcattgaggagctggtcaacatcacc 120
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Db 117 GGCCCTGTGCCTCCCTCTACAGCCCTCAGGGAGCTCATTTGAGGAGCTGGTCAACATCACC 176
QY 121 cagaatc---aggcatccctctgcaacgycagcatggtgtgagctcaacctgaccgcc 177
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Db 177 CAGAACACAGAGGCTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAACCTGACAGCT 236
QY 178 ggcattgactgcgcagctctagaatctctgatcaatgtctcgactgcagcccatccaa 237
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Db 237 GGCATGTACTGTGCAGCCCTGGAATCCCTGATCAACGTGTGAGGCTGCAGTGCCATCGAG 296
QY 238 aggaccagaggtgctgaaagcactgtgctctcaaaaag 276
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Db 297 AAGACCCAGAGGATGCTGACCGGATTCTGCCCGCACAAAG 335
RESULT 4
I34548 1290 bp DNA PAT 06-FEB-1997
LOCUS I34548
DEFINITION Sequence 1 from patent US 5596072.
ACCESSION I34548
VERSION I34548.1 GI:1825339
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1290)
AUTHORS Culpepper,J., McKenzie,A., Dang,W. and Zurawski,G.
TITLE Method of refolding human IL-13
JOURNAL Patent: US 5596072-A 1 21-JAN-1997;
FEATURES Location/Qualifiers
1. .1290
/organism="unknown"
BASE COUNT 308 a 335 c 336 g 311 t
ORIGIN





QY	1	atggcgctctggtgactgtggtcattgtctctcacctgcctcggtggtgccttgccctccccg	60
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QY	61	agccctgtgactccctcccaaccctcaaggagctcattgaggctggtcaacatcacc	120
Db	117	GGCCCTGTGCCCTCCCTCTACAGCCCTCAGGGAGCTCATTTAGGAGCTGGTCAACATCACC	176
QY	121	cagaatc---aggcatccctctgcaacggcagcatggtgtggagctcaacctgaccgcc	177
Db	177	CAGAACCAGAAGGCTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAACCTGACAGCT	236
QY	178	ggcatgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgccatccaa	237
Db	237	GACATGTACTGTGCAGCCCTTGAATCCCTGATCAACGTGTCAAGCTGCAGTGCCTCGAG	296
QY	238	aggaccagaggtctgaaagcactgtgtctctcaaaa	276
Db	297	AAGACCCAGAGGATGCTGAGCGGATTCTGCCCGCACAA	335
RESULT	7		
LOCUS	I58488	1297 bp	DNA
DEFINITION	Sequence 15 from patent US 5652123.	PAT	07-OCT-1997
ACCESSION	I58488		
VERSION	I58488.1	GI:2477726	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 1297)		
AUTHORS	Caput,D., Ferrara,P., Guillemot,J., Kaghad,M., Labit-Le Bouteiller,C., Leplatols,P., Magazin,M. and Minty,A.		
TITLE	Protein having interleukin 13 activity, recombinant DNA coding for this protein, transformed cells and microorganisms		
JOURNAL	Patent: US 5652123-A 15 29-JUL-1997;		
FEATURES	Location/Qualifiers		
Source	1..1297		
BASE COUNT	309 a 341 c 336 g 311 t		
ORIGIN	/organism="unknown"		
Query Match	68.1%;	Score 189.4;	DB 10; Length 1297;
Best Local Similarity	82.4%;	Pred. No. 1.1e-35;	
Matches	230; Conservative	0; Mismatches 46;	Indels 3; Gaps 1;
QY	1	atggcgctctggtgactgtggtcattgtctctcacctgcctcggtggtgccttgccctccccg	60
Db	57	ATGGCGCTTTTGTGACCAACGGTCATTGCTCTCACTTGCCCTTGGCGGCTTTGCCTCCCCA	116
QY	61	agccctgtgactccctcccaaccctcaaggagctcattgaggctggtcaacatcacc	120
Db	117	GGCCCTGTGCCCTCCCTCTACAGCCCTCAGGGAGCTCATTTAGGAGCTGGTCAACATCACC	176
QY	121	cagaatc---aggcatccctctgcaacggcagcatggtgtggagctcaacctgaccgcc	177
Db	177	CAGAACCAGAAGGCTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAACCTGACAGCT	236
QY	178	ggcatgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgccatccaa	237
Db	237	GACATGTACTGTGCAGCCCTTGAATCCCTGATCAACGTGTCAAGCTGCAGTGCCTCGAG	296
QY	238	aggaccagaggtctgaaagcactgtgtctctcaaaa	276
Db	297	AAGACCCAGAGGATGCTGAGCGGATTCTGCCCGCACAA	335
RESULT	8		
AF072807			
LOCUS	AF072807	343 bp	mRNA
DEFINITION	Bos taurus interleukin-13 precursor (IL-13) mRNA, partial cds.	MAM	21-JAN-2000

ACCESSION	AF072807		
VERSION	AF072807.1	GI:4558813	
KEYWORDS			
SOURCE	cow.		
ORGANISM	Bos taurus		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos.		
REFERENCE	1 (bases 1 to 343)		
AUTHORS	Trigona,W.L., Brown,W.C. and Estes,D.M.		
TITLE	Functional implications for signaling via the IL4R/IL13R complex on bovine cells		
JOURNAL	Vet. Immunol. Immunopathol. 72 (1-2), 73-79 (1999)		
MEDLINE	20080132		
PUBMED	10614495		
REFERENCE	2 (bases 1 to 343)		
AUTHORS	Trigona,W.T., Hirano,A. and Estes,D.M.		
TITLE	Direct Submission		
JOURNAL	Submitted (16-JUN-1998) Veterinary Pathobiology, University of Missouri-Columbia, W213 Veterinary Medicine Building, Columbia, MO 65211, USA		
FEATURES	Location/Qualifiers		
Source	1..343		
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gene	1..>343		
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	/protein_id="AAD22748.1"		
	/db_xref="GI:4558814"		
	/translation="MALLLTAVIVLICFGLTSPSPVPSATALKELIELVNTQNQK VPLCNGSMVWSLNLTSSTMYCAALDSLISNCSVIQRTKRLNALCPHKPSAKQVSSE YVRDTKIEVAQF"		
BASE COUNT	78 a 101 c 85 g 79 t		
ORIGIN			
Query Match	66.0%;	Score 183.4;	DB 7; Length 343;
Best Local Similarity	80.8%;	Pred. No. 3.8e-34;	
Matches	227; Conservative	0; Mismatches 51;	Indels 3; Gaps 1;
QY	1	atggcgctctggtgactgtggtcattgtctctcacctgcctcggtggtgccttgccctccccg	60
Db	1	ATGGCGCTCTTATTGACCGCGGTCAATTGTTCTTATCTGCTTGGTGGCCTCACCTCCCCA	60
QY	61	agccctgtgactccctcccaaccctcaaggagctcattgaggctggtcaacatcacc	120
Db	61	AGCCCTGTGCCCTTCTGCTACAGCCCTCAAGGAGCTCATTTAGAGAGCTGTTAATATCACC	120
QY	121	cagaatc---aggcatccctctgcaacggcagcatggtgtggagctcaacctgaccgcc	177
Db	121	CAGAACCAAGAGGTGCCGCTGTGCAATGGCAGCATGGTGTGGAGCCTCAACCTGACGAGC	180
QY	178	ggcatgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgccatccaa	237
Db	181	AGCATGTACTGTGCAGCCCTGGACTCCCTGATCAGCATCTCCAACCTGCAGTGTATCATA	240
QY	238	aggaccagaggtctgaaagcactgtgtctctcaaaa	278
Db	241	AGGACCAAGAGGATGCTGAATGCACCTCTGTCTCCTCACAGCC	281
RESULT	9		
A29950			
LOCUS	A29950	384 bp	DNA
DEFINITION	Nucleic acid fragment B.	PAT	23-JUN-1995
ACCESSION	A29950		
VERSION	A29950.1	GI:1249030	
KEYWORDS			

SOURCE synthetic construct.  
ORGANISM synthetic construct  
REFERENCE 1 (bases 1 to 384)  
AUTHORS Caput,D., Ferrara,P., Guillemot,J.C., Kaghad,M., Labit-le Bouteiller,C., Leplatois,P., Magazin,M. and Minty,A.  
TITLE Protein having cytokin type activity, recombinant DNA coding for this protein, transformed cells and microorganisms  
JOURNAL Patent: EP 0506574-A 23 30-SEP-1992;  
ELF SANOFI

FEATURES  
source Location/Qualifiers  
1..384  
/organism="synthetic construct"  
/db\_xref="taxon:32630"

BASE COUNT 97 a 104 c 99 g 84 t  
ORIGIN

Query Match 53.3%; Score 148.2; DB 9; Length 384;  
Best Local Similarity 81.8%; Pred. No. 1e-25;  
Matches 184; Conservative 0; Mismatches 38; Indels 3; Gaps 1;

QY 55 tccccgagccctgtgactccctcccccacccctcaaggagctcattgaggagctggtcaac 114  
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Db 16 TCCCCAGGCCCTGTGCCTCCCTCTACGGCCCTCAGGGAGCTCATTTGAGGAGCTGGTCAAC 75  
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QY 115 atcaccagaatc---aggcatccctctgcaacggcagcatgggtgtggagcgtcaacctg 171  
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Db 76 ATCACCAGAACCCAGAGAGGCTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAACCTG 135  
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QY 172 accgcggcatgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgcc 231  
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Db 136 ACAGCTGACATGTACTGTGCAGCCCTGGAATCCCTGATCAACGTTGTCAGGCTGCAGTGCC 195  
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QY 232 atccaaaggagccagaggatgctgaaagcactgtgctctcaaaaag 276  
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Query Match 53.3%; Score 148.2; DB 10; Length 384;  
Best Local Similarity 81.8%; Pred. No. 1e-25;  
Matches 184; Conservative 0; Mismatches 38; Indels 3; Gaps 1;

QY 55 tccccgagccctgtgactccctcccccacccctcaaggagctcattgaggagctggtcaac 114  
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Db 16 TCCCCAGGCCCTGTGCCTCCCTCTACGGCCCTCAGGGAGCTCATTTGAGGAGCTGGTCAAC 75  
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QY 115 atcaccagaatc---aggcatccctctgcaacggcagcatgggtgtggagcgtcaacctg 171  
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Db 76 ATCACCAGAACCCAGAGAGGCTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAACCTG 135  
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Query Match 53.1%; Score 147.6; DB 9; Length 336;  
Best Local Similarity 83.0%; Pred. No. 1.5e-25;  
Matches 181; Conservative 0; Mismatches 34; Indels 3; Gaps 1;

QY 62 gccctgtgactccctcccccacccctcaaggagctcattgaggagctggtcaacatcaccc 121  
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Db 2 GCCCTGTGCCTCCCTCTACAGCCCTCAGGGAGCTCATTTGAGGAGCTGGTCAACATCACCC 61  
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QY 122 agaatc---aggcatccctctgcaacggcagcatgggtgtggagcgtcaacctgaccgccc 178  
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Db 62 AGAACCAGAGAGGCTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAACCTGACAGCTG 121  
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Db 122 GCATGTACTGTGCAGCCCTGGAATCCCTGATCAACGTTGTCAGGCTGCAGTGCCATCGAGA 181  
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RESULT 12  
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DEFINITION Sequence 24 from patent US 5652123.  
ACCESSION I58494  
VERSION I58494.1 GI:2477732  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 336)  
AUTHORS Caput,D., Ferrara,P., Guillemot,J., Kaghad,M., Labit-Le Bouteiller,C., Leplatois,P., Magazin,M. and Minty,A.  
TITLE Protein having interleukin 13 activity, recombinant DNA coding for this protein, transformed cells and microorganisms  
JOURNAL Patent: US 5652123-A 24 29-JUL-1997;  
FEATURES Location/Qualifiers

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RESULT 11  
A29931  
LOCUS A29931 336 bp DNA PAT 23-JUN-1995  
DEFINITION Sequence coding for the mature cytokine like protein.  
ACCESSION A29931  
VERSION A29931.1 GI:1249019  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct  
REFERENCE 1 (bases 1 to 336)  
AUTHORS Caput,D., Ferrara,P., Guillemot,J.C., Kaghad,M., Labit-le Bouteiller,C., Leplatois,P., Magazin,M. and Minty,A.  
TITLE Protein having cytokin type activity, recombinant DNA coding for this protein, transformed cells and microorganisms  
JOURNAL Patent: EP 0506574-A 3 30-SEP-1992;  
ELF SANOFI

FEATURES  
source Location/Qualifiers  
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BASE COUNT 80 a 95 c 90 g 71 t  
ORIGIN

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Best Local Similarity 83.0%; Pred. No. 1.5e-25;  
Matches 181; Conservative 0; Mismatches 34; Indels 3; Gaps 1;

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QY 239 ggaccagagagatgctgaaagcactgtgctctcaaaaag 276  
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Db 182 AGACCCAGAGGATGCTGAGCGGATTTCTGCCCGCACAAAG 219  
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RESULT 12  
I58494  
LOCUS I58494 336 bp DNA PAT 07-OCT-1997  
DEFINITION Sequence 24 from patent US 5652123.  
ACCESSION I58494  
VERSION I58494.1 GI:2477732  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 336)  
AUTHORS Caput,D., Ferrara,P., Guillemot,J., Kaghad,M., Labit-Le Bouteiller,C., Leplatois,P., Magazin,M. and Minty,A.  
TITLE Protein having interleukin 13 activity, recombinant DNA coding for this protein, transformed cells and microorganisms  
JOURNAL Patent: US 5652123-A 24 29-JUL-1997;  
FEATURES Location/Qualifiers

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source      1. .336
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Query Match      53.1%; Score 147.6; DB 10; Length 336;
Best Local Similarity 83.0%; Pred. No. 1.5e-25;
Matches 181; Conservative 0; Mismatches 34; Indels 3; Gaps 1;

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QY 179 gcatgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgccatccaaa 238
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QY 239 ggaccagaggatgctgaaagcactgtgctctcaaaaag 276
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Db 182 AGACCCAGAGGATGCTGAGCGGGATTCTGCCCGGCACAAG 219

RESULT 13
AR027065
LOCUS      AR027065      425 bp      DNA      PAT      29-SEP-1999
DEFINITION      Sequence 4 from patent US 5856142.
ACCESSION      AR027065
VERSION      AR027065.1 GI:5937905
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unknown.
REFERENCE      1 (bases 1 to 425)
AUTHORS      Legoux,R., Maldonado,P. and Salome,M.
TITLE      Method for the extraction of periplasmic proteins from prokaryotic
            microorganisms in the presence of arginine
JOURNAL      Patent: US 5856142-A 4 05-JAN-1999;
FEATURES      Location/Qualifiers
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Matches 184; Conservative 0; Mismatches 41; Indels 3; Gaps 1;

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QY 112 aacatcacccagaatc---aggcatccctctgcaacggcgagcatggtgtggagcgtcaac 168
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QY 169 ctgaccgcgcgcatgtactgcgactctagaatctctgatcaatgtctccgactgcagc 228
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QY 229 gccatccaaaggaccagaggtgctgaaagcactgtgctctcaaaaag 276
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Db 235 GCCATCGAGAAGACCCAGAGGATGCTGAGCGGATTCTGCCCGGCACAAG 282

RESULT 14
I86198
LOCUS      I86198      425 bp      DNA      PAT      10-JUN-1998
DEFINITION      Sequence 4 from patent US 5700665.
ACCESSION      I86198
VERSION      I86198.1 GI:3205916
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unknown.
REFERENCE      1 (bases 1 to 425)
AUTHORS      Legoux,R., Maldonado,P. and Salome,M.
TITLE      Method for the extraction of periplasmic proteins from prokaryotic
            microorganisms in the presence of arginine
JOURNAL      Patent: US 5700665-A 4 23-DEC-1997;
FEATURES      Location/Qualifiers
source      1. .425
            /organism="unknown"
BASE COUNT      100 a      116 c      110 g      99 t
ORIGIN

Query Match      52.7%; Score 146.4; DB 10; Length 425;
Best Local Similarity 80.7%; Pred. No. 2.8e-25;
Matches 184; Conservative 0; Mismatches 41; Indels 3; Gaps 1;

QY 52 gccctcccgagccctgtgactccctcccaacccctcaaggagctcattgaggagctggtc 111
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QY 112 aacatcacccagaatc---aggcatccctctgcaacggcgagcatggtgtggagcgtcaac 168
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Db 235 GCCATCGAGAAGACCCAGAGGATGCTGAGCGGATTCTGCCCGGCACAAG 282

RESULT 15
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DEFINITION      Sequence 1 from Patent EP0725140.
ACCESSION      A52326
VERSION      A52326.1 GI:2851987
KEYWORDS
SOURCE      unidentified.
ORGANISM      unidentified.
REFERENCE      1 (bases 1 to 4410)
AUTHORS      Legoux,R., Maldonado,P. and Salome,M.
TITLE      Process of extraction of periplasmic proteins from prokaryotic
            microorganisms in the presence of arginine
JOURNAL      Patent: EP 0725140-A 1 07-AUG-1996;
COMMENT      SANOFI SA (FR)
            Other publication SK 10696 960904
            Other publication CZ 9600290 960814
            Other publication JP 8242879 960924
            Other publication FI 960427 960801
            Other publication PL 312543 960805
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763. .812
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Matches 184; Conservative 0; Mismatches 41; Indels 3; Gaps 1;

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Db 392 GCCTTCGCTGGCCCTGTGCTCCAGTACTGCCCTCAGGGAGCTCATTGAGGAGCTGGTC 451

Qy 112 aacatcacccagaaac---aggcatccctctgcaacgggcagcatggtgtggagcgtaaac 168
Db 452 AACATCACCCAGAACCAAGAGGCTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAAC 511

Qy 169 ctgaccgcccggcactgtactgcgcagctctagaatctctgatcaatgtctccgactgcagc 228
Db 512 CTGACAGCTGGCATGTACTGTGCAGCCCTGGAATCCCTGATCAACGTGTCAGGCTGCAGT 571

Qy 229 gccatccaaaaggacccagagatgctgaaagcaactgtgctctcaaaaag 276
Db 572 GCCATCGAGAGAGACCCAGAGGATGCTGAGCGGATTCTGCCCGCACAAAG 619
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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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Perfect score: 278  
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Scoring table: IDENTITY\_NUC  
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Searched: 678276 seqs, 291890651 residues

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SUMMARIES

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	36	37.2	13.4	66	20	232227	Human interleukin
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ALIGNMENTS

RESULT 1

Z55554

ID Z55554 standard; cDNA; 278 BP.

XX

AC Z55554;

XX

DT 14-MAR-2000 (first entry)

XX

DE Canine interleukin-13 (IL-13) cDNA probe.

XX

KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;

KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.

XX

OS Canis familiaris.

XX

PN WO9961618-A2.

XX

PD 02-DEC-1999.

XX

PF 28-MAY-1999; 99WO-US11942.

XX

PR 29-MAY-1998; 98US-0087306.

XX

PA (HESK-) HESKA CORP.

XX

PI Sim G, Yang S, Dreitz MJ, Wonderling RS;

XX

DR WPI; 2000-072623/06.

XX

PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,

PT useful for treating or preventing e.g. tumors or autoimmune disease

XX

PS Claim 1i; Page 229; 264pp; English.

XX

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CC Sequences 255552-255560 and 255561-255566 represent cDNA
CC sequences encoding canine interleukin-13 (IL-13) clones 80
CC and 78 respectively. The invention relates to canine
CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these
CC immunoregulatory proteins. The proteins, their associated
CC nucleic acids, specific antibodies and inhibitors may be used as
CC vaccines for therapeutic or prophylactic regulation of an immune
CC response in animals (particularly cats, dogs, horses and humans).
CC They may be used to treat autoimmune or infectious diseases including
CC allergies, tumours, inflammation and graft rejection, and to increase
CC the response from a co-administered antigen. The nucleotide sequences
CC can also be used for the recombinant production of a protein, while
CC nucleotide fragments are useful as probes, as amplification primers and
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
CC The proteins may be used to raise antibodies and to screen for
CC modulators of activity, while the antibodies may be used in detection,
CC and in drug targeting.
XX
SQ Sequence 278 BP; 58 A; 93 C; 69 G; 58 T; 0 other;

Query Match      100.0%; Score 278; DB 21; Length 278;
Best Local Similarity 100.0%; Pred. No. 2e-66;
Matches 278; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
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ID Z55563 standard; cDNA; 390 BP.
XX
AC Z55563;
XX
DT 14-MAR-2000 (first entry)
XX
DE Canine interleukin-13 (IL-13) clone 78 cDNA coding region.
XX
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
XX
OS Canis familiaris.
XX
PN WO9961618-A2.
XX
PD 02-DEC-1999.
XX
PF 28-MAY-1999; 99WO-US11942.
XX
PR 29-MAY-1998; 98US-0087306.
XX
PA (HESK-) HESKA CORP.
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XX
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;
XX
DR WPI; 2000-072623/06.
DR P-PSDB; Y58223.
XX
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,
PT useful for treating or preventing e.g. tumors or autoimmune disease
XX
XX Claim 1i; Page 238-239; 264pp; English.
XX
CC Sequences 255552-255560 and 255561-255566 represent cDNA
CC sequences encoding canine interleukin-13 (IL-13) clones 80
CC and 78 respectively. The invention relates to canine
CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these
CC immunoregulatory proteins. The proteins, their associated
CC nucleic acids, specific antibodies and inhibitors may be used as
CC vaccines for therapeutic or prophylactic regulation of an immune
CC response in animals (particularly cats, dogs, horses and humans).
CC They may be used to treat autoimmune or infectious diseases including
CC allergies, tumours, inflammation and graft rejection, and to increase
CC the response from a co-administered antigen. The nucleotide sequences
CC can also be used for the recombinant production of a protein, while
CC nucleotide fragments are useful as probes, as amplification primers and
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
CC The proteins may be used to raise antibodies and to screen for
CC modulators of activity, while the antibodies may be used in detection,
CC and in drug targeting.
XX
SQ Sequence 390 BP; 92 A; 117 C; 99 G; 82 T; 0 other;

Query Match      100.0%; Score 278; DB 21; Length 390;
Best Local Similarity 100.0%; Pred. No. 2.2e-66;
Matches 278; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atggcgctctggtgactgtggtcattgctcaccctgcctcgtggtgacctccccg 60
   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 atggcgctctggtgactgtggtcattgctcaccctgcctcgtggtgacctccccg 60

QY 61 agccctgtgactccctcccaaccctcaaggagctcattgaggagctggtcaacatcacc 120
   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 61 agccctgtgactccctcccaaccctcaaggagctcattgaggagctggtcaacatcacc 120

QY 121 cagaatcaggatccctctgcaacggcagcatggtgtggagcgtcaacctgaccgcggc 180
   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 cagaatcaggatccctctgcaacggcagcatggtgtggagcgtcaacctgaccgcggc 180

QY 181 atgtactgcgagctctagaatctctgatcaatgtctccgactgcagcgccatccaaagg 240
   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 atgtactgcgagctctagaatctctgatcaatgtctccgactgcagcgccatccaaagg 240

QY 241 acccagagatgctgaaagcactgtgctctcaaaaagcc 278
   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 acccagagatgctgaaagcactgtgctctcaaaaagcc 278

RESULT 3
Z55564/C
ID Z55564 standard; cDNA; 390 BP.
XX
AC Z55564;
XX
DT 14-MAR-2000 (first entry)
XX
DE Canine interleukin-13 (IL-13) clone 78 cDNA coding region complement.
XX
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
XX
```

```
OS Canis familiaris.
XX WO9961618-A2.
PN 02-DEC-1999.
XX 28-MAY-1999; 99WO-US11942.
XX 29-MAY-1998; 98US-0087306.
PR (HESK-) HESKA CORP.
XX Sim G, Yang S, Dreitz MJ, Wonderling RS;
PI WPI; 2000-072623/06.
XX P-PSDB; Y58223.
DR Nucleic acids encoding immunoregulatory proteins from cats or dogs,
XX useful for treating or preventing e.g. tumors or autoimmune disease
PT Claim 1i; Page 239; 264pp; English.
PS Sequences 255552-255560 and 255561-255566 represent cDNA
XX sequences encoding canine interleukin-13 (IL-13) clones 80
CC and 78 respectively. The invention relates to canine
CC IL-4, canine or feline Flt-3 ligand, canine IL-5, canine IL-13, feline
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these
CC immunoregulatory proteins. The proteins, their associated
CC nucleic acids, specific antibodies and inhibitors may be used as
CC vaccines for therapeutic or prophylactic regulation of an immune
CC response in animals (particularly cats, dogs, horses and humans).
CC They may be used to treat autoimmune or infectious diseases including
CC allergies, tumours, inflammation and graft rejection, and to increase
CC the response from a co-administered antigen. The nucleotide sequences
CC can also be used for the recombinant production of a protein, while
CC nucleotide fragments are useful as probes, as amplification primers and
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
CC The proteins may be used to raise antibodies and to screen for
CC modulators of activity, while the antibodies may be used in detection,
CC and in drug targetting.
XX Sequence 390 BP; 82 A; 99 C; 117 G; 92 T; 0 other;
SQ
Query Match 100.0%; Score 278; DB 21; Length 390;
Best Local Similarity 100.0%; Pred. No. 2.2e-66;
Matches 278; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 atggcgctctggtgactgtggtcattgctctcacctgcctcggtggccttgcctcccg 60
DB 390 ATGGCGCTCTGGTTGACTGTGGTTCATTGCTCTCACCTGCCCTCGGTGGCCTTGCCCTCCCG 331
QY 61 agccctgtgactccctcccaaccctcaaggagctcattgaggagctggtcaacatcacc 120
DB 330 AGCCCTGTGACTCCCTCCCAACCCTCAAGGAGCTCATTGAGGAGCTGGTCAACATCAAC 271
QY 121 cagaatcaggcatccctctgcaacgagcagcatggtgtggagcgtcaacctgaccgcccgc 180
DB 270 CAGAAATCAGGCATCCCTCTGCAACGGCAGCATGGTGTGGAGCGTCAACCTGACCGCCGC 211
QY 181 atgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgccatccaaagg 240
DB 210 ATGTACTGCGCAGCTCTAGAAATCTCTGATCAATGTCTCCGACTGCGAGCGCATCAAGG 151
QY 241 acccagaggatgctgaaagcactgtgctctcaaaagcc 278
DB 150 ACCCAGAGGATGCTGAAGCACTGTGCTCTCAAAAGCC 113
RESULT 4
255557
```

```
ID 255557 standard; cDNA; 393 BP.
XX
AC 255557;
XX
DT 14-MAR-2000 (first entry)
XX
DE Canine interleukin-13 (IL-13) clone 80 cDNA coding region.
XX
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
XX
OS Canis familiaris.
XX
PN WO9961618-A2.
XX
PD 02-DEC-1999.
XX
PF 28-MAY-1999; 99WO-US11942.
XX
PR 29-MAY-1998; 98US-0087306.
XX (HESK-) HESKA CORP.
XX Sim G, Yang S, Dreitz MJ, Wonderling RS;
PI WPI; 2000-072623/06.
XX P-PSDB; Y58221.
DR Nucleic acids encoding immunoregulatory proteins from cats or dogs,
XX useful for treating or preventing e.g. tumors or autoimmune disease
PT Claim 1i; Page 232-233; 264pp; English.
PS Sequences 255552-255560 and 255561-255566 represent cDNA
XX sequences encoding canine interleukin-13 (IL-13) clones 80
CC and 78 respectively. The invention relates to canine
CC IL-4, canine or feline Flt-3 ligand, canine IL-5, canine IL-13, feline
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these
CC immunoregulatory proteins. The proteins, their associated
CC nucleic acids, specific antibodies and inhibitors may be used as
CC vaccines for therapeutic or prophylactic regulation of an immune
CC response in animals (particularly cats, dogs, horses and humans).
CC They may be used to treat autoimmune or infectious diseases including
CC allergies, tumours, inflammation and graft rejection, and to increase
CC the response from a co-administered antigen. The nucleotide sequences
CC can also be used for the recombinant production of a protein, while
CC nucleotide fragments are useful as probes, as amplification primers and
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
CC The proteins may be used to raise antibodies and to screen for
CC modulators of activity, while the antibodies may be used in detection,
CC and in drug targetting.
XX
SQ Sequence 393 BP; 93 A; 118 C; 100 G; 82 T; 0 other;
Query Match 100.0%; Score 278; DB 21; Length 393;
Best Local Similarity 100.0%; Pred. No. 2.2e-66;
Matches 278; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 atggcgctctggtgactgtggtcattgctctcacctgcctcggtggccttgcctcccg 60
DB 1 atggcgctctggtgactgtggtcattgctctcacctgcctcggtggccttgcctcccg 60
QY 61 agccctgtgactccctcccaaccctcaaggagctcattgaggagctggtcaacatcacc 120
DB 61 agccctgtgactccctcccaaccctcaaggagctcattgaggagctggtcaacatcacc 120
QY 121 cagaatcaggcatccctctgcaacgagcagcatggtgtggagcgtcaacctgaccgcccgc 180
DB 121 cagaatcaggcatccctctgcaacgagcagcatggtgtggagcgtcaacctgaccgcccgc 180
```

QY 181 atgtactgcgcagtcttagaattctctgatcaatgtctccgactgcagcgccatccaaagg 240  
|||||  
Db 181 atgtactgcgcagtcttagaattctctgatcaatgtctccgactgcagcgccatccaaagg 240  
|||||  
QY 241 acccagaggatctgaaagcactgtgctctcctcaaaagcc 278  
|||||  
Db 241 acccagaggatctgaaagcactgtgctctcctcaaaagcc 278  
|||||  
RESULT 5  
Z55558/c  
ID Z55558 standard; cDNA; 393 BP.  
XX  
AC Z55558;  
XX  
DT 14-MAR-2000 (first entry)  
XX  
DE Canine interleukin-13 (IL-13) clone 80 cDNA coding region complement.  
DE  
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;  
immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.  
XX  
OS Canis familiaris.  
XX  
PN WO9961618-A2.  
XX  
PD 02-DEC-1999.  
XX  
PF 28-MAY-1999; 99WO-US11942.  
XX  
PR 29-MAY-1998; 98US-0087306.  
XX  
PA (HESK-) HESKA CORP.  
XX  
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;  
PI  
XX  
DR WPI; 2000-072623/06.  
DR  
DR P-PSDB; Y58221.  
XX  
XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
PT useful for treating or preventing e.g. tumors or autoimmune disease  
PT  
XX  
XX  
PS Claim 11; Page 233; 264pp; English.  
XX  
CC Sequences Z55552-Z55560 and Z55561-Z55566 represent cDNA  
CC sequences encoding canine interleukin-13 (IL-13) clones 80  
CC and 78 respectively. The invention relates to canine  
CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or  
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline  
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage  
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these  
CC immunoregulatory proteins. The proteins, their associated  
CC nucleic acids, specific antibodies and inhibitors may be used as  
CC vaccines for therapeutic or prophylactic regulation of an immune  
CC response in animals (particularly cats, dogs, horses and humans).  
CC They may be used to treat autoimmune or infectious diseases including  
CC allergies, tumours, inflammation and graft rejection, and to increase  
CC the response from a co-administered antigen. The nucleotide sequences  
CC can also be used for the recombinant production of a protein, while  
CC nucleotide fragments are useful as probes, as amplification primers and  
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
CC The proteins may be used to raise antibodies and to screen for  
CC modulators of activity, while the antibodies may be used in detection,  
CC and in drug targetting.  
XX  
SQ Sequence 393 BP; 82 A; 100 C; 118 G; 93 T; 0 other;

Query Match 100.0%; Score 278; DB 21; Length 393;  
Best Local Similarity 100.0%; Pred. No. 2.2e-66;  
Matches 278; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atggcgcctctgtgactgtggtcattgcctcacctgcctcgtggtgcctgcctcccg 60

Db 393 ATGCGCTCTGGTTGACTGTGGTCATTGCTCTCACCTGCTCGGTGGCCTTGCTCCCG 334  
|||||  
QY 61 agccctgtgactccctcccccaccctcaaggagctcattgagagctggtcaacatcacc 120  
|||||  
Db 333 AGCCTGTGACTCCCTCCCAACCCTCAAGGAGCTCATTGAGAGCTGGTCAACATCACC 274  
|||||  
QY 121 cagaatcaggcatccctctgcaagcgagcatggtgtggaggtcaacctgaccgcggc 180  
|||||  
Db 273 CAGAATCAGGCATCCCTCTGCAACGGCAGCATGGTGTGGAGCTCAACCTGACCGCGGC 214  
|||||  
QY 181 atgtactgcgcagtcttagaattctctgatcaatgtctccgactgcagcgccatccaaagg 240  
|||||  
Db 213 ATGTACTGCGCAGCTCTAGATCTCTGATCAATGTCTCCGACTGCAGGCCATCCAAAGG 154  
|||||  
QY 241 acccagaggatctgaaagcactgtgctctcctcaaaagcc 278  
|||||  
Db 153 ACCAGAGGATGCTGAAAGCACTGTGCTCTCTCAAAAGCC 116  
|||||  
RESULT 6  
Z55561  
ID Z55561 standard; cDNA; 1269 BP.  
XX  
AC Z55561;  
XX  
DT 14-MAR-2000 (first entry)  
XX  
DE Canine interleukin-13 (IL-13) clone 78 cDNA.  
DE  
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;  
immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.  
XX  
OS Canis familiaris.  
XX  
FH Key Location/Qualifiers  
FT CDS 57..449  
FT /\*tag= a  
FT /product= "Canine IL-13 clone 78"  
XX  
PN WO9961618-A2.  
XX  
PD 02-DEC-1999.  
XX  
PF 28-MAY-1999; 99WO-US11942.  
XX  
PR 29-MAY-1998; 98US-0087306.  
XX  
PA (HESK-) HESKA CORP.  
XX  
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;  
PI  
XX  
DR WPI; 2000-072623/06.  
DR  
DR P-PSDB; Y58223.  
XX  
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
PT useful for treating or preventing e.g. tumors or autoimmune disease  
XX  
PS Claim 11; Page 235-236; 264pp; English.  
XX  
CC Sequences Z55552-Z55560 and Z55561-Z55566 represent cDNA  
CC sequences encoding canine interleukin-13 (IL-13) clones 80  
CC and 78 respectively. The invention relates to canine  
CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or  
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline  
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage  
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these  
CC immunoregulatory proteins. The proteins, their associated  
CC nucleic acids, specific antibodies and inhibitors may be used as  
CC vaccines for therapeutic or prophylactic regulation of an immune  
CC response in animals (particularly cats, dogs, horses and humans).  
CC They may be used to treat autoimmune or infectious diseases including  
CC allergies, tumours, inflammation and graft rejection, and to increase







Db 1131 CAGAAATCAGGCATCCCTCTGCAACGGCAGCATGGTGTGGAGCGTCAACCTGACCGCGGC 1072

QY 181 atgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgccatccaaagg 240

Db 1071 ATGTACTGCGCAGCTCTAGAAATCTCTGATCAATGTCTCCGACTGCAGCGCCATCCAAAGG 1012

QY 241 acccagaggatgctgaaagcactgtgctctcaaaagcc 278

Db 1011 ACCCAGAGGATGCTGAAAGCACTGTGCTCTCAAAAGCC 974

RESULT 10

Z55553

ID Z55553 standard; cDNA; 272 BP.

XX

AC Z55553;

XX

DT 14-MAR-2000 (first entry)

XX

DE Canine interleukin-13 (IL-13) cDNA fragment nCaIL13-272.

XX

KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;

KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.

XX

OS Canis familiaris.

XX

PN WO9961618-A2.

XX

PD 02-DEC-1999.

XX

PF 28-MAY-1999; 99WO-US11942.

XX

PR 29-MAY-1998; 98US-0087306.

XX

PA (HESK-) HESKA CORP.

XX

PI Sim G, Yang S, Dreitz MJ, Wonderling RS;

XX

DR WPI; 2000-072623/06.

XX

PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,

PT useful for treating or preventing e.g. tumors or autoimmune disease

XX

PS Claim 1i; Page 228; 264pp; English.

XX

CC Sequences Z55552-Z55560 and Z55561-Z55566 represent cDNA

CC sequences encoding canine interleukin-13 (IL-13) clones 80

CC and 78 respectively. The invention relates to canine

CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or

CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline

CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage

CC colony-stimulating factor (GM-CSF), and nucleotides which encode these

CC immunoregulatory proteins. The proteins, their associated

CC nucleic acids, specific antibodies and inhibitors may be used as

CC vaccines for therapeutic or prophylactic regulation of an immune

CC response in animals (particularly cats, dogs, horses and humans).

CC They may be used to treat autoimmune or infectious diseases including

CC the response from a co-administered antigen. The nucleotide sequences

CC can also be used for the recombinant production of a protein, while

CC nucleotide fragments are useful as probes, as amplification primers and

CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).

CC The proteins may be used to raise antibodies and to screen for

CC modulators of activity, while the antibodies may be used in detection,

CC and in drug targeting.

XX

SQ Sequence 272 BP; 64 A; 91 C; 69 G; 48 T; 0 other;

Query Match 84.2%; Score 234; DB 21; Length 272;

Best Local Similarity 100.0%; Pred. No. 1.6e-54;

Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 tggccttgctccccgagccctgtgactccctcccccaacctcaaggagctcattgagga 104

Db 1 tggccttgctccccgagccctgtgactccctcccccaacctcaaggagctcattgagga 60

QY 105 gctggtcaacatcacccagaatcacaggcatccctctgcaacggcagcatggtgtggagcgt 164

Db 61 gctggtcaacatcacccagaatcacaggcatccctctgcaacggcagcatggtgtggagcgt 120

QY 165 caacctgaccgcggcgtactgtactgcgcagctctagaaatctctgatcaatgtctccgactg 224

Db 121 caacctgaccgcggcgtactgtactgcgcagctctagaaatctctgatcaatgtctccgactg 180

QY 225 cagcgccatccaaaggaccagaggatgctgaaagcactgtgctctcaaaagcc 278

Db 181 cagcgccatccaaaggaccagaggatgctgaaagcactgtgctctcaaaagcc 234

RESULT 11

Z55565

ID Z55565 standard; cDNA; 330 BP.

XX

AC Z55565;

XX

DT 14-MAR-2000 (first entry)

XX

DE Canine mature interleukin-13 (IL-13) clone 78 cDNA.

XX

KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;

KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.

XX

OS Canis familiaris.

XX

PN WO9961618-A2.

XX

PD 02-DEC-1999.

XX

PF 28-MAY-1999; 99WO-US11942.

XX

PR 29-MAY-1998; 98US-0087306.

XX

PA (HESK-) HESKA CORP.

XX

PI Sim G, Yang S, Dreitz MJ, Wonderling RS;

XX

DR WPI; 2000-072623/06.

DR P-PSDB; Y58224.

XX

PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,

PT useful for treating or preventing e.g. tumors or autoimmune disease

XX

PS Claim 1i; Page 239-240; 264pp; English.

XX

CC Sequences Z55552-Z55560 and Z55561-Z55566 represent cDNA

CC sequences encoding canine interleukin-13 (IL-13) clones 80

CC and 78 respectively. The invention relates to canine

CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or

CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline

CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage

CC colony-stimulating factor (GM-CSF), and nucleotides which encode these

CC immunoregulatory proteins. The proteins, their associated

CC nucleic acids, specific antibodies and inhibitors may be used as

CC vaccines for therapeutic or prophylactic regulation of an immune

CC response in animals (particularly cats, dogs, horses and humans).

CC They may be used to treat autoimmune or infectious diseases including

CC allergies, tumours, inflammation and graft rejection, and to increase

CC the response from a co-administered antigen. The nucleotide sequences

CC can also be used for the recombinant production of a protein, while

CC nucleotide fragments are useful as probes, as amplification primers and

CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).

CC The proteins may be used to raise antibodies and to screen for

CC modulators of activity, while the antibodies may be used in detection,

CC and in drug targeting.

XX



SQ Sequence 330 BP; 88 A; 96 C; 82 G; 64 T; 0 other;

Query Match 78.4%; Score 218; DB 21; Length 330;  
Best Local Similarity 100.0%; Pred. No. 3.6e-50;  
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 agccctgtgactccctcccccacccctcaaggagctcattgaggagctggtcaacatcacc 120  
|||||  
Db 1 agccctgtgactccctcccccacccctcaaggagctcattgaggagctggtcaacatcacc 60

QY 121 cagaatcaggcatccctctgcaacggcagcatggtgtggagcgtcaacctgaccgcggc 180  
|||||  
Db 61 cagaatcaggcatccctctgcaacggcagcatggtgtggagcgtcaacctgaccgcggc 120

QY 181 atgtactgcgagctctagaatctctgatcaatgtctccgactgcagcgccatccaaagg 240  
|||||  
Db 121 atgtactgcgagctctagaatctctgatcaatgtctccgactgcagcgccatccaaagg 180

QY 241 acccagaggatgctgaaagcactgtgctctcaaaaagcc 278  
|||||  
Db 181 acccagaggatgctgaaagcactgtgctctcaaaaagcc 218

RESULT 12  
Z55566/c

ID Z55566 standard; cDNA; 330 BP.

XX  
AC Z55566;  
XX

DT 14-MAR-2000 (first entry)

XX  
DE Canine mature interleukin-13 (IL-13) clone 78 cDNA complement.

XX  
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;  
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.  
XX  
OS Canis familiaris.  
XX  
PN WO9961618-A2.  
XX  
PD 02-DEC-1999.  
XX  
PF 28-MAY-1999; 99WO-US11942.  
XX  
PR 29-MAY-1998; 98US-0087306.  
XX  
PA (HESK-) HESKA CORP.  
XX  
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;  
XX  
XX WPI; 2000-072623/06.  
DR P-PSDB; Y58224.  
XX

PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
PT useful for treating or preventing e.g. tumors or autoimmune disease  
PS Claim 1i; Page 241; 264pp; English.  
XX

CC Sequences Z55552-Z55560 and Z55561-Z55566 represent cDNA  
CC sequences encoding canine interleukin-13 (IL-13) clones 80  
CC and 78 respectively. The invention relates to canine  
CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or  
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline  
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage  
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these  
CC immunoregulatory proteins. The proteins, their associated  
CC nucleic acids, specific antibodies and inhibitors may be used as  
CC vaccines for therapeutic or prophylactic regulation of an immune  
CC response in animals (particularly cats, dogs, horses and humans).  
CC They may be used to treat autoimmune or infectious diseases including  
CC allergies, tumours, inflammation and graft rejection, and to increase  
CC the response from a co-administered antigen. The nucleotide sequences

CC can also be used for the recombinant production of a protein, while  
CC nucleotide fragments are useful as probes, as amplification primers and  
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
CC The proteins may be used to raise antibodies and to screen for  
CC modulators of activity, while the antibodies may be used in detection,  
CC and in drug targetting.

XX  
SQ Sequence 330 BP; 64 A; 82 C; 96 G; 88 T; 0 other;

Query Match 78.4%; Score 218; DB 21; Length 330;  
Best Local Similarity 100.0%; Pred. No. 3.6e-50;  
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 agccctgtgactccctcccccacccctcaaggagctcattgaggagctggtcaacatcacc 120  
|||||  
Db 330 AGCCCTGTGACTCCCTCCCAACCCCTCAAGGAGCTCATTGAGGAGCTGGTCAACATCACC 271

QY 121 cagaatcaggcatccctctgcaacggcagcatggtgtggagcgtcaacctgaccgcggc 180  
|||||  
Db 270 CAGAATCAGGCATCCCTCTGCAACGCGCAGCATGCTGTGGAGCGTCAACCTGACCGCGGC 211

QY 181 atgtactgcgagctctagaatctctgatcaatgtctccgactgcagcgccatccaaagg 240  
|||||  
Db 210 ATGTACTGCGCAGCTCTAGAAATCTCTGATCAATGTCTCCGACTGCGAGGCCATCCAAAGG 151

QY 241 acccagaggatgctgaaagcactgtgctctcaaaaagcc 278  
|||||  
Db 150 ACCCAGAGGATGCTGAAAGCAGCTGTGCTCTCAAAAGCC 113

RESULT 13  
Z55559

ID Z55559 standard; cDNA; 333 BP.

XX  
AC Z55559;  
XX

DT 14-MAR-2000 (first entry)

XX  
DE Canine mature interleukin-13 (IL-13) clone 80 cDNA.

XX  
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;  
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.  
XX  
OS Canis familiaris.  
XX  
PN WO9961618-A2.  
XX  
PD 02-DEC-1999.  
XX  
PF 28-MAY-1999; 99WO-US11942.  
XX  
PR 29-MAY-1998; 98US-0087306.  
XX  
PA (HESK-) HESKA CORP.  
XX  
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;  
XX  
XX WPI; 2000-072623/06.  
DR P-PSDB; Y58222.

PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
PT useful for treating or preventing e.g. tumors or autoimmune disease  
PS Claim 1i; Page 233-234; 264pp; English.  
XX

CC Sequences Z55552-Z55560 and Z55561-Z55566 represent cDNA  
CC sequences encoding canine interleukin-13 (IL-13) clones 80  
CC and 78 respectively. The invention relates to canine  
CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or  
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline  
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage  
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these



CC immunoregulatory proteins. The proteins, their associated  
CC nucleic acids, specific antibodies and inhibitors may be used as  
CC vaccines for therapeutic or prophylactic regulation of an immune  
CC response in animals (particularly cats, dogs, horses and humans).  
CC They may be used to treat autoimmune or infectious diseases including  
CC allergies, tumours, inflammation and graft rejection, and to increase  
CC the response from a co-administered antigen. The nucleotide sequences  
CC can also be used for the recombinant production of a protein, while  
CC nucleotide fragments are useful as probes, as amplification primers and  
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
CC The proteins may be used to raise antibodies and to screen for  
CC modulators of activity, while the antibodies may be used in detection,  
CC and in drug targeting.

XX Sequence 333 BP; 89 A; 97 C; 83 G; 64 T; 0 other;

Query Match 78.4%; Score 218; DB 21; Length 333;  
Best Local Similarity 100.0%; Pred. No. 3.6e-50;  
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 agccctgtgactccctcccaaccctcaaggagctcattgaggagctggtcaacatcacc 120  
Db 1 agccctgtgactccctcccaaccctcaaggagctcattgaggagctggtcaacatcacc 60  
QY 121 cagaatcaggcatccctctgcaacgagcagcatggtgtggagctgaacctgacgcgcgc 180  
Db 61 cagaatcaggcatccctctgcaacgagcagcatggtgtggagctgaacctgacgcgcgc 120  
QY 181 atgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgccatccaaagg 240  
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QY 241 acccagaggatgctgaaagcactgtgtctctcaaaaagcc 278  
Db 181 acccagaggatgctgaaagcactgtgtctctcaaaaagcc 218

RESULT 14  
255560/c  
ID 255560 standard; CDNA; 333 BP.  
XX  
AC  
XX 255560;

DT 14-MAR-2000 (first entry)

XX Canine mature interleukin-13 (IL-13) clone 80 cDNA complement.

DE Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;  
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.

OS Canis familiaris.

XX WO9961618-A2.

PN 02-DEC-1999.

XX 28-MAY-1999; 99WO-US11942.

XX 29-MAY-1998; 98US-0087306.

PR (HESK-) HESKA CORP.

XX Sim G, Yang S, Dreitz MJ, Wonderling RS;

PI WPI; 2000-072623/06.

XX P-PSDB; Y58222.

DR Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
XX useful for treating or preventing e.g. tumors or autoimmune disease

PS Claim 1i; Page 235; 264pp; English.

XX

CC Sequences 255552-255560 and 255561-255566 represent cDNA  
CC sequences encoding canine interleukin-13 (IL-13) clones 80  
CC and 78 respectively. The invention relates to canine  
CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or  
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline  
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage  
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these  
CC immunoregulatory proteins. The proteins, their associated  
CC nucleic acids, specific antibodies and inhibitors may be used as  
CC vaccines for therapeutic or prophylactic regulation of an immune  
CC response in animals (particularly cats, dogs, horses and humans).  
CC They may be used to treat autoimmune or infectious diseases including  
CC allergies, tumours, inflammation and graft rejection, and to increase  
CC the response from a co-administered antigen. The nucleotide sequences  
CC can also be used for the recombinant production of a protein, while  
CC nucleotide fragments are useful as probes, as amplification primers and  
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
CC The proteins may be used to raise antibodies and to screen for  
CC modulators of activity, while the antibodies may be used in detection,  
CC and in drug targeting.

XX  
SQ Sequence 333 BP; 64 A; 83 C; 97 G; 89 T; 0 other;

Query Match 78.4%; Score 218; DB 21; Length 333;  
Best Local Similarity 100.0%; Pred. No. 3.6e-50;  
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 agccctgtgactccctcccaaccctcaaggagctcattgaggagctggtcaacatcacc 120  
Db 333 AGCCCTGTGACTCCCTCCCAACCCTCAAGGAGCTCATTGAGGAGCTGGTCAACATCACC 274  
QY 121 cagaatcaggcatccctctgcaacgagcagcatggtgtggagctgaacctgacgcgcgc 180  
Db 273 CAGAATCAGGCATCCCTCTGCAACGGCAGCATGTTGTGGAGCGTCAACCTGACCGCCGCG 214  
QY 181 atgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgccatccaaagg 240  
Db 213 ATGTACTGGCAGCTCTAGAAATCTCTGATCAATGTCTCCGACTGCAGCGCCATCCAAAGG 154  
QY 241 acccagaggatgctgaaagcactgtgtctctcaaaaagcc 278  
Db 153 ACCCAGAGGATGCTGAAAGCACTGTGCTCTCTCAAAAGCC 116

RESULT 15  
F21334  
ID F21334 standard; DNA; 1270 BP.  
XX  
AC F21334;  
XX  
DT 14-MAR-2001 (first entry)

XX Human low adenosine antisense oligonucleotide related sequence #2901.

DE Low adenosine antisense oligonucleotide; phosphorothioate; allergy;  
XX human; airway disorder; bronchoconstriction; lung inflammation;  
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;  
KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;  
KW respiratory obstruction; pulmonary obstruction; impeded respiration;  
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;  
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;  
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;  
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;  
KW cancer; ss.

XX Homo sapiens.

OS WO200062736-A2.

XX 26-OCT-2000.

XX 24-MAR-2000; 2000WO-US08020.

PF

Search completed: May 13, 2001, 14:28:54  
Job time: 18249 sec

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XX PR 06-APR-1999; 99US-0127958.
XX PA (UYEC-) UNIV EAST CAROLINA.
XX PA (NYCE/) NYCE J W.
XX PI Nyce JW;
XX WI WPI; 2000-679539/66.
XX PT Low adenosine (A) content antisense oligonucleotides which do not
XX PT trigger adenosine receptors during metabolism, useful e.g. for treating
XX PT cancers and respiratory obstructions -
XX PS Disclosure; Page 1336; 1592pp; English.
XX CC The present invention describes low adenosine (A) content antisense
CC CC oligonucleotides and compositions (I) comprising them. In the antisense
CC CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC CC expression and/or activity of target polypeptides associated with
CC CC lung/respiratory disorders and malignancies, such as stimulating and
CC CC activating peptide factors and transmitters, transcription factors,
CC CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC CC chemokines, endogenously produced specific and non-specific enzymes,
CC CC binding proteins, adhesion molecules and their receptors, cytokine and
CC CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC CC nervous system (CNS) and peripheral nervous and non-nervous system
CC CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC CC transmitters, defensins, growth factors, vasoactive peptides and
CC CC receptors, binding proteins and malignancy associated proteins. The
CC CC antisense oligonucleotides may be used in this way to treat disorders
CC CC including respiratory obstruction (especially pulmonary obstruction
CC CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
CC CC and/or surfactant hypoproduction which are associated with a disease or
CC CC condition selected from pulmonary vasoconstriction, inflammation,
CC CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC CC and/or cancer. F18434 to F21543 represent human polynucleotide fragments
CC CC and antisense oligonucleotides used in the exemplification of the
CC CC present invention.
XX SQ Sequence 1270 BP; 288 A; 335 C; 336 G; 311 T; 0 other;

Query Match      68.7%; Score 191; DB 21; Length 1270;
Best Local Similarity 82.8%; Pred. NO. 1e-42;
Matches 231; Conservative 0; Mismatches 45; Indels 3; Gaps

QY 1 atggcgctctgttgactgtggtcattgctctcaatgcctcggtggccttgcctccccg 60
Db | ||||| | ||||| ||||||| ||||| ||||| ||||| ||||| ||||| |||||
45 atggcgcttttgtgaccacggtcattgctctcaatgccttggcggcttgcctcccca 104
QY 61 agccctgtgactccctcccaccctcaaggagtcattgaggagctggtcaacatcac 120
Db | ||||| ||||| || ||||| ||||||| ||||||| ||||||| ||||||| |||||
105 ggccctgtgcctccctctacagccctcagggaagtcataggagctggtcaacatcac 164
QY 121 cagaatc---aggcatccctctgcaacggcagcatggtgtggagcgtcaacctgacgcc 177
Db | |||| | ||| | ||||| ||||||| ||||||| ||||||| ||||||| |||||
165 cagaaccagaaggctccgctctgcaatggcagcatgttatggagcatcaacctgacagct 224
QY 178 ggcatgtactgcgagctctagaatctctgatcaatgtctccgactgcagcgccatccaa 237
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225 ggcatgtactgtcagcccttggaatccctgatcaacgtgtcagggtgcagtgccatcgag 284
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285 aagacccagagatgctgagcggattctgccccgacaag 323

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 13, 2001, 14:20:49 ; Search time 226.02 Seconds  
(without alignments)  
214.758 Million cell updates/sec

Title: US-09-451-527-90  
Perfect score: 278  
Sequence: 1 atggcgctctgtgtgactgt.....gcactgtgctctcaaaagcc 278

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 302621 seqs, 87301344 residues

Total number of hits satisfying chosen parameters: 605242

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /cgnl\_7/ptodata/1/ina/5B\_COMB.seq:\*  
3: /cgnl\_7/ptodata/1/ina/6A\_COMB.seq:\*  
4: /cgnl\_7/ptodata/1/ina/6B\_COMB.seq:\*  
5: /cgnl\_7/ptodata/1/ina/PCTUS\_COMB.seq:\*  
6: /cgnl\_7/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	191	68.7	1290	5	PCT-US93-07645A-1 Sequence 1, Appli
3	191	68.7	1290	5	PCT-US93-07645-1 Sequence 1, Appli
4	189.4	68.1	1297	1	US-08-371-121-15 Sequence 15, Appli
5	148.2	53.3	384	1	US-08-371-121-17 Sequence 17, Appli
6	147.6	53.1	336	1	US-08-371-121-24 Sequence 24, Appli
7	146.4	52.7	425	1	US-08-594-469-4 Sequence 4, Appli
8	146.4	52.7	425	2	US-08-906-957-4 Sequence 4, Appli
9	146.4	52.7	4410	1	US-08-594-469-1 Sequence 1, Appli
10	146.4	52.7	4410	2	US-08-906-957-1 Sequence 1, Appli
11	146	52.5	336	1	US-08-371-121-2 Sequence 2, Appli
12	142.4	51.2	447	1	US-08-371-121-26 Sequence 26, Appli
13	142.4	51.2	1212	1	US-08-012-543-3 Sequence 3, Appli
14	142.4	51.2	1212	5	PCT-US93-07645A-3 Sequence 3, Appli
15	142.4	51.2	1212	5	PCT-US93-07645-3 Sequence 3, Appli
16	44.6	16.0	60	1	US-08-371-121-12 Sequence 12, Appli
17	44.6	16.0	102	1	US-08-371-121-10 Sequence 10, Appli
18	39.6	14.2	54	1	US-08-371-121-11 Sequence 11, Appli
19	39.6	14.2	96	1	US-08-371-121-9 Sequence 9, Appli
20	35.8	12.9	2249	3	US-08-814-052-19 Sequence 19, Appli
21	35.8	12.9	2300	3	US-08-814-052-18 Sequence 18, Appli
22	35.8	12.9	3183	2	US-08-939-218A-1 Sequence 1, Appli
23	35.8	12.9	3187	5	PCT-US95-06815-1 Sequence 1, Appli
24	35.8	12.9	3192	1	US-08-706-037-26 Sequence 26, Appli
25	35.8	12.9	3192	1	US-08-940-661A-1 Sequence 1, Appli
26	35.8	12.9	3192	2	US-09-083-485-1 Sequence 1, Appli
27	35.8	12.9	3192	2	US-09-005-397-26 Sequence 26, Appli

28	34.4	12.4	1322	4	US-09-128-450-27 Sequence 27, Appli
29	34.4	12.4	1521	1	US-08-496-855A-3 Sequence 3, Appli
30	34.4	12.4	1521	2	US-07-938-154-9 Sequence 9, Appli
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34	34.4	12.4	2450	3	US-08-467-574-9 Sequence 9, Appli
35	33.2	11.9	2712	3	US-09-025-691-4 Sequence 4, Appli
36	32.4	11.7	720	4	US-09-094-359-3 Sequence 3, Appli
37	32.4	11.7	720	4	US-09-094-359-7 Sequence 7, Appli
38	32.4	11.7	720	4	US-09-172-063-11 Sequence 11, Appli
39	32.4	11.7	720	4	US-09-172-063-13 Sequence 13, Appli
40	32.4	11.7	762	1	US-08-532-390-40 Sequence 40, Appli
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42	32.4	11.7	768	4	US-09-094-359-11 Sequence 11, Appli
43	32.4	11.7	850	4	US-09-062-102-2 Sequence 2, Appli
44	32.4	11.7	972	4	US-09-172-063-27 Sequence 27, Appli
45	32.4	11.7	972	4	US-09-172-063-29 Sequence 29, Appli

ALIGNMENTS

RESULT 1  
US-08-012-543-1  
; Sequence 1, Application US/08012543  
; Patent No. 5596072  
; GENERAL INFORMATION:  
; APPLICANT: Culpepper, Janice  
; APPLICANT: McKenzie, Andrew  
; APPLICANT: Dang, Warren  
; APPLICANT: de Waal Malefyt, Rene  
; APPLICANT: Heath, Andrew  
; APPLICANT: Aversa, Gregorio  
; APPLICANT: Briere, Francine  
; APPLICANT: Banchereau, Jacques  
; APPLICANT: de Vries, Jan  
; APPLICANT: Zurawski, Gerard  
; TITLE OF INVENTION: Human Interleukin-13  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/012,543  
; FILING DATE: 01-FEB-1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/933,416  
; FILING DATE: 21-AUG-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0302K1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-852-9196  
; TELEFAX: 415-496-1200  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1290 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA



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; FEATURE:
; NAME/KEY: CDS
; LOCATION: 45..443
US-08-012-543-1

Query Match          68.7%; Score 191; DB 1; Length 1290;
Best Local Similarity 82.8%; Pred. No. 4.1e-46;
Matches 231; Conservative 0; Mismatches 45; Indels 3; Gaps 1;

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QY 121 cagaatc---aggcatccctctgcaacggcagcatggtgtgagcgtcaacctgaccgcc 177
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RESULT 2
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; Sequence 1, Application PC/TUS9307645A
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Human Interleukin-13
; NUMBER OF SEQUENCES: 6
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.5
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07645A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/012543
; FILING DATE: 01-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/010977
; FILING DATE: 29-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/933416
; FILING DATE: 21-AUG-1992
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1290 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
PCT-US93-07645A-1

Query Match          68.7%; Score 191; DB 5; Length 1290;
Best Local Similarity 82.8%; Pred. No. 4.1e-46;
Matches 231; Conservative 0; Mismatches 45; Indels 3; Gaps 1;

QY 1 atggcgctctggtgactgtggtcattgctcaccctgcctcggtggccttgcctccccg 60
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QY 61 agccctgtgactccctcccccaccctcaaggagctcattgaggagctggtcaacatcacc 120
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QY 178 ggcattgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgccatccaa 237
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RESULT 2
PCT-US93-07645A-1
; Sequence 1, Application PC/TUS9307645A
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Human Interleukin-13
; NUMBER OF SEQUENCES: 6
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.5
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07645A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/012543
; FILING DATE: 01-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/010977
; FILING DATE: 29-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/933416
; FILING DATE: 21-AUG-1992
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1290 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
PCT-US93-07645A-1

Query Match          68.7%; Score 191; DB 5; Length 1290;
Best Local Similarity 82.8%; Pred. No. 4.1e-46;
Matches 231; Conservative 0; Mismatches 45; Indels 3; Gaps 1;

QY 1 atggcgctctggtgactgtggtcattgctcaccctgcctcggtggccttgcctccccg 60
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Db 105 GGCCCTGTGCCCTCCCTCTACAGCCCTCAGGGAGCTCATTGAGGAGCTGGTCAACATCACC 164
||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 121 cagaatc---aggcatccctctgcaacggcagcatggtgtgagcgtcaacctgaccgcc 177
||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 165 CAGAACCCAGAGAGGCTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAACCTGACAGCT 224
||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 178 ggcattgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgccatccaa 237
||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 225 GGCATGTACTGTGCAGCCCTGGAATCCCTGATCAACGTGTGAGGCTGCAGTGCATCGAG 284
||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 238 aggacccagaggatgctgaaagcactgtgctctcaaaaag 276
||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 285 AAGACCCAGAGGATGCTGAGCGGATTCTGCCCGCACAAAG 323
||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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Db 105 GGCCCTGTGCCCTCCCTCTACAGCCCTCAGGGAGCTCATTGAGGAGCTGGTCAACATCACC 164
||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 121 cagaatc---aggcatccctctgcaacggcagcatggtgtgagcgtcaacctgaccgcc 177
||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 165 CAGAACCCAGAGAGGCTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAACCTGACAGCT 224
||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 178 ggcattgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgccatccaa 237
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Db 225 GGCATGTACTGTGCAGCCCTGGAATCCCTGATCAACGTGTGAGGCTGCAGTGCATCGAG 284
||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 238 aggacccagaggatgctgaaagcactgtgctctcaaaaag 276
||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 285 AAGACCCAGAGGATGCTGAGCGGATTCTGCCCGCACAAAG 323
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RESULT 3
PCT-US93-07645-1
; Sequence 1, Application PC/TUS9307645
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Human Interleukin-13
; NUMBER OF SEQUENCES: 6
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.5
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07645
; FILING DATE: 19930818
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/012543
; FILING DATE: 01-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/010977
; FILING DATE: 29-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/933416
; FILING DATE: 21-AUG-1992
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1290 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
PCT-US93-07645-1

Query Match          68.7%; Score 191; DB 5; Length 1290;
Best Local Similarity 82.8%; Pred. No. 4.1e-46;
Matches 231; Conservative 0; Mismatches 45; Indels 3; Gaps 1;

QY 1 atggcgctctggtgactgtggtcattgctcaccctgcctcggtggccttgcctccccg 60
||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 45 ATGGCGCTTTTGTGACCACGGTCATTGCTCTCACTTGCCCTTGGCGGCTTGGCTCCCCA 104
||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 61 agccctgtgactccctcccccaccctcaaggagctcattgaggagctggtcaacatcacc 120
||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 105 GGCCCTGTGCCCTCCCTCTACAGCCCTCAGGGAGCTCATTGAGGAGCTGGTCAACATCACC 164
||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 121 cagaatc---aggcatccctctgcaacggcagcatggtgtgagcgtcaacctgaccgcc 177
||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 165 CAGAACCCAGAGAGGCTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAACCTGACAGCT 224
||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 178 ggcattgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgccatccaa 237
||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 225 GGCATGTACTGTGCAGCCCTGGAATCCCTGATCAACGTGTGAGGCTGCAGTGCATCGAG 284
||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 238 aggacccagaggatgctgaaagcactgtgctctcaaaaag 276
||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 285 AAGACCCAGAGGATGCTGAGCGGATTCTGCCCGCACAAAG 323
||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 384 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-371-121-17

Query Match 53.3%; Score 148.2; DB 1; Length 384;  
Best Local Similarity 81.8%; Pred. No. 5.6e-34;  
Matches 184; Conservative 0; Mismatches 38; Indels 3; Gaps 1;

QY 55 tccccgagccctgtgactccctcccccacccctcaaggagctcattgaggagctggtcaac 114  
||||| ||||||| ||||||| | ||||||| ||||||| ||||||| ||||||| |||||||  
Db 16 TCCCCAGGCCCTGTGCTCCCTCTACGGCCCTCAGGGAGCTCATTGAGGAGTGGTCAAC 75  
  
QY 115 atcaccagaaac---aggcatccctctgcaacggcagcagctggtgtggagcgtcaacctg 171  
||||| ||||||| | |||| | ||||||| ||||||| ||||||| ||||||| |||||||  
Db 76 ATCACCAGAACCAAGAGGCTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAACCTG 135  
  
QY 172 accgcggcagctactgcgcagctctagaatctctgatcaatgtctccgactgcagcgcc 231  
|| | ||||||| |||| | |||| | |||| | |||| | |||| | |||| | |||| |  
Db 136 ACAGCTGACATGCTACTGTGCAGCCCTGGAATCCCTGATCAACGTGTGAGGCTGCAGTGCC 195  
  
QY 232 atccaaaggaccagagatgctgaaagcactgtgctctcaaaaag 276  
|| | | ||||||| ||||||| |||| | |||| | |||| | |||| | |||| |  
Db 196 ATCGAGAAGACCCAGAGGATGCTGAGCGGATCTGCCCCGCACAAG 240

RESULT 6

US-08-371-121-24  
; Sequence 24, Application US/08371121  
; Patent No. 5652123

; GENERAL INFORMATION:  
; APPLICANT: CAPUT, Daniel  
; APPLICANT: FERRARA, Pascual  
; APPLICANT: GUILLEMOT, Jean-Claude  
; APPLICANT: LEPLATOIS, Pascal  
; APPLICANT: MINTY, Adrian  
; APPLICANT: KAGHAD, Mourad  
; APPLICANT: LABIT-LE BOUTEILLER, Christine  
; APPLICANT: MAGAZIN, Marilyn  
; TITLE OF INVENTION: Protein having a cytokine type  
; TITLE OF INVENTION: activity, recombinant DNA coding for this protein,  
; TITLE OF INVENTION: transformed cells and microorganisms.  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FOLEY & LARDNER  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington, D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/371,121  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/938,161  
; FILING DATE: 30-NOV-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/FR92/00280  
; FILING DATE: 27-MAR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 91 00137  
; FILING DATE: 08-JAN-1992  
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: FR 91 03904  
; FILING DATE: 29-MAR-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SAXE, Bernhard D.  
; REGISTRATION NUMBER: 28,665  
; REFERENCE/DOCKET NUMBER: 16781/383  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 672-5300  
; TELEFAX: (202) 672-5399  
; TELEX: 904136  
; INFORMATION FOR SEQ ID NO: 24:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 336 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-371-121-24

Query Match 53.1%; Score 147.6; DB 1; Length 336;  
Best Local Similarity 83.0%; Pred. No. 8e-34;  
Matches 181; Conservative 0; Mismatches 34; Indels 3; Gaps 1;

QY 62 gccctgtgactccctcccccacccctcaaggagctcattgaggagctggtcaacatcaccc 121  
||||| ||||||| ||||||| || |||| | ||||||| ||||||| ||||||| |||||||  
Db 2 GCCCTGTGCTCCCTCTACAGCCCTCAGGGAGCTCATTGAGGAGCTGGTCAACATCACCC 61  
  
QY 122 agaatc---aggcatccctctgcaacggcagcagctggtgtggagcgtcaacctgaccgcg 178  
|||| | |||| | ||||||| ||||||| |||| | |||| | |||| | |||| |  
Db 62 AGAACCAAGAGGCTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAACCTGACAGCTG 121  
  
QY 179 gcatgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgccatccaaa 238  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
Db 122 GCATGTACTGTGCAGCCCTGGAATCCCTGATCAACGTTGTCAGGCTGCAGTGCATCGAGA 181  
  
QY 239 ggaccagagagtgctgaaagcactgtgctctcaaaaag 276  
||||| ||||||| ||||||| || |||| | |||| | |||| | |||| |  
Db 182 AGACCCAGAGGATGCTGAGCGGATTTCTGCCCGCACAAAG 219

RESULT 7

US-08-594-469-4  
; Sequence 4, Application US/08594469  
; Patent No. 5700665

; GENERAL INFORMATION:  
; APPLICANT: LEGOUX, Richard  
; APPLICANT: MALDONADO, Paul  
; APPLICANT: SALOME, Marc  
; TITLE OF INVENTION: Method for the extraction of  
; TITLE OF INVENTION: periplasmic proteins of prokaryotic microorganisms in the  
; TITLE OF INVENTION: presence of arginine  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Bacon & Thomas  
; STREET: 625 Slaters Lane - Fourth Floor  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: USA  
; ZIP: 22314  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/594,469  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 95 01083  
; FILING DATE: 31-JAN-1995  
; ATTORNEY/AGENT INFORMATION:

NAME: FICHTER, Richard E  
REGISTRATION NUMBER: 26,382  
REFERENCE/DOCKET NUMBER: REF/LEGOUX  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 683-0500  
TELEFAX: (703) 683-1080  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 425 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-906-957-4

Query Match 52.7%; Score 146.4; DB 1; Length 425;  
Best Local Similarity 80.7%; Pred. No. 1.9e-33;  
Matches 184; Conservative 0; Mismatches 41; Indels 3; Gaps 1;  
QY 52 gcctcccgagccctgtgactccctcccaaccctcaaggagctcattgaggagctggtc 111  
Db 55 GCCTTCGCTGGCCCTGTGCTCCAGTACTGCCCTCAGGGAGCTCATTTGAGGAGCTGGTC 114  
QY 112 aacatcaccagaatc---aggcatccctctgcaacggcagcatggtgtgagcgtcaac 168  
Db 115 AACATCACCAGAACCCAGAGGCTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAAC 174  
QY 169 ctgaccgcggcatgtactgcagctctagaatctctgatcaatgtctccgactgcagc 228  
Db 175 CTGACAGCTGGCATGTACTGTGAGCCCTGGAATCCCTGTATCAACGTTGTCAAGCTGCAGT 234  
QY 229 gccatccaaaggaccagaggtgctgaaagcactgtgctctcaaaag 276  
Db 235 GCCATCGAGAAGACCCAGAGGATGCTGAGCGGATTCTGCCCGCACAAAG 282

RESULT 8  
US-08-906-957-4  
Sequence 4, Application US/08906957  
Patent No. 5856142  
GENERAL INFORMATION:  
APPLICANT: LEGOUX, Richard  
APPLICANT: MALDONADO, Paul  
APPLICANT: SALOME, Marc  
TITLE OF INVENTION: Method for the extraction of  
TITLE OF INVENTION: periplasmic proteins of prokaryotic microorganisms in the  
TITLE OF INVENTION: presence of arginine  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Bacon & Thomas  
STREET: 625 Slaters Lane - Fourth Floor  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: USA  
ZIP: 22314  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/906,957  
FILING DATE: 06-AUG-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/594,469  
FILING DATE:  
APPLICATION NUMBER: FR 95 01083  
FILING DATE: 31-JAN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: FICHTER, Richard E  
REGISTRATION NUMBER: 26,382

REFERENCE/DOCKET NUMBER: REF/LEGOUX  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 683-0500  
TELEFAX: (703) 683-1080  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 425 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-906-957-4

Query Match 52.7%; Score 146.4; DB 2; Length 425;  
Best Local Similarity 80.7%; Pred. No. 1.9e-33;  
Matches 184; Conservative 0; Mismatches 41; Indels 3; Gaps 1;  
QY 52 gcctcccgagccctgtgactccctcccaaccctcaaggagctcattgaggagctggtc 111  
Db 55 GCCTTCGCTGGCCCTGTGCTCCAGTACTGCCCTCAGGGAGCTCATTTGAGGAGCTGGTC 114  
QY 112 aacatcaccagaatc---aggcatccctctgcaacggcagcatggtgtgagcgtcaac 168  
Db 115 AACATCACCAGAACCCAGAGGCTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAAC 174  
QY 169 ctgaccgcggcatgtactgcagctctagaatctctgatcaatgtctccgactgcagc 228  
Db 175 CTGACAGCTGGCATGTACTGTGAGCCCTGGAATCCCTGTATCAACGTTGTCAAGCTGCAGT 234  
QY 229 gccatccaaaggaccagaggtgctgaaagcactgtgctctcaaaag 276  
Db 235 GCCATCGAGAAGACCCAGAGGATGCTGAGCGGATTCTGCCCGCACAAAG 282

RESULT 9  
US-08-594-469-1  
Sequence 1, Application US/08594469  
Patent No. 5700665  
GENERAL INFORMATION:  
APPLICANT: LEGOUX, Richard  
APPLICANT: MALDONADO, Paul  
APPLICANT: SALOME, Marc  
TITLE OF INVENTION: Method for the extraction of  
TITLE OF INVENTION: periplasmic proteins of prokaryotic microorganisms in the  
TITLE OF INVENTION: presence of arginine  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Bacon & Thomas  
STREET: 625 Slaters Lane - Fourth Floor  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: USA  
ZIP: 22314  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/594,469  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 95 01083  
FILING DATE: 31-JAN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: FICHTER, Richard E  
REGISTRATION NUMBER: 26,382  
REFERENCE/DOCKET NUMBER: REF/LEGOUX  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 683-0500  
TELEFAX: (703) 683-1080







CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/012,543  
FILING DATE: 01-FEB-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/933,416  
FILING DATE: 21-AUG-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Ching, Edwin P.  
REGISTRATION NUMBER: 34,090  
REFERENCE/DOCKET NUMBER: DX0302K1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-852-9196  
TELEFAX: 415-496-1200  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1212 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 70..465  
US-08-012-543-3

Query Match 51.2%; Score 142.4; DB 1; Length 1212;  
Best Local Similarity 71.4%; Pred. No. 3.4e-32;  
Matches 207; Conservative 0; Mismatches 71; Indels 12; Gaps 1;  
QY 1 atggcgctctggtgactgtggtcattgctctcaccctgcctcggtggtgcttgcctccccg 60  
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Db 70 ATGGCGCTCTGGGTGACTGCAGTCCTGGCTCTTGGCTTGGCTTGGTGGTCTGCGCGCCCA 129  
QY 61 agcc-----ctgtgactccctcccccacccctcaaggagctcattgaggagctg 108  
|||||  
Db 130 GGGCCGGTGCCCAAGATCTGTCTCTCCCTCTGACCCCTTAAGGAGCTTATTGAGGAGCTG 189  
QY 109 gtcaacatcaccagaatcaggcatccctctgcaacggcagcatggtgtggagcgtcaac 168  
|||||  
Db 190 AGCAACATCACACAAGACCAGACTCCCTGTGCAACGGCAGCATGGTATGGAGTGTGGAC 249  
QY 169 ctgaccgcccgcgtactgcgcagctctagaatctctgatcaatgtctccgactgcagc 228  
|||  
Db 250 CTGGCCGCTGGCGGTTCTGTGTAGCCCTGGATTCCCTGACCAACATCTCCAATTGCAAT 309  
QY 229 gccatccaaaggaccagagatgctgaaagcactgtgctctcaaaagcc 278  
|||||  
Db 310 GCCATCTACAGGACCCAGAGGATATTGCATGGCCCTCTGTAACCGCAAGGC 359

RESULT 14  
PCT-US93-07645A-3  
; Sequence 3, Application PC/TUS9307645A  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: Human Interleukin-13  
; NUMBER OF SEQUENCES: 6  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Macintosh 6.0.5  
; SOFTWARE: Microsoft Word 5.1a

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/07645A  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/012543  
FILING DATE: 01-FEB-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/010977  
FILING DATE: 29-JAN-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/933416  
FILING DATE: 21-AUG-1992  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1212 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
PCT-US93-07645A-3

Query Match 51.2%; Score 142.4; DB 5; Length 1212;  
Best Local Similarity 71.4%; Pred. No. 3.4e-32;  
Matches 207; Conservative 0; Mismatches 71; Indels 12; Gaps 1;  
QY 1 atggcgctctggtgactgtggtcattgctctcaccctgcctcggtggtgcttgcctccccg 60  
|||||  
Db 70 ATGGCGCTCTGGGTGACTGCAGTCCTGGCTCTTGGCTTGGCTTGGTGGTCTGCGCGCCCA 129  
QY 61 agcc-----ctgtgactccctcccccacccctcaaggagctcattgaggagctg 108  
|||||  
Db 130 GGGCCGGTGCCCAAGATCTGTCTCTCCCTCTGACCCCTTAAGGAGCTTATTGAGGAGCTG 189  
QY 109 gtcaacatcaccagaatcaggcatccctctgcaacggcagcatggtgtggagcgtcaac 168  
|||||  
Db 190 AGCAACATCACACAAGACCAGACTCCCTGTGCAACGGCAGCATGGTATGGAGTGTGGAC 249  
QY 169 ctgaccgcccgcgtactgcgcagctctagaatctctgatcaatgtctccgactgcagc 228  
|||  
Db 250 CTGGCCGCTGGCGGTTCTGTGTAGCCCTGGATTCCCTGACCAACATCTCCAATTGCAAT 309  
QY 229 gccatccaaaggaccagagatgctgaaagcactgtgctctcaaaagcc 278  
|||||  
Db 310 GCCATCTACAGGACCCAGAGGATATTGCATGGCCCTCTGTAACCGCAAGGC 359

RESULT 15  
PCT-US93-07645-3  
; Sequence 3, Application PC/TUS9307645  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: Human Interleukin-13  
; NUMBER OF SEQUENCES: 6  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Macintosh 6.0.5  
; SOFTWARE: Microsoft Word 5.1a  
; CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/07645  
FILING DATE: 19930818  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/012543  
FILING DATE: 01-FEB-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/010977  
FILING DATE: 29-JAN-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/933416  
FILING DATE: 21-AUG-1992  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1212 base pairs

; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
PCT-US93-07645-3

Query Match 51.2%; Score 142.4; DB 5; Length 1212;  
Best Local Similarity 71.4%; Pred. No. 3.4e-32;  
Matches 207; Conservative 0; Mismatches 71; Indels 12; Gaps 1;

QY	1	atggcgctctggtgactgtggtcattgctctcaccctgcctcggtggccttgccctccccg	60
Db	70	ATGGCGCTCTGGGTGACTGCAGTCTCTGGCTCTTGCTTGCCCTTGGTGGTCTCGCCGCCCCCA	129
QY	61	agcc-----ctgtgactccctcccccaaccctcaaggagctcattgaggagctg	108
Db	130	GGGCGGGTGCCCAAGATCTGTGTCTCTCCCTCTGACCCCTTAAGGAGCTTATTGAGGAGCTG	189
QY	109	gtcaacatcacccagaatcaggcatccctctgcaacggcagcatggtgtggagcgtaac	168
Db	190	AGCAACATCACACAAGACCAGACTCCCTGTGCAACGGCAGCATGGTATGGAGTGTGGAC	249
QY	169	ctgaccgccggcatgtactgcgagctctagaaatctctgatcaatgtctccgactgcagc	228
Db	250	CTGGCCGCTGGCGGGTTCTGTGTAGCCCTGGATTCCCTGACCAACATCTCCCAATTGCAAT	309
QY	229	gccatccaaaggaccagagatgctgaaagcactgtgctctcaaaaagcc	278
Db	310	GCCATCTACAGGACCCAGAGGATATTGCATGGCCTCTGTAAACCGCAAGGC	359

Search completed: May 13, 2001, 14:20:52  
Job time: 17803 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 13, 2001, 11:39:46 ; Search time 5997.24 Seconds  
(without alignments)  
404.959 Million cell updates/sec

Title: US-09-451-527-90  
Perfect score: 278  
Sequence: 1 atggcgctctgtgtgactgt.....gcactgtgctctcaaaagcc 278

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 9623517 seqs, 4368049070 residues

Total number of hits satisfying chosen parameters: 19247034

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:\*  
1: gb\_estl1:\*  
2: gb\_est2:\*  
3: gb\_est3:\*  
4: gb\_est4:\*  
5: gb\_est5:\*  
6: gb\_est6:\*  
7: gb\_est7:\*  
8: gb\_est8:\*  
9: gb\_est9:\*  
10: gb\_est10:\*  
11: gb\_est11:\*  
12: gb\_est12:\*  
13: gb\_est13:\*  
14: gb\_est14:\*  
15: gb\_est15:\*  
16: gb\_est16:\*  
17: gb\_est17:\*  
18: gb\_est18:\*  
19: gb\_est19:\*  
20: gb\_est20:\*  
21: gb\_est21:\*  
22: gb\_est22:\*  
23: gb\_est23:\*  
24: gb\_est24:\*  
25: gb\_est33:\*  
26: gb\_est34:\*  
27: gb\_est35:\*  
28: gb\_est36:\*  
29: gb\_est37:\*  
30: gb\_est38:\*  
31: gb\_est39:\*  
32: gb\_est40:\*  
33: em\_estba:\*  
34: em\_estfun:\*  
35: em\_esthum1:\*  
36: em\_esthum2:\*  
37: em\_esthum3:\*  
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177: em\_gss\_hum1:\*  
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188: em\_gss\_inv3:\*  
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190: em\_gss\_pln1:\*  
191: em\_gss\_pln2:\*  
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193: em\_gss\_rod1:\*  
194: em\_gss\_rod2:\*  
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198: em\_gss\_vrt1:\*  
199: em\_gss\_vrt2:\*  
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226: gb\_gss26:\*  
227: gb\_gss27:\*  
228: gb\_gss28:\*  
229: gb\_gss29:\*  
230: gb\_gss30:\*  
231: gb\_gss31:\*  
232: gb\_gss32:\*  
233: gb\_gss33:\*  
234: gb\_gss34:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	Score	Match	Length	DB	ID	Description
No.							
1		43.4	15.6	581	219	AZ305110	AZ305110 1M0005P05
2		40	14.4	463	24	AI712497	AI712497 UI-R-AF1-
C 3		37.8	13.6	994	231	CNS040ZX	AL300678 Tetraodon
4		36.8	13.2	576	141	BE907816	BE907816 601501924
5		36.6	13.2	329	146	BF292210	BF292210 WHE2208_A
6		36.4	13.1	277	137	BE593226	BE593226 WS1_99_B0
C 7		36.4	13.1	411	201	AQ001086	AQ001086 CIT-HSP-2
8		36.4	13.1	537	166	BE357229	BE357229 DGI_147_B
9		35.6	12.8	230	167	BE498968	BE498968 WHE0969_G
C 10		35.6	12.8	1070	136	BE536034	BE536034 601062471
C 11		35.2	12.7	177	103	AI909438	AI909438 IL-BT208-
12		35.2	12.7	570	24	AI746678	AI746678 ul06b05.y
13		35	12.6	359	17	AI209519	AI209519 b0e07a1.f
14		34.8	12.5	507	138	BE705147	BE705147 SC02_08f0
C 15		34.6	12.4	965	217	AZ201624	AZ201624 SP_0053_A
16		34.4	12.4	462	143	BF039993	BF039993 BP250023B
17		34.4	12.4	544	13	AA880435	AA880435 vw89f07.r
18		34.4	12.4	553	106	AU075583	AU075583 AU075583

19	34.4	12.4	700	113	AW318852	un08d12.y
20	34.4	12.4	712	115	AW475303	un64b04.y
21	34.4	12.4	1056	144	BF143984	601791238
22	34.2	12.3	477	151	BF625277	HVSMEA000
23	34.2	12.3	535	161	BE032541	131940 MA
24	34.2	12.3	546	161	BE032543	131942 MA
25	34.2	12.3	616	106	AU066538	AU066538
26	34.2	12.3	691	150	BF620464	HVSMEC001
27	34	12.2	341	163	BE127683	DEPA1432
28	34	12.2	370	166	BE363650	WS1_64_G1
29	34	12.2	562	166	BE361027	BS361027
30	34	12.2	704	230	CNS02PBO	
31	34	12.2	1122	141	BE889888	
32	33.8	12.2	498	150	BF606532	
33	33.6	12.1	537	29	AV387571	
34	33.6	12.1	727	164	BE216356	HV_CEB001
35	33.6	12.1	891	151	BF685554	602140603
36	33.6	12.1	902	106	AL522415	AL522415
37	33.4	12.0	619	173	BG112663	602282217
38	33.4	12.0	669	211	AQ780112	HS_3169_A
39	33.4	12.0	752	212	AQ849747	LMAJFV1_1
40	33.4	12.0	818	212	AQ849972	
41	33.2	11.9	462	164	BE228410	
42	33.2	11.9	487	22	AI598187	
43	33.2	11.9	616	15	AI062250	
44	33.2	11.9	621	175	C97983	
45	33.2	11.9	683	15	AI064071	

ALIGNMENTS

```
RESULT 1
AZ305110      581 bp      DNA      29-SEP-2000
LOCUS      1M0005P05R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION      clone UUGC1M0005P05 R, DNA sequence.
ACCESSION      AZ305110
VERSION      AZ305110.1 GI:10341800
KEYWORDS      house mouse.
SOURCE      Mus musculus
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE      1 (bases 1 to 581)
AUTHORS      Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
      Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Reilly
      ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
      and Wright,D.,Weiss,R.
TITLE      Mouse whole genome scaffolding with paired end reads from 10kb
      plasmid inserts
JOURNAL      Unpublished (2000)
COMMENT      Contact: Robert B. Weiss
      University of Utah Genome Center
      University of Utah
      Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
      84112, USA
      Tel: 801 585 5606
      Fax: 801 585 7177
      Email: ddunn@genetics.utah.edu
      Insert Length: 10000 Std Error: 0.00
      Plate: 0005 row: P column: 05
      Seq primer: CACACAGGAACACAGCTATGACC
      Class: plasmid ends
      High quality sequence stop: 581.
FEATURES      Location/Qualifiers
      source      1..581
      /organism="Mus musculus"
      /strain="C57BL/6J"
      /db_xref="taxon:10090"
      /clone="UUGC1M0005P05"
      /clone_lib="Mouse 10kb plasmid UUGC1M library"
      /sex="Male"
```

```
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gii4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
```

BASE COUNT 169 a 139 c 153 g 120 t  
ORIGIN

Query Match 15.6%; Score 43.4; DB 219; Length 581;  
Best Local Similarity 76.8%; Pred. No. 0.14;  
Matches 53; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 1 atggcgctctgtgactgtgtcattgtcctcactgcctcggtgccttgcctccccg 60  
|||||  
Db 513 ATGGCCCTCTGGTGACTGCAGTCCCTGGCTCTTGCTTGCTTGCTGCGCGCCCA 572

QY 61 agccctgtg 69  
| | | | |

Db 573 GGGCCGGTG 581

RESULT 2  
AI712497  
LOCUS AI712497 463 bp mRNA EST 08-JUN-1999  
DEFINITION UI-R-AF1-aap-b-12-0-UI.s1 UI-R-AF1 Rattus norvegicus cDNA clone  
 UI-R-AF1-aap-b-12-0-UI 3', mRNA sequence.  
ACCESSION AI712497  
VERSION AI712497.1 GI:5016297  
KEYWORDS EST.  
SOURCE Norway rat.  
ORGANISM Rattus norvegicus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.

REFERENCE 1 (bases 1 to 463)  
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.  
TITLE Normalization and subtraction: two approaches to facilitate gene  
 discovery  
JOURNAL Genome Res. 6 (9), 791-806 (1996)  
MEDLINE 97044477  
COMMENT Contact: Soares, MB  
 Program for Rat Gene Discovery and Mapping  
 University of Iowa  
 451 Eckstein Medical Research Building Iowa City, IA 52242, USA  
 Tel: 319 335 8250  
 Fax: 319 335 9565  
 Email: msoares@blue.weeg.uiowa.edu  
 Oligo-dT track not found, Not I site shown in beginning of sequence  
 is likely internal to the message. cDNA Library Preparation: M.B.  
 Soares Lab Clone distribution: clones will be available through  
 Research Genetics (www.resgen.com)  
 Seq primer: M13 Forward  
 POLYA=No. Location/Qualifiers  
 1..463  
 /organism="Rattus norvegicus"  
 /strain="Sprague-Dawley"

FEATURES source

















DH10B"		304 a	178 c	184 g	297 t	2 others	
BASE COUNT							
ORIGIN							
Query Match	12.4%;	Score 34.6;	DB 217;	Length 965;			
Best Local Similarity	50.3%;	Pred. NO. 39;					
Matches 85;	Conservative	0;	Mismatches 84;	Indels 0;	Gaps 0;		
QY	47	gccttgccctcccgagccctgtgtgactccctcccaacccctcaaggagctcattgaggagc	106				

Search completed: May 13, 2001, 11:39:51  
Job time: 16466 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 13, 2001, 14:16:12 ; Search time 9342.78 Seconds  
(without alignments)  
2055.246 Million cell updates/sec

Title: US-09-451-527-91  
Perfect score: 1302  
Sequence: 1 ctacgacctgcctgctcttc.....aaaaaaaaaaaaaaaaaaaa 1302

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1283235 seqs, 7373929652 residues  
Total number of hits satisfying chosen parameters: 2566470

Minimum DB seq length: 0  
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

- GenEmbl:\*
- 1: gb\_bal:\*
- 2: gb\_ba2:\*
- 3: gb\_ba3:\*
- 4: gb\_in1:\*
- 5: gb\_in2:\*
- 6: gb\_in3:\*
- 7: gb\_om:\*
- 8: gb\_ov:\*
- 9: gb\_pat1:\*
- 10: gb\_pat2:\*
- 11: gb\_ph:\*
- 12: gb\_pl1:\*
- 13: gb\_pl2:\*
- 14: gb\_pl3:\*
- 15: gb\_pl4:\*
- 16: em\_bal:\*
- 17: em\_ba2:\*
- 18: em\_fun:\*
- 19: em\_htgo\_hum:\*
- 20: em\_htgo\_inv:\*
- 21: em\_htgo\_rod:\*
- 22: em\_htg\_hum1:\*
- 23: em\_htg\_hum2:\*
- 24: em\_htg\_hum3:\*
- 25: em\_htg\_hum4:\*
- 26: em\_htg\_hum5:\*
- 27: em\_htg\_hum6:\*
- 28: em\_htg\_hum7:\*
- 29: em\_htg\_hum8:\*
- 30: em\_htg\_inv1:\*
- 31: em\_htg\_inv2:\*
- 32: em\_htg\_Other:\*
- 33: em\_htg\_rod:\*
- 34: em\_hum1:\*
- 35: em\_hum2:\*
- 36: em\_hum3:\*
- 37: em\_hum4:\*
- 38: em\_hum5:\*
- 39: em\_hum6:\*
- 40: em\_hum7:\*
- 41: em\_in:\*
- 42: em\_om:\*
- 43: em\_or:\*

- 44: em\_ov:\*
- 45: em\_pat:\*
- 46: em\_ph:\*
- 47: em\_pl:\*
- 48: em\_ro:\*
- 49: em\_sts:\*
- 50: em\_sy:\*
- 51: em\_un:\*
- 52: em\_vi:\*
- 53: gb\_sts1:\*
- 54: gb\_sts2:\*
- 55: gb\_sts3:\*
- 56: gb\_sy:\*
- 57: gb\_un:\*
- 58: gb\_vil:\*
- 59: gb\_vil2:\*
- 60: gb\_htg1:\*
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- 83: gb\_htg24:\*
- 84: gb\_htg25:\*
- 85: gb\_prl:\*
- 86: gb\_pr2:\*
- 87: gb\_pr3:\*
- 88: gb\_pr4:\*
- 89: gb\_pr5:\*
- 90: gb\_pr6:\*
- 91: gb\_pr7:\*
- 92: gb\_pr8:\*
- 93: gb\_pr9:\*
- 94: gb\_rol:\*
- 95: gb\_ro2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1302	100.0	1302	7	AF244915 Canis fam
2	890	68.4	213343	78	AF276990 Canis fam
3	408.4	31.4	213343	78	AF276990 Canis fam
4	378	29.0	1270	93	L06801 Homo sapien
5	378	29.0	1282	92	X69079 H.sapiens 1
6	378	29.0	1290	10	I34548 Sequence 1
7	376.4	28.9	1297	9	A29948 Coding sequ
8	376.4	28.9	1297	10	I58488 Sequence 15
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10	232.2	17.8	3520	7	AJ132441 Bos tauru
11	219.8	16.9	343	7	AF072807 Bos tauru









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QY 642 gccagccgggtgcccctcctcgtcgtcacttcaacacgctgagggaaagcactgcatt 701
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Db 113727 GCCAGCGGGTGGCCTTCCTCCGCTGCACCTTCATCAACGCTGAGGAAAGCACTGCAT 113786

QY 702 cccatgactgtccccctcctcagagcaaatgcagcattacagtgaggagagatatgtgtg 761
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Db 113787 CCCATGACTGTCCCTCCTCAGAGCAAAGTGCAGCATTACAGTGGAGGCAGATATGTGTG 113846

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Db 113847 GGAGGGGTCTTGCTGTACCTGGGAGTGGCACAGACATGTTTCTTCTAAGCCTTATTAT 113906

QY 822 tattgtgtgtatttaacaaagtgtctttgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgag 881
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QY 882 ctg9ggggccagtgactcgg9gttttagagagagtcctcctgggaataagcactgtgtgtaaaatt 941
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QY 942 ctgctacctcactggggtcctggg9ccgacacaggggacaggggacagggagaaaggtcagagatgc 1001
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Db 114027 CTGCTACCTCACTGGGATCGTGGGGCCGACACAGGGGACAGGAGAAAGGTCAGAGATGC 114086

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Db 114087 TGCTGT 114092
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RESULT 4
HUMIL13A HUMIL13A 1270 bp mRNA PRI 22-JUL-1993
LOCUS Homo sapiens interleukin 13 mRNA, complete cds.
DEFINITION L06801
ACCESSION L06801
VERSION L06801.1 GI:186275
KEYWORDS cytokine; growth factor; interleukin 13; regulatory protein.
SOURCE Homo sapiens cDNA to mRNA.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1270)
AUTHORS McKenzie,A.N.J., Culpepper,J.A., de Waal Malefyt,R., Briere,F.,
Punnonen,J., Aversa,G., Sato,A., Dang,W., Cocks,B.G., Menon,S., de
Vries,J.E., Banchereau,J. and Zurawski,G.R.
TITLE Interleukin-13, a T cell-derived cytokine that regulates human
monocyte and B cell function
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 90, 3735-3739 (1993)
MEDLINE 93234572
FEATURES
source Location/Qualifiers
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/db_xref="taxon:9606"
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polyA_site 1270
BASE COUNT 288 a 335 c 336 g 311 t
ORIGIN

Query Match 29.0%; Score 378; DB 93; Length 1270;
Best Local Similarity 66.2%; Pred. No. 3.9e-71;
Matches 780; Conservative 0; Mismatches 290; Indels 108; Gaps 12;

QY 21 cctcgctcctcgtcattggctcgtgggtcccatggcgctcgtggtgactgtggtcattgc 80
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QY 81 tctcaactgcctcgtggtgacctcctccctcccgagccctgtgactcctcccccacacctcaa 140
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QY 141 ggagctcattgaggagctggtcaacatcacccagaatc---aggcatccctctctgcaacgg 197
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Db 134 GGAGCTCATTTGAGGAGCTGGTCAACATCACCCAGAACCCAGAGAGGCTCCGCTCTGCAATGG 193

QY 198 cagcatggtgtgagcgtcaacctgaccgcccggcgtgctactgctgagcgtctagaaatctct 257
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Db 194 CAGCATGGTATGGAGCATCAACCTGACAGCTGGCATGTACTGTGACGCCCTGGAATCCCT 253

QY 258 gatcaatgtctccgactgcagcgccatccaaaaggacccagaggtgctgaaagcactgtg 317
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Db 254 GATCAACGTGTCAAGCTGCAGTGGSCAGTTTCCAGCTTGCAATGTCCGAGACACCAAAATCGA 313

QY 318 ctctcaaaagccccgaggcaggtccaggtccagtgaaacgcagccgagacacacaaaattga 377
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Db 314 CCGCACAAAGGTCTCAGCTGGSCAGTTTCCAGCTTGCAATGTCCGAGACACCAAAATCGA 373

QY 378 agtgatccagttggtgaaaaaacctgctcacctatgtaaagggagtttatcgccatggaaa 437
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Db 374 GGTGGCCCACTTTGTAAAGGACCTGCTCTTACATTTAAAGAAACTTTTCGCGAGGGACG 433

QY 438 ttccagatgaagcatgaaaaaacttagcatccttatctgtagacca-gacctgaccactta 496
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QY 497 agttccagattcatttttcttcgacgtcacaaaatttcttagggaggtggggg----- 551
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QY 609 ctgagccccagccacccctgccttggtgcatggggccacgcccgggtgcccctcctcgtc- 667
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Db 609 ----AGCCGACCTCAGCCTTCCCTTGGCCAGGGCTCAGCCTGGTGGGCTCCTCTGTGCC 664

QY 668 ----tgcacttcataacgctgagggaaagcactgcataccatgactgtccccctcctcag 723
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Db 665 AGGGCCCTGAGCTCGGTGGACCCAGGGATGACATGTCCCTACACCCCTCCCTGCCCCTAG 724

QY 724 agcaaatgacagcattacagtggagg-----cagatatgtgtgggagggg----- 769
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Db 725 AGCACACTGTAGCATTACAGTGGGTGCCCCCTTGGCCAGACATGTGTTGGGACAGGGACC 784

QY 770 -----tcttgctgtacctgggagtggtggcacagacatgtttcttcttagcctta 816
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Db 785 CACTTCACACACAGGCAACTGAGGCAGACAGCAGCTCAGGCACACTTCTTCTTGGTCTTA 844

QY 817 ttattattgtgtgtattttaaacaaagtgtctttgtgtgtgtgtgtgtgtgtgtgtgtgtg--- 873
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QY 1009 gtcctgccactcagcagctggccctcagccaagcagtaatttatgttttctctgtattt 1068
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Db 1085 GTCTGCCAGCCAGCAGCCAGCTCTCAGCCAAACGAGTAATTTATTTGTTTCTCCTCGTATT 1144

QY 1069 aaagttaagaaaataataatgttatcaaaagagttaata 1106
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ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 384)  
AUTHORS Caput,D., Ferrara,P., Guillemot,J., Kaghad,M., Labit-Le  
Boutellier,C., Leplatois,P., Magazin,M. and Minty,A.  
TITLE Protein having interleukin.13 activity, recombinant DNA coding for  
this protein, transformed cells and microorganisms  
JOURNAL Patent: US 5652123-A 17 29-JUL-1997;  
FEATURES Location/Qualifiers  
source 1..384  
/organism="unknown"  
BASE COUNT 97 a 104 c 99 g 84 t  
ORIGIN

Query Match 16.1%; Score 209.4; DB 10; Length 384;  
Best Local Similarity 76.3%; Pred. No. 5.1e-35;  
Matches 271; Conservative 0; Mismatches 81; Indels 3; Gaps 1;

QY 106 tccccgagccctgtgactccctcccccaaccctcaaggagctcattgaggagctggtcaac 165  
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QY 166 atcacccagaatc---aggcatccctctgcaacggcagcagcatgggtgtggagcgtcaacctg 222  
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Db 76 ATCACCCAGAACCCAGAGGCTCGCTCTGCAATGGCAGCATGGTATGGAGCATCAACCTG 135

QY 223 accgcccgatgtactgcgagctctagaatctctgatcaatgtctccgactgcagcgcc 282  
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Db 136 ACAGCTGACATGTACTGTGCAGCCCTGGAAATCCCTGATCAACGTGTGAGGCTGCAGTGCC 195

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Db 196 ATCGAGAAGACCCAGAGGATGCTGAGCGGATCTGCCCGCACAAAGGTCTCAGCTGGGCAG 255

QY 343 atttccagtgaaacgcagccgagacaccaaattgaagtgtccagttgtgtaaaaacctg 402  
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Db 256 TTTTCCAGCTTGCATGTCCGAGACACCAAAATCGAGGTGGCCCCAGTTTGTAAAGGACCTG 315

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RESULT 14  
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LOCUS AR027065 425 bp DNA PAT 29-SEP-1999  
DEFINITION Sequence 4 from patent US 5856142.  
ACCESSION AR027065  
VERSION AR027065.1 GI:5937905  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 425)  
AUTHORS Legoux,R., Maldonado,P. and Salome,M.  
TITLE Method for the extraction of periplasmic proteins from prokaryotic  
microorganisms in the presence of arginine  
JOURNAL Patent: US 5856142-A 4 05-JAN-1999;  
FEATURES Location/Qualifiers  
source 1..425  
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BASE COUNT 100 a 116 c 110 g 99 t  
ORIGIN

Query Match 15.9%; Score 207.6; DB 9; Length 425;  
Best Local Similarity 75.7%; Pred. No. 1.3e-34;  
Matches 271; Conservative 0; Mismatches 84; Indels 3; Gaps 1;

QY 103 gcctccccgagccctgtgactccctcccccaaccctcaaggagctcattgaggagctggtc 162  
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QY 163 aacatcacccagaatc---aggcatccctctgcaacggcagcagcatgggtgtggagcgtcaac 219  
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QY 340 cagatttccagtgaacgcagccgagacaccaaattgaagtgtatccagttggtgaaaaaac 399  
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RESULT 15  
I86198  
LOCUS I86198 425 bp DNA PAT 10-JUN-1998  
DEFINITION Sequence 4 from patent US 5700665.  
ACCESSION I86198  
VERSION I86198.1 GI:3205916  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 425)  
AUTHORS Legoux,R., Maldonado,P. and Salome,M.  
TITLE Method for the extraction of periplasmic proteins from prokaryotic  
microorganisms in the presence of arginine  
JOURNAL Patent: US 5700665-A 4 23-DEC-1997;  
FEATURES Location/Qualifiers  
source 1..425  
/organism="unknown"  
BASE COUNT 100 a 116 c 110 g 99 t  
ORIGIN

Query Match 15.9%; Score 207.6; DB 10; Length 425;  
Best Local Similarity 75.7%; Pred. No. 1.3e-34;  
Matches 271; Conservative 0; Mismatches 84; Indels 3; Gaps 1;

QY 103 gcctccccgagccctgtgactccctcccccaaccctcaaggagctcattgaggagctggtc 162  
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Db 55 GCCTTCGCTGGCCCTGTGCCTCCCACTGCTGAGGAGCTGAGGAGCTGAGGAGCTGGTC 114

QY 163 aacatcacccagaatc---aggcatccctctgcaacggcagcagcatgggtgtggagcgtcaac 219  
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Db 115 AACATCACCCAGAACCCAGAGGCTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAAC 174

QY 220 ctgaccgcccggcatgtactgcgagctctagaatctctgatcaatgtctccgactgcagc 279  
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Db 235 GCCATCGAGAAGACCCAGAGGATGCTGAGCGGATTTCTGCCCGCACAAAGGTCTCAGCTGGG 294

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Search completed: May 13, 2001, 14:20:29  
Job time: 19109 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 13, 2001, 14:28:54 ; Search time 472.02 Seconds  
(without alignments)  
1610.278 Million cell updates/sec

Title: us-09-451-527-91  
Perfect score: 1302  
Sequence: 1 ctacgacctgcctgtcttc.....aaaaaaaaaaaaaaaa 1302

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 678276 seqs, 291890651 residues

Total number of hits satisfying chosen parameters: 1356552

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Match	Length	ID	Description
1	1302	100.0	1302	21	Canine interleukin
2	1302	100.0	1302	21	Canine interleukin
3	1251	96.1	1269	21	Canine interleukin
4	1251	96.1	1269	21	Canine interleukin
5	393	30.2	393	21	Canine interleukin
6	393	30.2	393	21	Canine interleukin
7	378	29.0	1270	21	Human low adenosin
8	378	29.0	1270	21	Human adenosine re
9	378	29.0	1282	21	Human low adenosin
10	378	29.0	1282	21	Human adenosine re
11	378	29.0	1290	15	Sequence encoding

12	378	29.0	6952	21	F21333
13	378	29.0	6952	21	A35211
14	378	29.0	14978	21	F21338
15	378	29.0	14978	21	A35216
16	377	29.0	390	21	Z55563
17	377	29.0	390	21	Z55564
18	374.8	28.8	1297	13	Q28947
19	333	25.6	333	21	Z55559
20	333	25.6	333	21	Z55560
21	317	24.3	330	21	Z55565
22	317	24.3	330	21	Z55566
23	278	21.4	278	21	Z55554
24	272	20.9	272	21	Z55553
25	207	15.9	1212	15	Q56693
26	203.4	15.6	336	13	Q28944
27	201.8	15.5	336	13	Q28943
28	169	13.0	5670	21	F21331
29	169	13.0	5670	21	F21337
30	169	13.0	5670	21	A35209
31	169	13.0	5670	21	A35215
32	150	11.5	166	21	Z55552
33	72.2	5.5	612	21	C98862
34	71.2	5.5	202	21	C98563
35	70.2	5.4	2323	19	V59524
36	70	5.4	4064	21	A07587
37	69.6	5.3	2604	21	A48576
38	69.4	5.3	1377	21	C98083
39	69.4	5.3	3712	21	F21873
40	69.2	5.3	1984	20	X52252
41	68.8	5.3	1835	20	X27245
42	68.4	5.3	1740	21	Z36914
43	68.4	5.3	1801	21	Z36893
44	68.2	5.2	2517	21	C90463
45	68.2	5.2	2549	10	N91467

ALIGNMENTS

RESULT 1  
Z55555  
ID Z55555 standard; cDNA; 1302 BP.  
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AC Z55555;  
XX  
DT 14-MAR-2000 (first entry)  
XX  
DE Canine interleukin-13 (IL-13) clone 80 cDNA.  
XX  
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;  
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.  
XX  
OS Canis familiaris.  
XX  
FH Key Location/Qualifiers  
FT CDS 52..447  
FT /\*tag= a  
FT /product= "Canine IL-13 clone 80"  
XX  
PN WO9961618-A2.  
XX  
PD 02-DEC-1999.  
XX  
PF 28-MAY-1999; 99WO-US11942.  
XX  
PR 29-MAY-1998; 98US-0087306.  
XX  
PA (HESK-) HESKA CORP.  
XX  
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;  
XX WPI; 2000-072623/06.  
DR P-PSDB; Y58221.







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Canis familiaris.
Key      Location/Qualifiers
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WO9961618-A2.

02-DEC-1999.

28-MAY-1999; 99WO-US11942.

29-MAY-1998; 98US-0087306.

(HESK - ) HESKA CORP.

Slm G, Yang S, Dreitz MJ, Wonderling RS;

WPI; 2000-072623/06.

1577001, 9993 1

**Nucleic acids encoding immunoregulatory proteins from cats or dogs, useful for treating or preventing e.g. tumors or autoimmune disease**

Claim 11; Page 235-236; 264pp; English.

Sequences Z5552-255560 and Z55561-255566 represent cDNA sequences encoding canine interleukin-13 (IL-13) clones 80 and 78 respectively. The invention relates to canine

IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline

interferon- $\alpha$  (IFN- $\alpha$ ) and feline granulocyte macrophage colony-stimulating factor (GM-CSF), and nucleotides which encode these

immunoregulatory proteins. The proteins, their associated

nucleic acids, specific antibodies and inhibitors may be used as

vaccines for therapeutic or prophylactic regulation of an immune response in animals (particularly cats, dogs, horses and humans).

They may be used to treat autoimmune or infectious diseases including allergies, tumours, inflammation and graft rejection, and to increase

the response from a co-administered antigen. The nucleotide sequences can also be used for the recombinant production of a protein, while

nucleotide fragments are useful as probes, as amplification primers and as sources of inhibitory therapeutics (e.g., antisense oligonucleotides)

The proteins may be used to raise antibodies and to screen for modulators of activity, while the antibodies may be used in detection,

Sequence 1269 BP; 302 A; 320 C; 340 G; 307 T; 0 other;

Query Match	96.1%	Score 1251;	DB 21;	Length 1269;
Best Local Similarity	99.8%	Pred. No. 7.1e-254;		
Matches 1264;	Conservative	0;	Mismatches 0;	Indels 3;
				Gaps 1;

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— — — — —

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Qy 61 tggttgactgtggtcattgctctcacctgcctcggccttgcctccccgagccctgtg 120

Db 66 tgggtgactgtgggtcattgctctcacctgcctcggtggccttgcctccccgagccctgtg 125

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Db 126 actccctcccccaacctcaaggagctcattgaggagctggtcaacatcaccagaatcag 185

Qy 241 gcagctctagaatctctgatcaatgtctccgactgcagcqcacatccaaaagqaccagagq 300

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Db	306	atgctgaaagcactgtgctctcaaaagcccgcggcgagg- -gattccagtgaaacgcagc	362
QY	361	cgagacacaaaaattgaagtgcacagttgggtgaaaaaacctgctcacctatgttaagggga	420
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QY	421	gtttatcgccatggaaaatttcagatgaagcatgaaaaacttagcatccttatctgtagacc	480
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QY	481	cagacctgaccacttaagtccagattcattttttttccgcagcgtcacaaaaatttcttagg	540
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QY	541	gaggtgggggggggagaaacatttctcagctgggacctaagcctgcacgcctgcct	600
Db	543	gaggtgggggggggagaaacatttctcagctgggacctaagcctgcacgcctgcct	602
QY	601	ccatggagctgagcccgagccacccctgccttggtgcatggggcccagccgggtggccctc	660
Db	603	ccatggagctgagcccgagccacccctgccttggtgcatggggcccagccgggtggccctc	662
QY	661	ctcgtctgcacttcatcaacgctgagggaagcactgcattcccccatgactgtccccctct	720
Db	663	ctcgtctgcacttcatcaacgctgagggaagcactgcattcccccatgactgtccccctct	722
QY	721	cagagcaaaagtgcagcattacagtgaggagcagatatgtgtgggaggggtcttgcgtgac	780
Db	723	cagagcaaaagtgcagcattacagtgaggagcagatatgtgtgggaggggtcttgcgtgac	782
QY	781	ctgggagtgccacagacatgtttcttcttagccttatttatttattgtgtgtattttaaac	840
Db	783	ctgggagtgccacagacatgtttcttcttagccttatttatttattgtgtgtattttaaac	842
QY	841	aagtgtctttgtgtgctggggacagggagtgcttgagcctggggcccagtgactcg	900
Db	843	aagtgtctttgtgtgctggggacagggagtgcttgagcctggggcccagtgactcg	902
QY	901	ggtttagagagtcctcctgggaataagcactgtgtgtataaattctgtacctcactgggac	960
Db	903	ggtttagagagtcctcctgggaataagcactgtgtgtataaattctgtacctcactgggac	962
QY	961	ctggggccgacacaggggacagggagaaaaaggtcagagatgctgctcttgtctgccactca	1020
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QY	1021	gcagctggccctcagccaaagcagtaatttattgttttcttctgtatttaaagttaagaaa	1080
Db	1023	gcagctggccctcagccaaagcagtaatttattgttttcttctgtatttaaagttaagaaa	1082
QY	1081	taaaaatatgtatcaaaagagtttaataatatatagaagagtagcctaaaaaggctgcatttg	1140
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QY	1141	gtgtgtgtggccaggccggggtgggggggaggggtgtgttgcactgaatgtgctcttt	1200
Db	1143	gtgtgtgtggccaggccggggtgggggggaggggtgtgttgcactgaatgtgctcttt	1202
QY	1201	cactgacttttgtcaaacctggaagccagaaaaataaagatgggtgacaagagaaaaaaaaaa	1260
Db	1203	cactgacttttgtcaaacctggaagccagaaaaataaagatgggtgacaagagaaaaaaaaaa	1262
QY	1261	aaaaaaaa 1267	
Db	1263	aaaaaa 1269	

## RESULT 4



Z55562/c  
ID 255562 standard; cDNA; 1269 BP.  
XX  
AC Z55562;  
XX  
DT 14-MAR-2000 (first entry)  
XX  
DE Canine interleukin-13 (IL-13) clone 78 cDNA complement.  
XX  
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;  
immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.  
XX  
OS Canis familiaris.  
XX  
FH Key Location/Qualifiers  
FT CDS complement (821..1213)  
FT /\*tag= a  
FT /product= "Canine IL-13 clone 78"  
XX  
PN WO9961618-A2.  
XX  
PD 02-DEC-1999.  
XX  
PF 28-MAY-1999; 99WO-US11942.  
XX  
PR 29-MAY-1998; 98US-0087306.  
XX  
PA (HESK-) HESKA CORP.  
XX  
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;  
XX  
DR WPI; 2000-072623/06.  
DR P-PSDB; Y58223.  
XX  
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
PT useful for treating or preventing e.g. tumors or autoimmune disease  
XX  
PS Claim 1i; Page 237-238; 264pp; English.  
XX  
CC Sequences Z55552-Z55560 and Z55561-Z55566 represent cDNA  
CC sequences encoding canine interleukin-13 (IL-13) clones 80  
CC and 78 respectively. The invention relates to canine  
CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or  
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline  
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage  
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these  
CC immunoregulatory proteins. The proteins, their associated  
CC nucleic acids, specific antibodies and inhibitors may be used as  
CC vaccines for therapeutic or prophylactic regulation of an immune  
CC response in animals (particularly cats, dogs, horses and humans).  
CC They may be used to treat autoimmune or infectious diseases including  
CC allergies, tumours, inflammation and graft rejection, and to increase  
CC the response from a co-administered antigen. The nucleotide sequences  
CC can also be used for the recombinant production of a protein, while  
CC nucleotide fragments are useful as probes, as amplification primers and  
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
CC The proteins may be used to raise antibodies and to screen for  
CC modulators of activity, while the antibodies may be used in detection,  
CC and in drug targeting.  
XX  
SQ Sequence 1269 BP; 307 A; 340 C; 320 G; 302 T; 0 other;

Query Match 96.1%; Score 1251; DB 21; Length 1269;  
Best Local Similarity 99.8%; Pred. No. 7.1e-254;  
Matches 1264; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

Qy 1 ctacgacctgcctgctcttccctcgctcctcctgcatggctctgggtccatggcgctc 60  
|||||  
Db 1264 CTACGACCTGCTCTTCCCTCGCTCCTCGATTGGCTCTGGGCTCCATGGCGCTC 1205  
|||||  
Qy 61 tgggtgactgtggtcattgctctcacctgcctcggtggccttgccctcccccagccctgtg 120  
|||||

Db 1204 TGGTTGACTGTGGTCATTGCTCTCACCTGCCTCGGTGGCCTTGCTTCCCGAGCCCTGTG 1145  
Qy 121 actccctcccaaccctcaaggagctcattgaggagctggtcaacatcacccagaatcag 180  
|||||  
Db 1144 ACTCCCTCCCAACCCTCAAGGAGCTCATTGAGGAGCTGGTCAACATCACCCAGAATCAG 1085  
Qy 181 gcatccctctgcaacggcagcatggtgtggagcgtcaacacctgaccgcggcgaatgtactgc 240  
|||||  
Db 1084 GCATCCCTCTGCAACGGCAGCATGGTGTGGAGCGTCAACCTGACCGCGGCATGTACTGC 1025  
Qy 241 gcagctctagaatctctgatcaatgtctccgactgcagcgccatcccaaggaccagagg 300  
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Db 1024 GCAGCTCTAGAATCTCTGATCAATGTCTCCGACTGCAGCGCCATCCAAAGGACCCAGAGG 965  
Qy 301 atgtgaaagcactgtgctctcaaaagcccgcgaggcagagatttccagtgaaacgcagc 360  
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Db 964 ATGCTGAAAGCACTGTGCTCTCAAAAGCCCGCGGAGG---GATTTCCAGTGAACGCAGC 908  
Qy 361 cgagacacacaaaattgaagtgatccagttggtgaaaaaacctgctcacctatgtaaggga 420  
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Db 907 CGAGACACCAAAATTGAAGTGATCCAGTTGGTGAAAAACCTGCTCACCTATGTAAAGGGA 848  
Qy 421 gttatcgccatggaatttcagatgaagcatgaaaacttagcatccttatctgtagacc 480  
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Db 847 GTTTATCGCCATGGAATTTCAGATGAAGCATGAAAAACTTAGCATCCTTATCTGTAGACC 788  
Qy 481 cagacctgaccacttaagtccagattcaattttcttccgacgtcaaaaatttcttagg 540  
|||||  
Db 787 CAGACCTGACCACCTTAAGTTCCAGATTCAATTTTCTTTCCGACGTCACAAATTTCTTAGG 728  
Qy 541 gagtgggggggggagaaaccatttccctcagctgggacacctcagcctgcacgcctgcct 600  
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Db 727 GAGGTGGGGGGGGGAGAACCATTTCTCAGCTGGGACCTCAGCCCTGCACCGCCTGCCT 668  
Qy 601 ccattggagctgagccacgcaacccctgccttggctgcatggggccagccgggtggccctc 660  
|||||  
Db 667 CCATGGAGCTGAGCCACCCACCCCTGCTTGGTGCATGGGGCCACAGCCGGTGGCCCTC 608  
Qy 661 ctccgtctgcacttcatcaacgctgagggaaagcactgcatacccatgactgtccccctcct 720  
|||||  
Db 607 CTCCGTCTGCACTTCATCAACGCTGAGGAAAGCACTGCATCCCATGACTGTCCCTCCT 548  
Qy 721 cagagaaaagtgcagcattacagtgaggcagatatgtgtgggaggggtcttctgtgtac 780  
|||||  
Db 547 CAGAGCAAAAGTGCAGCATTACAGTGGAGGCAGATATGTGTGGAGGGGTCTTGTGTATC 488  
Qy 781 ctgggagtggcacagacatgtttcttcttagccttatttattattgtgtatttataaac 840  
|||||  
Db 487 CTGGGAGTGGCACAGACATGTTTCTTTTAGCCCTTATTTATTTGTTGTTATTTAAAC 428  
Qy 841 aagtctcttgttctgtgctggggacagggagtggtgagctggggggccagtgactcg 900  
|||||  
Db 427 AAGTGTCTTTGTTGTGTGGGACAGGAGTGGCTTGGAGCTGGGGGCCAGTGACTCG 368  
Qy 901 ggttagagagtcctcctgggaataagcactgtgtgtaaaattctgctacctcactgggac 960  
|||||  
Db 367 GGTTAGAGAGTCCCTGGGAATAAGCACTGTGTGTAATAATTCGTCTACCTCACTGGGATC 308  
Qy 961 ctggggccgacacaggggacaggaaggggtcagagatgctgctctgtctgctgccactca 1020  
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Db 307 CTGGGGCCGACACAGGGGACAGGAGAAAGGTCAGAGATGCTGCTCTTGTCTGCCACTCA 248  
Qy 1021 gcagctggccctcagccaaagcagtaatttattgttttctccttgatttaaagtaagaa 1080  
|||||  
Db 247 GCAGCTGGCCCTCAGCCCAAGCAGTAATTTATTGTTTTTCTCTTGTATTTAAAGTAAAGAA 188  
Qy 1081 taaaatatgttatcaaaagagttaataatatatagaagagtagcctaaaggctgcatgtg 1140  
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Db 187 TAAATATGTTATCAAAAGAGTTAATAATATATATAGAGAGTAGCCTAAAGAGGCTGCATTTG 128  
Qy 1141 gtgtgtgtggccagggcggggtggggggggagggtgtgtgtcactgaatgtgctcttt 1200  
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Db 127 GTGTGTGTGGCCAGGCCGGGGGGGTGGGGGGGGAGGGGTGTTGTCTACTGAATGTGCTCTTT 68



QY 1201 cactgacttgtcaaacaggcagaaataaagatgtgacaagagaaaaa 1260  
|||||  
Db 67 CACTGACTTTGTCAAACTGGAAGCCAGAAATAAAGATGGTGACAAGAAAAA 8  
QY 1261 aaaaaa 1267  
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Db 7 AAAAAA 1

RESULT 5  
Z55557  
ID Z55557 standard; cDNA; 393 BP.  
XX  
AC Z55557;  
XX  
DT 14-MAR-2000 (first entry)  
XX  
DE Canine interleukin-13 (IL-13) clone 80 cDNA coding region.  
XX  
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;  
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.  
XX  
OS Canis familiaris.  
XX  
PN WO9961618-A2.  
XX  
PD 02-DEC-1999.  
XX  
PF 28-MAY-1999; 99WO-US11942.  
XX  
PR 29-MAY-1998; 98US-0087306.  
XX  
PA (HESK-) HESKA CORP.  
XX  
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;  
XX  
DR WPI; 2000-072623/06.  
DR P-PSDB; Y58221.  
XX  
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
PT useful for treating or preventing e.g. tumors or autoimmune disease  
XX  
PS Claim 11; Page 232-233; 264pp; English.  
XX  
CC Sequences Z55552-Z55560 and Z55561-Z55566 represent cDNA  
CC sequences encoding canine interleukin-13 (IL-13) clones 80  
CC and 78 respectively. The invention relates to canine  
CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or  
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline  
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage  
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these  
CC immunoregulatory proteins. The proteins, their associated  
CC nucleic acids, specific antibodies and inhibitors may be used as  
CC vaccines for therapeutic or prophylactic regulation of an immune  
CC response in animals (particularly cats, dogs, horses and humans).  
CC They may be used to treat autoimmune or infectious diseases including  
CC allergies, tumours, inflammation and graft rejection, and to increase  
CC the response from a co-administered antigen. The nucleotide sequences  
CC can also be used for the recombinant production of a protein, while  
CC nucleotide fragments are useful as probes, as amplification primers and  
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
CC The proteins may be used to raise antibodies and to screen for  
CC modulators of activity, while the antibodies may be used in detection,  
CC and in drug targeting.  
XX  
SQ Sequence 393 BP; 93 A; 118 C; 100 G; 82 T; 0 other;

Query Match 30.2%; Score 393; DB 21; Length 393;  
Best Local Similarity 100.0%; Pred. No. 8.2e-74;  
Matches 393; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 atggcgctctgttgactgtggtcattgtctcactgcctcggtggcctgcctccccg 111  
|||||  
Db 1 atggcgctctgttgactgtggtcattgtctcactgcctcggtggcctgcctccccg 60  
QY 112 agccctgtgactccctcccaaccctcaaggagctcattgaggagctggccaacatcacc 171  
|||||  
Db 61 agccctgtgactccctcccaaccctcaaggagctcattgaggagctggccaacatcacc 120  
QY 172 cagaatcaggcatccctctgcaacggcagcatggtgtggagcgtcaacctgaccgcggc 231  
|||||  
Db 121 cagaatcaggcatccctctgcaacggcagcatggtgtggagcgtcaacctgaccgcggc 180  
QY 232 atgtactgcgagctctagaaatctctgataatgtctccgactgcagcgcatccaaagg 291  
|||||  
Db 181 atgtactgcgagctctagaaatctctgataatgtctccgactgcagcgcatccaaagg 240  
QY 292 acccagaggatgctgaaagcactgtgctctcaaaagcccgaggcagattccagt 351  
|||||  
Db 241 acccagaggatgctgaaagcactgtgctctcaaaagcccgaggcagattccagt 300  
QY 352 gaacgcagcgagacacacaaattgaagtatccagttggtgaaaaaacctgctcacctat 411  
|||||  
Db 301 gaacgcagcgagacacacaaattgaagtatccagttggtgaaaaaacctgctcacctat 360  
QY 412 gtaaggggagtttatcgccatggaaatttcaga 444  
|||||  
Db 361 gtaaggggagtttatcgccatggaaatttcaga 393

RESULT 6  
Z55558/c  
ID Z55558 standard; cDNA; 393 BP.  
XX  
AC Z55558;  
XX  
DT 14-MAR-2000 (first entry)  
XX  
DE Canine interleukin-13 (IL-13) clone 80 cDNA coding region complement.  
XX  
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;  
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.  
XX  
OS Canis familiaris.  
XX  
PN WO9961618-A2.  
XX  
PD 02-DEC-1999.  
XX  
PF 28-MAY-1999; 99WO-US11942.  
XX  
PR 29-MAY-1998; 98US-0087306.  
XX  
PA (HESK-) HESKA CORP.  
XX  
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;  
XX  
DR WPI; 2000-072623/06.  
DR P-PSDB; Y58221.  
XX  
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
PT useful for treating or preventing e.g. tumors or autoimmune disease  
XX  
PS Claim 11; Page 233; 264pp; English.  
XX  
CC Sequences Z55552-Z55560 and Z55561-Z55566 represent cDNA  
CC sequences encoding canine interleukin-13 (IL-13) clones 80  
CC and 78 respectively. The invention relates to canine  
CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or  
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline  
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage  
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these  
CC immunoregulatory proteins. The proteins, their associated  
CC nucleic acids, specific antibodies and inhibitors may be used as



```

Db 254 gatcaacgtgtcaggctgcagtgccatgcagaaagacccagaggtgctgagcggattctg 313
Qy 318 ctctcaaaaagcccgaggcagagatttccagtgaacgcagccgagacacacaaaattga 377
Db 314 ccgcacaaggctcagctggcaggttttccagcttgcatgtccgagacacaaaatcga 373
Qy 378 agtgatccagttggtgaaaaaacctgctcacctatgtaaggaggagtttatcgccatgaaa 437
Db 374 ggtggccagtttgtaaaggacctgctcttacatttaagaaaacttttctgcgagggacg 433
Qy 438 ttccagatgaagcatgaaaaacttagcatccttatctgtagaccca-gacctgacactta 496
Db 434 gttcaactgaaacttcgaa---agcatcattatttcagagacagacctgactattga 489
Qy 497 agttccagattcatttttcttccgacgtcacaaatttcttagggaggtggggg---- 551
Db 490 agttgcagattcatttttcttcttgatgtcaaaatgtcttggttagcgggaaggaggg 549
Qy 552 ---gggggagaaacatttccctcagctgggacctcagccctgcacccgctgcctccatggag 608
Db 550 ttagggagggttaaaattccttagcttagacctagacctagcctgtgtgcctcttcagcct- 608
Qy 609 ctgagccacagccacctgccttgggtgcattggggccacgggtggccctcctccgtc- 667
Db 609 ----agccgacctcagccttcccttgcgccagggtcagcctggtggcctcctctgtcc 664
Qy 668 ----tgcacttcatcaacgctgagggaaagcactgcacatcccatgactgtccctcctcag 723
Db 665 agggccctgagctcgggtggaccaggggatgacatgtcccctacacccctccctgcctag 724
Qy 724 agcaaagtcagcattacagtggagg-----cagatatgtgtgggaggggg---- 769
Db 725 agcacactgtgacattacagtgggtgcccccttgcacagacatgtggtggacaggggacc 784
Qy 770 -----tcttgctgtacctggagtgagcagacagacagcagcagcacttcttcttgctta 816
Db 785 cacttcacacacaggcgaactgaggcagacagacagcagcagcacttcttcttgctta 844
Qy 817 ttattattgtgtgtattttaaaagaagtgtcttctgtgtgtgctgggacagggagt- 873
Db 845 ttattattgtgtgtattttaaatgagtgtgttctgtcacctgtgggattggggaagact 904
Qy 874 -----gcttgagctgggggccccagtgactcgggttaga----- 908
Db 905 gtggctgtgacacttgagccaaagggttcagagactcaggccccagcactaaaagcagt 964
Qy 909 -----gagtcacctgggaataagcactgtgtgtaaaattctgctacctcactgggat 959
Db 965 ggacccccaggagtccttgtaataagtaactgtgtacagaattctgctacctcactgggt 1024
Qy 960 cctggggcc-----gacacaggggacagggagaaagggtcagagatgctgctctt 1008
Db 1025 cctggggcctcggagcctcatccgaggcaggtcaggtcaggaggggcagaaacgcgctcct 1084
Qy 1009 gtctgccactcagcagctggccctcagccaaagcagtaatttattgttttctctgtattt 1068
Db 1085 gtctgccagccagcagcagctctcagccaaagcagtaatttattgttttctctgtattt 1144
Qy 1069 aaagttaagaaataataatgttatcaaaagagttaata 1106
Db 1145 aa-----atattaaatatgttagcaaaagagttaata 1175
```

RESULT 8  
A35212  
ID A35212 standard; DNA; 1270 BP.  
XX  
AC A35212;  
XX

DT 28-JUL-2000 (first entry)

XX Human adenosine receptor related polynucleotide 2nd SEQ ID NO:86.  
DE

```

XX Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW phosphorothioate; impaired respiration; inflammation; allergy;
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX Homo sapiens.
OS
XX WO200009525-A2.
PN
XX 24-FEB-2000.
PD
XX 03-AUG-1999; 99WO-US17712.
XX
PR 03-AUG-1998; 98US-0095212.
XX
PA (UYEC-) UNIV EAST CAROLINA.
XX
PI Nyce JW;
XX
DR WPI; 2000-205971/18.
XX
PT New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstriction, inflammation, allergies, asthma, hypertension,
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers
XX
PS Disclosure; Page 1251-1252; 1343pp; English.
XX
CC The present invention describes a new composition comprising an antisense
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antiasthmatic, cytostatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
CC impeded respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC carcinomas, and cancers which may metastasise to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of the
CC ONs reduces side effects. The A-containing ONs break down with the
CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. A32313 to A3512 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last
CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences
CC differ from the previously named sequences. SEQ ID NO:11 to 1680 (A32323
CC to A33992) are specifically claimed ONs from the present invention.
CC N.B. Sequences given in the disclosure of the present invention do not
CC match up with their corresponding SEQ ID NO: sequences given in the
CC sequence listing.
XX
SQ Sequence 1270 BP; 288 A; 335 C; 336 G; 311 T; 0 other;
```

Query Match 29.0%; Score 378; DB 21; Length 1270;  
Best Local Similarity 66.2%; Pred. No. 1.6e-70;  
Matches 780; Conservative 0; Mismatches 290; Indels 108; Gaps 12;

```

Qy 21 cctcgctcctcctgcattggctctggggtcccatggcgctctggtgactgtggtcattgc 80
   |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 14 cctcaatcctctcctgtgtggcactgggcctcatggcgcttttgtgaccacggtcattgc 73
   |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Qy 81 tctcaactgcctcggtggccttgctccctcccgagccctgtgactccctcccaaccctcaa 140
   |||| |||| || || || || || || || || || || || || || || || || || ||
Db 74 tctcaactgcttgccggcgttgcttgcctcccgaggccctgtgcctcctctacagcctcag 133
```



QY 141 ggagctcattgaggagctggtcaacatcacccagaatc---aggcatccctctctgcaacgg 197  
|||||  
Db 134 ggagctcattgaggagctggtcaacatcacccagaacccagaaggctccgctctgcaatgg 193  
QY 198 cagcatggtgtgagcgtcaacctgaccgcccgcgtactgctgagcagctctagaatctct 257  
|||||  
Db 194 cagcatggtatggagcatcaacctgacagctggcatgtactgtcagccctggaatccct 253  
QY 258 gatcaatgtctccgactgcaggccatccaaaggacccagaggatgctgaaagcactgtg 317  
|||||  
Db 254 gatcaacgtgtcaggctgcagtgccatcgagaagacccagaggatgctgagcggattctg 313  
QY 318 ctctcaaaagcccgccgagcagatctccagtgaaacgcagccgagacaccaaattga 377  
|||  
Db 314 cccgcacaaggtctcagctggcaggttttccagcttgcatgtccgagacaccaaatacga 373  
QY 378 agtgatccagttggtgaaaaaacctgctcaccttatgttaaggggagtttatcgccatggaaa 437  
|||  
Db 374 ggtgcccagtttgtaaaggacctgctcttacatttaaagaaacttttctcgaggagcg 433  
QY 438 tttcagatgaagcatgaaaaacttagcatccttatctgtagaccca-gacctgaccactta 496  
|||||  
Db 434 gttcaactgaaactcgaa---agcatcattatttgcagagacagacctgactattga 489  
QY 497 agttccagattcatttttcttcgcagctcacaaatttctlaggaggtggggg---- 551  
|||||  
Db 490 agttgcagattcatttttcttctgtatgtcaaaatgtcttggtagcggaaggagg 549  
QY 552 ---gggggagaacacatttctcagctgggacctcagcctgacccgcctgcctccatggag 608  
|||  
Db 550 ttagggagggtaaaaattccttagcttagacctcagcctgctgctcccgtcttcagcct- 608  
QY 609 ctgagcccagccacctgcttgggtgcatggggcccagccgggtgcccctcctccgctc- 667  
|||  
Db 609 ----agccgacctcagccttcccttgcccagggtcagcctggtggcctcctctgtgc 664  
QY 668 ----tgcacttcatacagctgagggaaagcactgcatacccatgactgtcccctcctcag 723  
|  
Db 665 agggccctgagctcgtggaccacagggtgacatgtccctacacccctccctgccttag 724  
QY 724 agcaaagtgcagcattacagtggagg-----cagatatgtgtggaggggg---- 769  
|||||  
Db 725 agcacactgtagcattacagtgggtgcccccttgcccaggtcagcctggtggcctcctgtgc 784  
QY 770 -----tcttgctgtacactgggagtgggcccagtgactcgggtttaga----- 908  
|||  
Db 785 cacttcacacacaggaactgaggcagacagcagctcagcagcacttcttcttggcttta 844  
QY 817 ttattattgtgtattataaacaagtgtcttcttgttctgctggggacagggagtg--- 873  
|||||  
Db 845 ttattattgtgtattataaagtgtgttctgacccgttgggattggggaagact 904  
QY 874 -----gcttgagactggggggcccagtgactcgggtttaga----- 908  
|||||  
Db 905 gtggctgctggcacttggagccaaagggttcagagactcaggggcccagcactaaagcagt 964  
QY 909 -----gagtcacctgggaataagcactgtgtgtataaattctgctacctcactgggat 959  
|||||  
Db 965 ggacccaggaggtccctggtaataagactgtgttacagaattctgctacctcactggggt 1024  
QY 960 cctgggggccc-----gacacagggggacagggagaaagggtcagagatgctgctctt 1008  
|||||  
Db 1025 cctgggggctcgagcctcatccgagggcagggtcaggagagggggcagaacagcgctcct 1084  
QY 1009 gtctgccactcagcagctggccctcagccaaagcagtaatttatgttttctctgtattt 1068  
|||||  
Db 1085 gtctgccagccagcagcctcagcctcagccaaagcagtaatttatgttttctctgtattt 1144  
QY 1069 aaagttaagaaataaataatgttatcaaaagagttaata 1106  
|||  
Db 1145 aa-----atattaaataatgttagcaaaagagttaata 1175

RESULT 9  
F21332  
ID F21332 standard; DNA; 1282 BP.  
XX  
XX F21332;  
DT 14-MAR-2001 (first entry)  
XX  
DE Human low adenosine antisense oligonucleotide related sequence #2899.  
XX  
KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;  
human; airway disorder; bronchoconstriction; lung inflammation;  
surfactant depletion; respiratory; bronchodilator; antiinflammatory;  
immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;  
respiratory obstruction; pulmonary obstruction; impeded respiration;  
surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;  
respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;  
pulmonary hypertension; emphysema; pulmonary transplantation rejection;  
chronic obstructive pulmonary disease; pulmonary infection; bronchitis;  
cancer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200062736-A2.  
XX  
PD 26-OCT-2000.  
XX  
PF 24-MAR-2000; 2000WO-US08020.  
XX  
PR 06-APR-1999; 99US-0127958.  
XX  
PA (UYEC-) UNIV EAST CAROLINA.  
PA (NYCE/) NYCE J W.  
PI Nyce JW;  
XX  
DR WPI; 2000-679539/66.  
XX  
PT Low adenosine (A) content antisense oligonucleotides which do not  
PT trigger adenosine receptors during metabolism, useful e.g. for treating  
PT cancers and respiratory obstructions -  
PS  
XX Disclosure; Page 1333-1334; 1592pp; English.  
CC The present invention describes low adenosine (A) content antisense  
CC oligonucleotides and compositions (I) comprising them. In the antisense  
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.  
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,  
CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.  
CC The antisense oligonucleotides and (I) can be used to down-regulate the  
CC expression and or activity of target polypeptides associated with  
CC lung/respiratory disorders and malignancies, such as stimulating and  
CC activating peptide factors and transmitters, transcription factors,  
CC immunoglobulins and antibodies, antibody receptors, cytokines and  
CC chemokines, endogenously produced specific and non-specific enzymes,  
CC binding proteins, adhesion molecules and their receptors, cytokine and  
CC chemokine receptors, adenosine receptors, bradykinin receptors, central  
CC nervous system (CNS) and peripheral nervous and non-nervous system  
CC receptors, CNS and peripheral nervous and non-nervous system peptide  
CC transmitters, defensins, growth factors, vasoactive peptides and  
CC receptors, binding proteins and malignancy associated proteins. The  
CC antisense oligonucleotides may be used in this way to treat disorders  
CC including respiratory obstruction (especially pulmonary obstruction  
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)  
CC and/or surfactant hypoproduction which are associated with a disease or  
CC condition selected from pulmonary vasoconstriction, inflammation,  
CC allergies, asthma, impeded respiration, respiratory distress syndrome  
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary  
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),  
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,  
CC and/or cancer. F18434 to F21543 represent human polynucleotide fragments  
CC and antisense oligonucleotides used in the exemplification of the



CC present invention.  
XX  
SQ Sequence 1282 BP; 293 A; 341 C; 337 G; 311 T; 0 other;  
  
Query Match 29.0%; Score 378; DB 21; Length 1282;  
Best Local Similarity 66.2%; Pred. No. 1.6e-70;  
Matches 780; Conservative 0; Mismatches 290; Indels 108; Gaps 12;  
  
Qy 21 cctcgctcctcctgcaattggctctgggctccatggcgtctctggtgactgtggtcattgc 80  
Dbb 26 cctcaatcctcctcctgctggcactggcctcctcctcctcctcctcctcctcctcctc 85  
  
Qy 81 tctcacctgcctcctggtggccttgccctcccgagccctgtgactccctccccaacctcaa 140  
Dbb 86 tctcacttgccctggcggttggcctcccccagggcctgtgctcctctacagccctcag 145  
  
Qy 141 ggagctcattgagagctggtcaacatcacccagaatc--aggcatccctctgcaacgg 197  
Dbb 146 ggagctcattgagagctggtcaacatcacccagaaccagaaggctcctcctgcaatgg 205  
  
Qy 198 cagcatggtgtggagcgtcaaacctgacccgcccgcctgactgctgagcgtctagaaatctct 257  
Dbb 206 cagcatggtatggagcatcaacctgacagctgacagctgactgtgacgacctggaatccct 265  
  
Qy 258 gatcaatgtctcctgactgcagcgccatccaaaagacccagaggtgctgaaagcactgtg 317  
Dbb 266 gatcaacgtgtcagctgcagtgccatcgagagacccagaggtgctgagcgattctg 325  
  
Qy 318 ctctcaaaagcccgggcagggcagattttccagtgaacgcagccgagacacacaaaattga 377  
Dbb 326 ccgcacaaaggtctcagctggcgagttttccagctgcatgtccgagacacacaaaatcga 385  
  
Qy 378 agtgatccagttggtgaaaaaacctgctcacctatgtaaggggagtttatcgccatggaaa 437  
Dbb 386 ggtggcccagtttgtaaaggacctgtctttacatttaaaagaaactttttcgcgagggacg 445  
  
Qy 438 tttcagatgaagcatgaaaacttagcatccttatctgtagaccca-gacctgacacactta 496  
Dbb 446 gttcaactgaaacttcgaa---agcatcattatttgcagagacagacctgactattga 501  
  
Qy 497 agttccagattcatttttttccgacgtcacaaaatttcttagggaggtggggg----- 551  
Dbb 502 agttgcagattcatttttcttctgtatgtcaaaaatgtcttggttagggggaaggagg 561  
  
Qy 552 ---gggggagaaacatttccctcagctgggacctcagcctgcacccgctgcctccatggag 608  
Dbb 562 ttaggggagggttaaaattccttagcttagacctcagcctgtgctgcccgtcttcagcct- 620  
  
Qy 609 ctgagcccagcccccctgccttggtgcatggggcccgagccgggtggccctcctccgtc- 667  
Dbb 621 ---agccagcctcagccttcccccttgcccaggggtcagcctggtggcctcctctgtcc 676  
  
Qy 668 ----tgacttcaacagctgaggggaaagcaactgcatcccatgactgtccctcctcag 723  
Dbb 677 agggccctgagctcgtgtggaccagggtgacatgtccctacacccctccctgcccctag 736  
  
Qy 724 agcaaatgacagcattacagtggagg-----cagatatgtgtgggaggggg----- 769  
Dbb 737 agcacactgtagcattacagtgggtgcccccttgccagacatgtggtggagacagggacc 796  
  
Qy 770 -----tcttgctgtacctgggagtgggcacagacatgtttcttcttagcctta 816  
Dbb 797 cacttcacacacagggcaactgagggcacagacagcagctcaggcacacttctcttggtctta 856  
  
Qy 817 tttattattgtgtgtattttaaacaagtgtctttgtgtgtgtgtgggacagggagtg--- 873  
Dbb 857 tttattattgtgtgtattttaaatgagtgtgtttgtaccctgtgggattggggaagact 916  
  
Qy 874 -----gcttggagctgggggccccagtgactcgggttaga----- 908  
Dbb 917 gtggctgtggcactgtggagccaaagggttcagagactcaggggccccagcactaaagcagt 976

Qy 909 -----gagtcctcctgggaataagcactgtgtgtataaaattctgctacctcactgggat 959  
Dbb 977 ggacccccaggagtccttgtaataagtaactgtgtacagaattctgctacctcactggggt 1036  
  
Qy 960 cctgggggc-----gacacaggggacagaggagaaaggggtcagagatgctgctctt 1008  
Dbb 1037 cctggggcctcgagcctcatccgagcgaggtcaggagaggggcagaaacagccgctcct 1096  
  
Qy 1009 gtctgccactcagcagctggccctcagcccaagcagtaattattgttttctcctgtattt 1068  
Dbb 1097 gtctgccagccagcagcagctctcagcccaacgagtaattattgttttctcctgtattt 1156  
  
Qy 1069 aaagttaagaaaaataaatatgtttatcaaaagagtttaata 1106  
Dbb 1157 aa-----atattaatatgttagcaaaagagtttaata 1187  
  
RESULT 10  
A35210  
ID A35210 standard; DNA; 1282 BP.  
XX  
AC A35210;  
XX  
DT 28-JUL-2000 (first entry)  
XX  
DE Human adenosine receptor related polynucleotide 2nd SEQ ID NO:84.  
XX  
KW Human; adenosine receptor; low adenosine antisense oligonucleotide;  
KW phosphorothioate; impaired respiration; inflammation; allergy;  
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;  
KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;  
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;  
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;  
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;  
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200009525-A2.  
XX  
PD 24-FEB-2000.  
XX  
PF 03-AUG-1999; 99WO-US17712.  
XX  
PR 03-AUG-1998; 98US-0095212.  
XX  
PA (UYEC-) UNIV EAST CAROLINA.  
XX  
PI Nyce JW;  
XX  
DR WPI; 2000-205971/18.  
XX  
PT New antisense oligonucleotides useful for treating e.g. pulmonary  
PT vasoconstriction, inflammation, allergies, asthma, hypertension,  
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or  
PT cancers -  
XX  
PS Disclosure; Page 1249-1250; 1343pp; English.  
XX  
CC The present invention describes a new composition comprising an antisense  
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets  
CC nucleic acids involved in bronchoconstriction, allergies, and/or  
CC inflammation. The ON can have antiinflammatory, antiallergic,  
CC antiasthmatic, cytostatic and analgesic activities. The compositions are  
CC useful for the treatment of diseases associated with inflammation,  
CC impaired airways, including lung disease and diseases whose secondary  
CC effects afflict the lungs of a subject. They can be used for treating  
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,  
CC impeded respiration, respiratory distress syndrome, pain, cystic  
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive  
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,  
CC carcinomas, and cancers which may metastasize to the lungs, including  
CC breast and prostate cancer. The reduction of the adenosine content of the











PT bronchitis, emphysema, respiratory distress syndrome, ischemia or  
PT cancers  
XX  
PS Disclosure; Page 1250-1251; 1343pp; English.  
XX  
CC The present invention describes a new composition comprising an antisense  
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets  
CC nucleic acids involved in bronchoconstriction, allergies, and/or  
CC inflammation. The ON can have antiinflammatory, antiallergic,  
CC antiasthmatic, cytostatic and analgesic activities. The compositions are  
CC useful for the treatment of diseases associated with inflammation,  
CC impaired airways, including lung disease and diseases whose secondary  
CC effects afflict the lungs of a subject. They can be used for treating  
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,  
CC impeded respiration, respiratory distress syndrome, pain, cystic  
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive  
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,  
CC carcinomas, and cancers which may metastasise to the lungs, including  
CC breast and prostate cancer. The reduction of the adenosine content of the  
CC ONs reduces side effects. The A-containing ONs break down with the  
CC release of deoxyadenosine which activates adenosine receptors causing  
CC bronchoconstriction and inflammation. A3213 to A35312 represent the  
CC nucleotide sequences given in the sequence listing from the present  
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last  
CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences  
CC differ from the previously named sequences. SEQ ID NO:11 to 1680 (A32323  
CC to A33992) are specifically claimed ONs from the present invention.  
CC N.B. Sequences given in the disclosure of the present invention do not  
CC match up with their corresponding SEQ ID NO: sequences given in the  
CC sequence listing.

XX  
SQ Sequence 6952 BP; 1536 A; 2017 C; 1919 G; 1480 T; 0 other;

Query Match 29.0%; Score 378; DB 21; Length 6952;  
Best Local Similarity 66.2%; Pred. No. 2.7e-70;  
Matches 780; Conservative 0; Mismatches 290; Indels 108; Gaps 12;

Qy 21 cctcgctcctcctgcatgttgctggctccatggcgctctgttgactgtggtcattgc 80  
Db 5696 cctcaatcctctcctgttgacactgggcctcatggcgcttctgttgaccacggtcattgc 5755  
Qy 81 tctcacctgcctcgttggtggccttgcctccccgagccctgtgactccctccccacccctcaa 140  
Db 5756 tctcacctgccttggcggttgcctccccagccctgtgctcctctacagccctcag 5815  
Qy 141 ggagctcattgagagctggtcaacatcacccagaatc---aggcatccctctgcaacgg 197  
Db 5816 ggagctcattgagagctggtcaacatcacccagaacccagaaggctccgctctgcaatgg 5875  
Qy 198 cagcatggtgtgagcgtcaacactgaccgcgcggtactgtactgcgagctctagaatctct 257  
Db 5876 cagcatggtatggagcatcaacctgacagctggcatgtactgtgcagccctggaaatcct 5935  
Qy 258 gatcaatgtctcgcgactgcagcgccatccaaaggaccagaggatgctgaaagcactgtg 317  
Db 5936 gatcaacgtgtcaggctgcagtgccatcgagaagaccagaggatgctgagcggattctg 5995  
Qy 318 ctctcaaaaagccgcggcagggcagatttccagtgaaacgcagccgagacaccaaattga 377  
Db 5996 ccgcacaaaggctcagctgggcagtttccagcttgcagctgcatgctccgagacaccaaattcga 6055  
Qy 378 agtgatccagttggtgaaaaacactgctcacctatgtaaaggggagtttatcgccatgaaa 437  
Db 6056 ggtggccagtttgtaaaggacctgctcttacattaaagaaacttttctcgagggagc 6115  
Qy 438 ttctcagatgaagcatgaaaacttagcatccttattctgtagaccca-gacctgaccactta 496  
Db 6116 gttcaactgaaacttcgaa---agcatcattatttgacagacagggacctgactattga 6171  
Qy 497 agttccagattcatttttcttccgacgtcacaaatttcttagggaggtggggg---- 551  
Db 6172 agttgcagattcatttttcttctctgatgtcaaaaatgtcttggttaggcgggaaggaggg 6231

Qy 552 ---ggggagagaaccatttctcagctgggagacctcagcctgcacccgcctgcctccatggag 608  
Db 6232 ttaggggagggtataaattctcttagcttagacctcagcctgtgtgcctgtcttcagcct- 6290  
Qy 609 ctgagccagagccacccctgccttggctgcatggggcccgagccgggtggccctcctccgtc- 667  
Db 6291 ---agcgacctcagccttcccttggccagggctcagcctggtgggctcctctctgtcc 6346  
Qy 668 ---tgacctcatcaacgctgagggaaagcactgcatcccatgactgtccccctcctcag 723  
Db 6347 agggccctgagctcgtggaccacgggatgacatgtccctacacccctccctcctgacctag 6406  
Qy 724 agcaaatgcagcattacagtggagg-----cagatatgtgtgggagggg---- 769  
Db 6407 agcacactgtagcattacagtgggtgcccccttgcacacatgtgtgtgggacagggacc 6466  
Qy 770 -----tcttgcgtgtacctgggggcccagtgactcggttttaga----- 908  
Db 6467 cacttcacacacaggaactgaggcagacagcagcagcagcagcacttcttcttcttctta 816  
Qy 817 ttattattgtgtgtattttaaacaagtgtcttcttcttcttcttcttcttcttcttcttctt 873  
Db 6527 ttattattgtgtgtattttaaagtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 6586  
Qy 874 -----gcttgagctgggggcccagtgactcggttttaga----- 908  
Db 6587 gtggctgctggcacttgagccaaaggttccagagactcagggccccagcactaaagcagt 6646  
Qy 909 -----gagtcctcctgggaataagcactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 959  
Db 6647 ggaccccgaggagtccttgtaataagtactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 6706  
Qy 960 cctgggggc-----gacacaggggagacaggaaggggtcagagatgctgtcttt 1008  
Db 6707 cctggggcctcggagcctcatccgagcgaggtcaggggtcagagaggggcagaaagcgcctct 6766  
Qy 1009 gtctgacctcagcagctggccctcagccaaagcagtaatttattgttttcttctgtattt 1068  
Db 6767 gtctgcccagcagcagcagctctcagcctcagcaaacagtaatttattgttttcttctgtattt 6826  
Qy 1069 aaagttaagaaataaaatatgttatcaaaagagttaata 1106  
Db 6827 aa-----atattaaatatgttagcaaaagagttaata 6857

RESULT 14  
F21338

ID F21338 standard; DNA; 14978 BP.

XX

AC F21338;

XX

DT 14-MAR-2001 (first entry)

XX

DE Human low adenosine antisense oligonucleotide related sequence #2905.

XX

KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;

KW human; airway disorder; bronchoconstriction; lung inflammation;

KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;

KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;

KW respiratory obstruction; pulmonary obstruction; impeded respiration;

KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;

KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;

KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;

KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;

KW cancer; ss.

XX Homo sapiens.

OS

XX WO200062736-A2.

PN

XX 26-OCT-2000.

PD

XX

PF 24-MAR-2000; 2000WO-US08020.  
XX  
PR 06-APR-1999; 99US-0127958.  
XX  
XX (UYEC-) UNIV EAST CAROLINA.  
PA (NYCE/) NYCE J W.  
XX  
PI Nyce JW;  
XX  
DR WPI; 2000-679539/66.  
XX  
XX Low adenosine (A) content antisense oligonucleotides which do not  
PT trigger adenosine receptors during metabolism, useful e.g. for treating  
PT cancers and respiratory obstructions  
XX  
PS Disclosure; Page 1339-1343; 1592pp; English.  
XX  
CC The present invention describes low adenosine (A) content antisense  
CC oligonucleotides and compositions (I) comprising them. In the antisense  
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.  
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,  
CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.  
CC The antisense oligonucleotides and (I) can be used to down-regulate the  
CC expression and or activity of target polypeptides associated with  
CC lung/respiratory disorders and malignancies, such as stimulating and  
CC activating peptide factors and transmitters, transcription factors,  
CC immunoglobulins and antibodies, antibody receptors, cytokines and  
CC chemokines, endogenously produced specific and non-specific enzymes,  
CC binding proteins, adhesion molecules and their receptors, cytokine and  
CC chemokine receptors, adenosine receptors, bradykinin receptors, central  
CC nervous system (CNS) and peripheral nervous and non-nervous system  
CC receptors, CNS and peripheral nervous and non-nervous system  
CC transmitters, defensins, growth factors, vasoactive peptides and  
CC receptors, binding proteins and malignancy associated proteins. The  
CC antisense oligonucleotides may be used in this way to treat disorders  
CC including respiratory obstruction (especially pulmonary obstruction  
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)  
CC and/or surfactant hypoproduction which are associated with a disease or  
CC condition selected from pulmonary vasoconstriction, inflammation,  
CC allergies, asthma, impeded respiration, respiratory distress syndrome  
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary  
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),  
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,  
CC and/or cancer. F18434 to F21543 represent human polynucleotide fragments  
CC and antisense oligonucleotides used in the exemplification of the  
CC present invention.  
XX  
SQ Sequence 14978 BP; 3793 A; 3676 C; 3696 G; 3813 T; 0 other;

Query Match 29.0%; Score 378; DB 21; Length 14978;  
Best Local Similarity 66.2%; Pred. No. 3.3e-70;  
Matches 780; Conservative 0; Mismatches 290; Indels 108; Gaps 12;

QY 21 cctgcgtcctcctgcattggcttgggctccatggcgctctgtgtgactgtgtgactgtgtcattgc 80  
DB 14 cctcaatcctctcctgttggcactgggcctcatggcgcttttgtgaccacgggtcattgc 73

QY 81 tctcacctgcctcgttggccttgcctccccgagccctgtgactcccccccccaacctcaa 140  
DB 74 tctcacttgccttggcgttggctccccagggccctgtgcctccccctctacagccctcag 133

QY 141 ggagctcattgaggagctggtcaacatcacccagaaac---aggcatccctctgcaacgg 197  
DB 134 ggagctcattgaggagctggtcaacatcacccagaaacagaggtccgctctgcaatgg 193

QY 198 cagcatggtgtgagcgtcaacctgaccgcccggcatgtactgcgagagctctagaaatctct 257  
DB 194 cagcatggtatggagcatcaacctgacagctggcatgtactgtgacgcccctggaatccct 253

QY 258 gatcaatgtctccgactgcagcgccatcccaaggaccagaggtactgctgaaagcactgtg 317  
DB 254 gatcaacgtgtcagggtcagtgccatcgcagaagaccagaggtactgctgagcggtattctg 313

QY 318 ctctcaaaaagcccgccaggggcagattttccagtgaaacacgagccgagacacacaaaattga 377  
DB 314 cccgcacaaaggtctcagctgggcagttttccagcttgcatgtccgagacacacaaaatcga 373

QY 378 agtgatccagttggtgaaaaacctgctcacctatgtaaagggagtttatcgccatggaaa 437  
DB 374 ggtggcccgagttttaaaggacctgctcttacatttaaagaaactttttcgcgaggagc 433

QY 438 tttcagatgaagcatgaaaaacttagcatccttatctgtagaccca-gacctgaccactta 496  
DB 434 gttcaactgaaacttcgaa---agcatcattatttgcagagacagacctgactattga 489

QY 497 agttccagattcatttttttttccgacgtcacaaaatttcttagggaggtgggggg---- 551  
DB 490 agttgcagattcatttttttttctgtatgtcaaaaaatgtcttgggtagcggggaaggagg 549

QY 552 ---gggggagaaacatttctcagctgggacctcagcctcagcctgacccgctgcctccatggag 608  
DB 550 ttaggggaggggtaaaaattccttagcttagacctcagcctgctgtgctgccttctcagcct- 608

QY 609 ctgagcccgagccacccctgcttggctgcatggggcccgagcggtggccctcctccgtc- 667  
DB 609 ---agcgacctcagccttcccccttggccagggctcagcctggtggccctcctctgtcc 664

QY 668 ---tgcacttcatcaacgctgaggggaaagcactgcacccatgactgtccccctcctcag 723  
DB 665 agggccctgagctcgtggaccacgggatgacatgtccctacacccctccccctgccttag 724

QY 724 agcaaaagtgcagcattacagtggagg-----cagatatgtgtgggagggg---- 769  
DB 725 agcacactgtagcattacagtgggtgcccccttgccagacatgtggtggacagggacc 784

QY 770 -----tcttgtgtacctgggagtggtggcagacacatgtttcttcttagcctta 816  
DB 785 cacttcacacagggcaactgaggcagacagcagctcagggcacttcttcttggctta 844

QY 817 tttattattgtgtgtattttaaacaaagtgtcttgtttgtgctgggggacagggagtg--- 873  
DB 845 tttattattgtgtgtattttaaatagtggtgtttgtcaccgttgggattggggaagact 904

QY 874 -----gcttggagctggggggcccgactgactcgggttaga----- 908  
DB 905 gtggctgctggcacttggagccaaagggttcagagactcagggccccagcactaaaagcagt 964

QY 909 -----gagtcctcctgggaataagcactgtgtgtataaaattctgtacctcactgggat 959  
DB 965 ggaccccgaggtccctggtaataagtactgtgtacagaattctgtacctcactggggt 1024

QY 960 cctgggggccc-----gacacaggggacagggagaaaaggttcagagatgctgctctt 1008  
DB 1025 cctggggcctcggagcctcatccgagggcagggtcaggagagggggcagaacagccgctcct 1084

QY 1009 gtctgccactcagcagctggccctcagccaagcagtaatttattgttttctctgtattt 1068  
DB 1085 gtctgccagccagcagcagctctcagccaacgagtaatttattgttttctctgtattt 1144

QY 1069 aaagttaagaaaataaataatgttatcaaaagagtttaata 1106  
DB 1145 aa-----atattaaatatgttagcaaaagagtttaata 1175

RESULT 15  
A35216  
ID A35216 standard; DNA; 14978 BP.  
XX  
AC A35216;  
XX  
DT 28-JUL-2000 (first entry)  
XX  
DE Human adenosine receptor related polynucleotide 2nd SEQ ID NO:90.  
XX  
KW Human; adenosine receptor; low adenosine antisense oligonucleotide;



Search completed: May 13, 2001, 14:29:52  
Job time: 18307 sec

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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: May 13, 2001, 14:20:52 ; Search time 226.02 Seconds  
(without alignments)  
1005.808 Million cell updates/sec

Title: US-09-451-527-91  
Perfect score: 1302  
Sequence: 1 ctacgacctgcctgctcttc.....aaaaaaaaaaaaaaaaaaaa 1302

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 302621 seqs, 87301344 residues

Total number of hits satisfying chosen parameters: 605242

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_NA: \*  
1: /cgnl\_7/ptodata/1/ina/5A\_COMB.seq: \*  
2: /cgnl\_7/ptodata/1/ina/5B\_COMB.seq: \*  
3: /cgnl\_7/ptodata/1/ina/6A\_COMB.seq: \*  
4: /cgnl\_7/ptodata/1/ina/6B\_COMB.seq: \*  
5: /cgnl\_7/ptodata/1/ina/PCTUS\_COMB.seq: \*  
6: /cgnl\_7/ptodata/1/ina/backfiles1.seq: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	378	29.0	1290	1	US-08-012-543-1
2	378	29.0	1290	5	PCT-US93-07645A-1
3	378	29.0	1290	5	PCT-US93-07645-1
4	376.4	28.9	1297	1	US-08-371-121-15
5	209.4	16.1	384	1	US-08-371-121-17
6	207.6	15.9	425	1	US-08-594-469-4
7	207.6	15.9	425	2	US-08-906-957-4
8	207.6	15.9	4410	1	US-08-594-469-1
9	207.6	15.9	4410	2	US-08-906-957-1
10	207	15.9	1212	1	US-08-012-543-3
11	207	15.9	1212	5	PCT-US93-07645A-3
12	207	15.9	1212	5	PCT-US93-07645-3
13	203.4	15.6	336	1	US-08-371-121-24
14	201.8	15.5	336	1	US-08-371-121-2
15	176	13.5	447	1	US-08-371-121-26
16	68.2	5.2	2550	6	5258287-23
17	68	5.2	1023	1	US-08-252-966B-16
18	67.8	5.2	1882	4	US-09-370-253-1
19	67.2	5.2	2447	2	US-09-014-969-14
20	67.2	5.2	7218	1	US-08-232-463-14
21	67	5.1	1817	1	US-08-473-981A-5
22	67	5.1	1817	2	US-08-474-087-5
23	66.4	5.1	903	5	PCT-US95-06406A-21
24	66	5.1	1512	2	US-08-909-965C-8
25	65.8	5.1	1066	1	US-08-157-101A-4
26	65.2	5.0	260	2	US-08-520-678A-29
27	65	5.0	2010	1	US-07-864-475A-4

28	65	5.0	2010	2	US-08-468-249A-4	Sequence 4, Appli
29	64.8	5.0	2671	6	5168051-9	Patent No. 5168051
30	64.4	4.9	227	2	US-08-520-678A-28	Sequence 28, Appl
31	64.4	4.9	1558	1	US-08-467-607-2	Sequence 2, Appli
32	64.4	4.9	1558	2	US-08-469-362-2	Sequence 2, Appli
33	64.4	4.9	1558	2	US-08-850-392-2	Sequence 2, Appli
34	64.2	4.9	1733	3	US-09-073-569-1	Sequence 1, Appli
35	64	4.9	1582	3	US-08-545-196B-10	Sequence 10, Appl
36	64	4.9	1582	3	US-08-545-196B-12	Sequence 12, Appl
37	63.8	4.9	1307	2	US-08-960-022-17	Sequence 17, Appl
38	63.8	4.9	2233	1	US-08-496-631-1	Sequence 1, Appli
39	63.4	4.9	144	1	US-08-702-344-26	Sequence 26, Appl
40	63.4	4.9	270	2	US-08-520-678A-30	Sequence 30, Appl
41	63.4	4.9	1098	3	US-09-248-335-35	Sequence 35, Appl
42	63.4	4.9	1134	3	US-09-248-335-29	Sequence 29, Appl
43	63.4	4.9	6671	1	US-08-280-443-1	Sequence 1, Appli
44	63.4	4.9	6671	1	US-08-457-459-1	Sequence 1, Appli
45	63.4	4.9	6671	1	US-08-555-678-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1  
US-08-012-543-1  
; Sequence 1, Application US/08012543  
; Patent No. 5596072  
; GENERAL INFORMATION:  
; APPLICANT: Culpepper, Janice  
; APPLICANT: McKenzie, Andrew  
; APPLICANT: Dang, Warren  
; APPLICANT: de Waal Malefyt, Rene  
; APPLICANT: Heath, Andrew  
; APPLICANT: Aversa, Gregorio  
; APPLICANT: Briere, Francine  
; APPLICANT: Banchereau, Jacques  
; APPLICANT: de Vries, Jan  
; APPLICANT: Zurawski, Gerard  
; TITLE OF INVENTION: Human Interleukin-13  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/012,543  
; FILING DATE: 01-FEB-1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/933,416  
; FILING DATE: 21-AUG-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0302K1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-852-9196  
; TELEFAX: 415-496-1200  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1290 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA

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;
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 45..443
US-08-012-543-1

Query Match      29.0%; Score 378; DB 1; Length 1290;
Best Local Similarity 66.2%; Pred. No. 4.3e-86;
Matches 780; Conservative 0; Mismatches 290; Indels 108; Gaps 12;

QY 21 cctcgctcctcctgcattggctctggtggtccatggcgctctggttgactgtggtcattgc 80
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 14 CCTCAATCCTCTCCTGTGGCACTGGGCCCTCATGGCGCTTTTGTGACCACGGTCAATTGC 73

QY 81 tctcacctgcctcggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 140
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 74 TCTCACTTGGCGGCTTTGCCTCCCCAGGCCCTGTGCCTCCCTCTACAGCCCTCAG 133

QY 141 ggagctcattgaggagctggtcaacatcacccagaatc---aggcatccctctgcaacgg 197
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 134 GGAGCTCATTTGAGGAGCTGGTCAACATCACCCAGACCAGAGAGGCTCGCTCTGCAATGG 193

QY 198 cagcatggtgtggtgagcgtcaacctgacccggcgatgtactgcgagctctagaatctct 257
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 194 CAGCATGGTATGGAGCATCAACCTGACAGCTGGCATGTACTGTGCAGCCCTGGAATCCCT 253

QY 258 gatcaatgctccgactgcagcgccatccaaaggaccagaggtgctgaaagcaactgtg 317
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 254 GATCAACGTGTCAGGCTGCAGTGCCATCGAGAGACCCAGAGGATGCTGAGCGGATTCTG 313

QY 318 ctctcaaaagcccgaggcagggcagagatttccagtgaaacgcagccagacacccaaattga 377
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 314 CCCGCACAAGGTCTCAGCTGGGCAGTTTTCCAGCTTGCAATGTCGAGACACCAAAATCGA 373

QY 378 agtgatccagttggtgaaacacctgctcacctatgtaaggggagtttatcgccatggaaa 437
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 374 GGTGGCCCAAGTTTCTAAAGGACCTGCTCTTACATTTAAAGAAACTTTTTCGGGAGGACG 433

QY 438 ttccagatgaagcatgaaacttagcatcctcttatctgtagaccca-gacctgaccactta 496
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 434 GTTCAACTGAACCTCGAA---AGCATCATTTATTGCAGAGACAGGACCTGACTATTGA 489

QY 497 agttccagattcattttcttccgacgtcacaaatttcttagggaggtggtggggg----- 551
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 490 AGTTGCAGATTCTATTTCTTCTGTATGTCAAAAATGTCTTGGGTAGGGGGGAAGGAGGG 549

QY 552 ---gggggagaaaccttctcagctgggacccagcctgacccgctgacctccatggag 608
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 550 TTAGGGAGGGGTAAAAATTCCTTAGCTTAGACCTCAGCCTGTGCTGCCCGTCTTCAGCCT- 608

QY 609 ctgagccagcagccctcctgtggtgcatggggcccgagcgggtggccctcctccgtc- 667
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Db 609 ----AGCCGACCTCAGCCTTCCCTTGTGCCAGGGCTCAGCCTGGTGGCCCTCCTCTGTCC 664

QY 668 ----tgcacttcatcaacgctgagggaaagcactgcatcccatgactgtccctcctcag 723
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Db 665 AGGGCCCTGAGCTCGGTGGACCCAGGGATGACATGTCCCTACACCCCTCCCTGCCCTAG 724

QY 724 agcaaaagtgcagcattacagtggagg-----cagatatgtgtggaggggggg----- 769
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Db 725 AGCACACTGTAGCATTACAGTGGGTGCCCCCTTGGCCAGACATGTGGTGGGACAGGGACC 784

QY 770 -----tcttgctgtacctgggagtggcacagacatgtttcttcttagcctta 816
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Db 785 CACTTCACACAGGCAACTGAGGCAGACAGCAGCTCAGGCACACATTCTTCTTGGTCTTA 844

QY 817 ttattattgtgtgtatttaacaaagtgtctttgtttgtgctggggacagggagtgt--- 873
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Db 845 TTTATTATTGTGTGTTATTAAATGAGTGTGTTGTACCGTTTGGGGATTGGGGAAGACT 904

QY 874 -----gcttggagctggggggccagtgactcgggtttaga----- 908
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Db 905 GTGGCTGCTGGCACTTGGAGCCCAAGGTTTCAGAGACTCAGGGCCCCCAGCACTAAAGCAGT 964
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QY 909 -----gagtcctctgggaataagcaactgtgtgtataaaattctgtacctcaactgggat 959
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Db 965 GGACCCAGGAGTCCCTGGTAATAAGTACTGTGTACAGAATTCTGCTACCTCACTGGGGT 1024

QY 960 cctggggcc-----gacacagggggacagagagaagggtcagagatgctgctctt 1008
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Db 1025 CCTGGGCGCTCGGAGCCTCATCCGAGGAGGGTCAAGGAGGGGAGAGAGCCGCTCCT 1084

QY 1009 gtctgcaactcagcagctggtggtcctcagccaaagcagtaatttttcttctgtattt 1068
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QY 1069 aaagttaagaaaaataatatgtttatcaaaagagttaata 1106
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Db 1145 AA-----ATATTAAATATGTTAGCAAAAGAGTTAATA 1175

RESULT 2
PCT-US93-07645A-1
; Sequence 1, Application PC/TUS9307645A
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Human Interleukin-13
; NUMBER OF SEQUENCES: 6
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.5
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07645A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/012543
; FILING DATE: 01-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/010977
; FILING DATE: 29-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/933416
; FILING DATE: 21-AUG-1992
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1290 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
PCT-US93-07645A-1
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Query Match      29.0%; Score 378; DB 5; Length 1290;
Best Local Similarity 66.2%; Pred. No. 4.3e-86;
Matches 780; Conservative 0; Mismatches 290; Indels 108; Gaps 12;

QY 21 cctcgctcctcctgcattggtctgtgggtcccatggcgctctggttgactgtggtcattgc 80
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Db 14 CCTCAATCCTCTCCTGTGGCACTGGGCCCTCATGGCGCTTTTGTGACCACGGTCAATGC 73

QY 81 tctcacctgcctcggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 140
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Db 74 TCTCACTTGGCGGCTTTGGCCTCCCCAGGCCCTGTGCCTCCCTCTACAGCCCTCAG 133

QY 141 ggagctcattgaggagctggtcaacatcacccagaatc---aggcatccctctgcaacgg 197
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 134 GGAGCTCATTTGAGGAGCTGGTCAACATCACCCAGAACCCAGAGGCTCCGCTCTGCAATGG 193

QY 198 cagcatggtgtggtgagcgtcaacctgacccggcgatgtactgcgagctctagaatctct 257
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 194 CAGCATGGTATGGAGCATCAACCTGACAGCTGGCATGTACTGTGACGACCCCTGGAATCCCT 253

QY 258 gatcaatgtctccgactgcagcgccatccaaaggaccagaggtgctgaaagcactgtg 317
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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[illegible]

```

RESULT 11
PCT-US93-07645A-3
; Sequence 3, Application PC/TUS9307645A
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Human Interleukin-13
; NUMBER OF SEQUENCES: 6
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.5
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07645A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/012543
; FILING DATE: 01-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/010977
; FILING DATE: 29-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/933416
; FILING DATE: 21-AUG-1992
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1212 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
PCT-US93-07645A-3

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Query Match	15.9%;	Score 207;	DB 5;	Length 1212;
Best Local Similarity	56.8%;	Pred. No. 4.7e-43;		
Matches 715; Conservative	0;	Mismatches 415;	Indels 129;	Gaps 13;

[illegible]



```

; APPLICATION NUMBER: FR 91 03904
; FILING DATE: 29-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 16781/383
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 336 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
;
US-08-371-121-24

Query Match 15.6%; Score 203.4; DB 1; Length 336;
Best Local Similarity 77.8%; Pred. No. 2.le-42;
Matches 259; Conservative 0; Mismatches 71; Indels 3; Gaps 1;

QY 113 gccctgtgactccctcccaaccctcaaggagctcattgaggagtggtcaacatcaccc 172
Db 2 GCCCTGTGCCTCCCTCTACAGCCCTCAGGGAGCTCATTGAGGAGTGGTCAACATCACCC 61

QY 173 agaatc--aggcatccctctgaaacgagcagcatggtgtggagcgtcaacacctgaccgccg 229
Db 62 AGAACCAGAGGGTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAACCTGACAGCTG 121

QY 230 gcatgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgccatccaa 289
Db 122 GCATGTACTGTGCAGCCCTGGAATCCCTGATCAACGTGTACGGCTGCAGTGCCATCGAGA 181

QY 290 ggaccagagcagcagacacaaattgaaagtatccagttggtgaaaaaacctgctcacct 349
Db 182 AGACCCAGAGGATGCTGAGCGGATTCTGCCCGCACAAAGTGTGATCAACGTGCAGTGCCATCGAGA 181

QY 350 gtgaacgcagccgcagacacccaaattgaagtatccagttggtgaaaaaacctgctcacct 409
Db 242 GCTTGCATGTCGAGACACCAAAATCGAGGTGGCCCCAGTTTGTAAAGGACCTGCTCTTAC 301

QY 410 atgtaaggggagtttatcgccatggaaatttca 442
Db 302 ATTTAAAGAAACTTTTTCGCGAGGACGGTTTCA 334

RESULT 14
US-08-371-121-2
; Sequence 2, Application US/08371121
; Patent No. 5652123
; GENERAL INFORMATION:
; APPLICANT: CAPUT, Daniel
; APPLICANT: FERRARA, Pascual
; APPLICANT: GUILLEMOT, Jean-Claude
; APPLICANT: LEPLATOIS, Pascal
; APPLICANT: MINTY, Adrian
; APPLICANT: KAGHAD, Mourad
; APPLICANT: LABIT-LE BOUTEILLER, Christine
; APPLICANT: MAGAZIN, Marilyn
; TITLE OF INVENTION: Protein having a cytokine type
; TITLE OF INVENTION: activity, recombinant DNA coding for this protein,
; TITLE OF INVENTION: transformed cells and microorganisms.
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/371,121
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/938,161
; FILING DATE: 30-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR92/00280
; FILING DATE: 27-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91 00137
; FILING DATE: 08-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91 03904
; FILING DATE: 29-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 16781/383
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 336 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
;
US-08-371-121-2

Query Match 15.5%; Score 201.8; DB 1; Length 336;
Best Local Similarity 77.5%; Pred. No. 5.3e-42;
Matches 258; Conservative 0; Mismatches 72; Indels 3; Gaps 1;

QY 113 gccctgtgactccctcccaaccctcaaggagctcattgaggagtggtcaacatcaccc 172
Db 2 GCCCTGTGCCTCCCTCTACAGCCCTCAGGGAGCTCATTGAGGAGTGGTCAACATCACCC 61

QY 173 agaatc--aggcatccctctgaaacgagcagcatggtgtggagcgtcaacacctgaccgccg 229
Db 62 AGAACCAGAGGGTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAACCTGACAGCTG 121

QY 230 gcatgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgccatccaa 289
Db 122 ACATGTACTGTGCAGCCCTGGAATCCCTGATCAACGTGTGATCAACGTGCAGTGCCATCGAGA 181

QY 290 ggaccagagcagcagacacccaaattgaagtatccagttggtgaaaaaacctgctcacct 349
Db 182 AGACCCAGAGGATGCTGAGCGGATTCTGCCCGCACAAAGTGTGATCAACGTGCAGTGCCATCGAGA 181

QY 350 gtgaacgcagccgcagacacccaaattgaagtatccagttggtgaaaaaacctgctcacct 409
Db 242 GCTTGCATGTCGAGACACCAAAATCGAGGTGGCCCCAGTTTGTAAAGGACCTGCTCTTAC 301

QY 410 atgtaaggggagtttatcgccatggaaatttca 442
Db 302 ATTTAAAGAAACTTTTTCGCGAGGACGGTTTCA 334

RESULT 15
US-08-371-121-26
; Sequence 26, Application US/08371121
; Patent No. 5652123
; GENERAL INFORMATION:
; APPLICANT: CAPUT, Daniel
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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: May 13, 2001, 11:39:51 ; Search time 5997.24 Seconds  
(without alignments)  
1896.606 Million cell updates/sec

Title: US-09-451-527-91  
Perfect score: 1302  
Sequence: 1 ctacgacctgcctgcctcttc.....aaaaaaaaaaaaaaaaaaaaa 1302

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 9623517 seqs, 4368049070 residues

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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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C 3	96.2	7.4		430	10	AA646049	AA646049 vs34d01.r
C 4	81.2	6.2		431	105	AL513947	AL513947 AL513947
C 5	81	6.2		300	105	AL513837	AL513837 AL513837
C 6	80	6.1		596	111	AW129722	AW129722 xe23b07.x
C 7	79.8	6.1		407	103	AI921379	AI921379 wo24b03.x
C 8	78.6	6.0		967	229	CNS00JUP	AL077063 Drosophll
C 9	78.4	6.0		248	17	AI224992	AI224992 qw95a10.x
C 10	78.2	6.0		319	104	AI950892	AI950892 wx56f05.x
C 11	78.2	6.0		351	110	AW089036	AW089036 xc79a04.x
C 12	78.2	6.0		1290	105	AL514843	AL514843 AL514843
C 13	77.8	6.0		339	22	AI609594	AI609594 tw28d06.x
C 14	77.6	6.0		506	105	AL514437	AL514437 AL514437
C 15	77.2	5.9		733	110	AW074172	AW074172 xb08g08.x
C 16	77.2	5.9		968	225	AZ682070	AZ682070 ENTGO02TR
C 17	77	5.9		297	103	AI871697	AI871697 wm51c05.x
C 18	77	5.9		903	174	BG178352	BG178352 602330117

C 19	76.8	5.9	389	110	AW084869
C 20	76.8	5.9	1101	105	AL513871
C 21	76.4	5.9	423	103	AI922215
C 22	75.6	5.8	261	111	AW169790
C 23	75.6	5.8	358	105	AL515173
C 24	75.4	5.8	272	103	AI9222707
C 25	75.4	5.8	288	18	AI290154
C 26	75.4	5.8	304	23	AI633330
C 27	75.4	5.8	324	23	AI635942
C 28	75.4	5.8	392	23	AI654672
C 29	75.4	5.8	444	104	AI954507
C 30	75.4	5.8	514	111	AW167228
C 31	75.4	5.8	517	104	AI934137
C 32	75.4	5.8	872	230	CNS027E7
C 33	75.4	5.8	1036	229	CNS00599
C 34	75.2	5.8	175	103	AI922577
C 35	75.2	5.8	305	105	AL045620
C 36	75.2	5.8	428	112	AW188539
C 37	75.2	5.8	436	105	AL514063
C 38	75.2	5.8	498	22	AI554186
C 39	75.2	5.8	956	142	BE964016
C 40	75	5.8	336	105	AL515323
C 41	75	5.8	357	102	AI818977
C 42	75	5.8	383	105	AL513789
C 43	75	5.8	400	20	AI431327
C 44	75	5.8	476	110	AW080357
C 45	75	5.8	829	166	BE421175

ALIGNMENTS

RESULT 1					
AI208823/c					
LOCUS	AI208823	534 bp	mRNA	EST	29-NOV-1998
DEFINITION	qg38e05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1837472 3' similar to gb:L06801 INTERLEUKIN-13 PRECURSOR (HUMAN);, mRNA sequence.				
ACCESSION	AI208823				
VERSION	AI208823.1 GI:3770765				
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	1 (bases 1 to 534)				
TITLE	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index				
JOURNAL	Unpublished (1997)				
COMMENT	Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email: Robert_Strausberg@nih.gov cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html Insert Length: 1082 Std Error: 0.00 Seq primer: -40UP from Gibco High quality sequence stop: 350. Location/Qualifiers 1. .534 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:1837472" /clone_lib="Soares_testis_NHT" /sex="male" /lab_host="DH10B" /note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA				
FEATURES	source				

BASE COUNT	132 a	143 c	115 g	142 t
ORIGIN	was prepared from mRNA obtained from Clontech Laboratories, Inc., and primed with a Not I - oligo(dT) primer [5', TGTTACCAATCTGAAGTGGGAGCGCGCCCAATTTTGTGTTTTTTT 3']. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo. "			

Query Match	7.8%	Score 101;	DB 17;	Length 534;
Best Local Similarity	64.4%	Pred. No. 2e-12;		
Matches 244;	Conservative 0;	Mismatches 80;	Indels 55;	Gaps 4;
QY 776	tgtacctgggagtggcacagacatgtttcttcttagcccttattattgtgtgtatt	835		
Db 473	TGAGCCAGACAGCAGCTCAGCACACTCTTCTTGGTCTATTATTATTGTGTATT	414		
QY 836	taaacaaagtgtctttgttgtgtgtgggacagggagtg	880		
Db 413	TAAATGAGTGTGTTGTCACCGTTGGGGATTGGGAAGACTGTGGCTGCTGGCAC	354		
QY 881	gctggggggcccagtgactcgggttttaga	918		
Db 353	GCCAAAGGTTTCAGAGACTCAGGGCCCCCAGCACA	294		
QY 919	gaataagcactgtgtgtataaattctgtacctcactcgtggatcctgggcccgcacagggg	978		
Db 293	TAATAAGTACTGTGTACAGAAATTCTGTCTACCTCACTGGGGTCTCTGGGCGCTC	234		
QY 979	acagga	1027		
Db 233	ATCCGAGGCAGGGTCAGGAGAGGGGCAGAACACGCGCTCCTGTCTGCCAGCCAG	174		
QY 1028	gccctcagccaagcagtaatttattgttttcttctgtattttaagtaagaaaaata	1087		
Db 173	GCTCTCAGCCAACGAGTAATTTATTGTTTTCCTCGTATTAA	121		
QY 1088	tgttatcaaaagaggttaata	1106		
Db 120	TGTTAGCAAGAGTTAATA	102		

RESULT 2					
AA905851/c					
LOCUS	AA905851	517 bp	mRNA	EST	19-MAY-1998
DEFINITION	oj87e03.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1505308 3' similar to gb:L06801 INTERLEUKIN-13 PRECURSOR (HUMAN);, mRNA sequence.				
ACCESSION	AA905851				
VERSION	AA905851.1 GI:3040974				
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 517)				
AUTHORS	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.				
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index				
JOURNAL	Unpublished (1997)				
COMMENT	Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email: Robert_Strausberg@nih.gov This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Trace considered overall poor quality Insert Length: 1437 Std Error: 0.00 Seq primer: -40ml3 fwd. Et from Amersham High quality sequence stop: 1. Location/Qualifiers				
FEATURES					



















Search completed: May 13, 2001, 11:40:07  
Job time: 16482 sec

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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: May 13, 2001, 14:20:29 ; Search time 9342.78 Seconds  
(without alignments)  
620.362 Million cell updates/sec

Title: US-09-451-527-94  
Perfect score: 393  
Sequence: 1 atggcgctctgttgactgt.....atcgccatggaaatttcaga 393

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1283235 seqs, 7373929652 residues

Total number of hits satisfying chosen parameters: 2566470

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl:

- 1: gb\_bal:\*
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- 3: gb\_ba3:\*
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- 8: gb\_ov:\*
- 9: gb\_pat1:\*
- 10: gb\_pat2:\*
- 11: gb\_ph:\*
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- 13: gb\_pl2:\*
- 14: gb\_pl3:\*
- 15: gb\_pl4:\*
- 16: em\_bal:\*
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- 18: em\_fun:\*
- 19: em\_htgo\_hum:\*
- 20: em\_htgo\_inv:\*
- 21: em\_htgo\_rod:\*
- 22: em\_htg\_hum1:\*
- 23: em\_htg\_hum2:\*
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- 63: gb\_htg4:\*
- 64: gb\_htg5:\*
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- 87: gb\_pr3:\*
- 88: gb\_pr4:\*
- 89: gb\_pr5:\*
- 90: gb\_pr6:\*
- 91: gb\_pr7:\*
- 92: gb\_pr8:\*
- 93: gb\_pr9:\*
- 94: gb\_ro1:\*
- 95: gb\_ro2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	393	100.0	1302	7	AF244915	AF244915 Canis fam
2	246.8	62.8	1270	93	HUMIL13A	L06801 Homo sapien
3	246.8	62.8	1282	92	HSNC30	X69079 H.sapiens i
4	246.8	62.8	1290	10	I34548	I34548 Sequence 1
5	245.2	62.4	417	88	AF043334	AF043334 Homo sapi
6	245.2	62.4	1297	9	A29948	A29948 Coding sequ
7	245.2	62.4	1297	10	I58488	I58488 Sequence 15
8	219.8	55.9	343	7	AF072807	AF072807 Bos tauru
9	204	51.9	384	9	A29950	A29950 Nucleic aci
10	204	51.9	384	10	I58489	I58489 Sequence 17
11	203.4	51.8	336	9	A29931	A29931 Sequence co



12	203.4	51.8	336	10	I58494	I58494 Sequence 24
13	202.2	51.5	425	9	AR027065	AR027065 Sequence
14	202.2	51.5	425	10	I86198	I86198 Sequence 4
15	202.2	51.5	4410	9	A52326	A52326 Sequence 1
16	202.2	51.5	4410	9	AR027062	AR027062 Sequence
17	202.2	51.5	4410	10	I86195	I86195 Sequence 1
18	201.8	51.3	336	9	A29930	A29930 Sequence co
19	201.8	51.3	336	10	I58481	I58481 Sequence 2
20	159.2	40.5	447	10	I58495	I58495 Sequence 26
21	159.2	40.5	1207	94	MUSSTCPE	M23504 Mus musculu
22	159.2	40.5	1212	10	I34549	I34549 Sequence 3
23	153.8	39.1	443	94	RATIL13A	L26913 Rattus Norv
24	130.8	33.3	213343	78	AF276990	AF276990 Canis fam
C 25	101.8	25.9	3714	93	HUM11DC99Z	L42080 Homo sapien
26	101.8	25.9	4600	93	HUMIL13B	L13029 Human inter
27	101.8	25.9	4740	93	HSU10307	U10307 Human inter
28	101.8	25.9	5670	93	HSU31120	U31120 Human inter
C 29	101.8	25.9	50282	85	AC004039	AC004039 Homo sapi
30	101.8	25.9	78469	75	AC074127	AC074127 Homo sapi
C 31	101.8	25.9	78469	75	AC074127	AC074127 Homo sapi
32	92.2	23.5	3520	7	BTA132441	AJ132441 Bos tauru
C 33	70.6	18.0	3395	93	HUM11DC98Z	L42079 Homo sapien
34	61.6	15.7	4376	94	MUSIL13A	L13028 Mouse inter
C 35	61.6	15.7	142732	88	AC084392	AC084392 Homo sapi
C 36	61.6	15.7	159500	94	AC005742	AC005742 Mus muscu
37	61.6	15.7	237823	66	AC020886	AC020886 Mus muscu
38	44.6	11.3	60	9	A29941	A29941 Oligonucleo
39	44.6	11.3	60	10	I58485	I58485 Sequence 12
40	44.6	11.3	102	9	A29939	A29939 Sequence co
41	44.6	11.3	102	10	I58483	I58483 Sequence 10
42	40.8	10.4	1008	94	RATNACHRR5	M33952 Rat neurona
43	40.8	10.4	2461	95	RNU42976	U42976 Rattus norv
C 44	40.8	10.4	38390	3	SC2H12	AL359215 Streptomy
45	39.6	10.1	54	9	A29940	A29940 Sequence co

ALIGNMENTS

RESULT	1
AF244915	
LOCUS	1302 bp mRNA MAM 16-OCT-2000
DEFINITION	Canis familiaris interleukin-13 mRNA, complete cds.
ACCESSION	AF244915
VERSION	AF244915.1 GI:7528273
KEYWORDS	.
SOURCE	dog.
ORGANISM	Canis familiaris
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE	1 (bases 1 to 1302)
AUTHORS	Yang, S., Boroughs, K.L. and McDermott, M.J.
TITLE	Canine interleukin-13: molecular cloning of full-length cDNA and expression of biologically active recombinant protein
JOURNAL	J. Interferon Cytokine Res. 20 (9), 779-785 (2000)
MEDLINE	20485146
PUBMED	11032397
REFERENCE	2 (bases 1 to 1302)
AUTHORS	Yang, S.
TITLE	Direct Submission
JOURNAL	Submitted (13-MAR-2000) Allergy and Immunology, Heska Corporation, 1613 Prospect Parkway, Fort Collins, CO 80525, USA
FEATURES	Location/Qualifiers
source	1. .1302
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CDS	52. .447
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	/db_xref="GI:7528274"
	/translation="MALWLTVVIALTCLGLASPSVPTSPTLKELIEELVNITQNA"

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448. .1302					
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Best Local Similarity	100.0%	Pred. No. 3.9e-91;			
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QY	1	atggcgctctgttgactgtgtgctcattgctctcactgcctcgctcggtgcttgcctcccg	60		
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QY	61	agccctgtgactccctcccccaccctcaaggagctcattgaggagctggtcaacatcacc	120		
Db	112	AGCCCTGTGACTCCCTCCCAACCCCTCAAGGAGCTCATTGAGGAGCTGGTCAACATCACC	171		
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QY	181	atgtactgcgcagctctagaaatctctgatcaatgtctccgactgcagcgccatccaaag	240		
Db	232	ATGTACTGCGCAGCTCTAGAAATCTCTGATCAATGTCTCCGACTGCGAGCGCCATCCAAGG	291		
QY	241	accagagagatgctgaaagcactgtgctctcaaaagccgcgcgcgcgcgcgcgcgcgc	300		
Db	292	ACCCAGAGGATGCTGAAAGCACTGTGCTCTCAAAAGCCCGCGGCGAGGCAGATTTCAGT	351		
QY	301	gaacgcagccgagacacacacaaattgaagtgcacagttggtgaaacacacctgctcacctat	360		
Db	352	GAACGAGCGGAGACACCAAAATTGAAGTGATCCAGTTGGTGAAAAACCTGCTCACCTAT	411		
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Db	412	GTAAGGGGAGTTTATCGCCATGGAATTTTTCAGA	444		
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HUMIL13A	HUMIL13A	1270 bp	mRNA	PRI	22-JUL-1993
LOCUS	Homo sapiens interleukin 13 mRNA, complete cds.				
DEFINITION	L06801				
ACCESSION	L06801.1	GI:186275			
VERSION					
KEYWORDS	cytokine; growth factor; interleukin 13; regulatory protein.				
SOURCE	Homo sapiens				
ORGANISM	Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE	1 (bases 1 to 1270)				
AUTHORS	McKenzie, A.N.J., Culpepper, J.A., de Waal Malefyt, R., Briere, F., Punnonen, J., Aversa, G., Sato, A., Dang, W., Cocks, B.G., Menon, S., de Vries, J.E., Banchereau, J. and Zurawski, G.R.				
TITLE	Interleukin-13, a T cell-derived cytokine that regulates human monocyte and B cell function				
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 90, 3735-3739 (1993)				
MEDLINE	93234572				
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RESULT 6
A29948 LOCUS A29948 1297 bp DNA PAT 23-JUN-1995
DEFINITION Coding sequence for protein with cytokine like activity.
ACCESSION A29948
VERSION A29948.1 GI:1249028
KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial construct.
REFERENCE 1 (bases 1 to 1297)
AUTHORS Caput,D., Ferrara,P., Guillemot,J.C., Kaghad,M., Labit-le
Bouteiller,C., Leplatois,P., Magazin,M. and Minty,A.
TITLE Protein having cytokin type activity, recombinant DNA coding for
this protein, transformed cells and microorganisms
JOURNAL Patent: EP 0506574-A 21 30-SEP-1992;
ELF SANOFI
FEATURES
source Location/Qualifiers
1..1297
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/translacion="MHPLLNPLLLALGLMALLLTIVIALTCLGGFASGPVPPSTALR
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BASE COUNT 309 a 341 c 336 g 311 t
ORIGIN
Query Match 62.4%; Score 245.2; DB 9; Length 1297;
Best Local Similarity 78.2%; Pred. No. 5e-53;
Matches 308; Conservative 0; Mismatches 83; Indels 3; Gaps 1;
QY 1 atggcgctctggtgactgtgtcattgctctcacctgcctgggtggccttgcctccccg 60
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QY 298 agtgaacgcagccgagacaccaaattgaagtgtatccagttggtgaaacacctgctcacc 357
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RESULT 7
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DEFINITION Sequence 15 from patent US 5652123.
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ACCESSION I58488
VERSION I58488.1 GI:2477726
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1297)
AUTHORS Caput,D., Ferrara,P., Guillemot,J., Kaghad,M., Labit-Le
Bouteiller,C., Leplatois,P., Magazin,M. and Minty,A.
TITLE Protein having interleukin 13 activity, recombinant DNA coding for
this protein, transformed cells and microorganisms
JOURNAL Patent: US 5652123-A 15 29-JUL-1997;
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Best Local Similarity 78.2%; Pred. No. 5e-53;
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Db 57 ATGGCGCTTTTGTGACCACGGTCATTGCTCTCACTTGCCCTTGGCGGCTTTGCCCTCCCCA 116
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Db 417 CATTTAAAGAAACTTTTTCGCGAGGGACGGTTCA 450
RESULT 8
AF072807 LOCUS AF072807 343 bp mRNA MAM 21-JAN-2000
DEFINITION Bos taurus interleukin-13 precursor (IL-13) mRNA, partial cds.
ACCESSION AF072807
VERSION AF072807.1 GI:4558813
KEYWORDS
SOURCE cow.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 343)
AUTHORS Trigona,W.L., Brown,W.C. and Estes,D.M.
TITLE Functional implications for signaling via the IL4R/IL13R complex on
bovine cells
JOURNAL Vet. Immunol. Immunopathol. 72 (1-2), 73-79 (1999)
MEDLINE 20080132
PUBMED 10614495
REFERENCE 2 (bases 1 to 343)
AUTHORS Trigona,W.T., Hirano,A. and Estes,D.M.
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TITLE Direct Submission  
JOURNAL Submitted (16-JUN-1998) Veterinary Pathobiology, University of Missouri-Columbia, W213 Veterinary Medicine Building, Columbia, MO 65211, USA

FEATURES  
source Location/Qualifiers  
1..343  
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/db\_xref="GI:4558814"  
/translation="MALLLTAVILVICFGGLTSPSPVPSATALKELIEELVNITQNK  
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BASE COUNT 78 a 101 c 85 g 79 t  
ORIGIN

Query Match 55.9%; Score 219.8; DB 7; Length 343;  
Best Local Similarity 79.6%; Pred. No. 2e-46;  
Matches 273; Conservative 0; Mismatches 67; Indels 3; Gaps 1;

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Db 181 AGCATGTACTGTGAGCCCTGGACTCCCTGATCAGCATCTCCAACCTGCAGTGTATCCAA 240  
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QY 298 agtgaacgcagcgagacacacaaattgaagtgatccagttgg 340  
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RESULT 9  
A29950  
LOCUS A29950 384 bp DNA PAT 23-JUN-1995  
DEFINITION Nucleic acid fragment B.  
ACCESSION A29950  
VERSION A29950.1 GI:1249030  
KEYWORDS synthetic construct.  
SOURCE synthetic construct.  
ORGANISM artificial construct.  
REFERENCE 1 (bases 1 to 384)  
AUTHORS Caput,D., Ferrara,P., Guillemot,J.C., Kaghad,M., Labit-le Bouteiller,C., Leplatois,P., Magazin,M. and Minty,A.  
TITLE Protein having cytokin type activity, recombinant DNA coding for this protein, transformed cells and microorganisms  
JOURNAL Patent: EP 0506574-A 23 30-SEP-1992;  
ELF SANOFI  
FEATURES Location/Qualifiers  
source 1..384  
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BASE COUNT 97 a 104 c 99 g 84 t  
ORIGIN

Query Match 51.9%; Score 204; DB 9; Length 384;  
Best Local Similarity 77.1%; Pred. No. 2.3e-42;  
Matches 262; Conservative 0; Mismatches 75; Indels 3; Gaps 1;

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LOCUS I58489 384 bp DNA PAT 07-OCT-1997  
DEFINITION Sequence 17 from patent US 5652123.  
ACCESSION I58489  
VERSION I58489.1 GI:2477727  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 384)  
AUTHORS Caput,D., Ferrara,P., Guillemot,J., Kaghad,M., Labit-Le Bouteiller,C., Leplatois,P., Magazin,M. and Minty,A.  
TITLE Protein having interleukin 13 activity, recombinant DNA coding for this protein, transformed cells and microorganisms  
JOURNAL Patent: US 5652123-A 17 29-JUL-1997;  
FEATURES Location/Qualifiers  
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/organism="unknown"

BASE COUNT 97 a 104 c 99 g 84 t  
ORIGIN

Query Match 51.9%; Score 204; DB 10; Length 384;  
Best Local Similarity 77.1%; Pred. No. 2.3e-42;  
Matches 262; Conservative 0; Mismatches 75; Indels 3; Gaps 1;

QY 55 tccccgagccctgtgactccctcccccaaccctcaaggagctcattgaggagctggtcaac 114  
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Db 16 TCCCCAGGCCCTGTGCCTCCCTCTACGGCCCTCAGGGAGCTCATTTGAGGAGCTGGTCAAC 75  
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Qy 229 gccatccaaaggacccagagatgctgaaagcactgtgtctctcaaaaagcccgaggcaggg 288

Db 235 GCCATCGAGAGACCCAGAGGATGCTGAGCGGATTTGCCCCACAAAGTCTCAGCTGGG 294

Qy 289 cagatttccagtgaacgcagccgagacacccaaaattgaagtgatccagttggtgaaaaac 348

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Db 355 CTGCTCTTACATTAAAGAAACTTTTTCGCGAGGGACGGTTCA 397

RESULT 14

LOCUS I86198 425 bp DNA PAT 10-JUN-1998

DEFINITION Sequence 4 from patent US 5700665.

ACCESSION I86198

VERSION I86198.1 GI:3205916

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 425)

AUTHORS Legoux,R., Maldonado,P. and Salome,M.

TITLE Method for the extraction of periplasmic proteins from prokaryotic microorganisms in the presence of arginine

JOURNAL Patent: US 5700665-A 4 23-DEC-1997;

FEATURES

source Location/Qualifiers

1. .425

/organism="unknown"

BASE COUNT 100 a 116 c 110 g 99 t

ORIGIN

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Best Local Similarity 76.4%; Pred. No. 6.7e-42;

Matches 262; Conservative 0; Mismatches 78; Indels 3; Gaps 1;

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Qy 112 aacatcacccagaatc---aggcatccctctgcaaacggcgagcatggtgtgagcgtcaac 168

Db 115 AACATCACCCAGAACCAAGGCTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAAC 174

Qy 169 ctgaccgcgggaatgtactgcgcagctctagaatctctgatcaatgtctccgactgcagc 228

Db 175 CTGACAGCTGGCATGTACTGTGCAGCCCTGGAATCCCTGATCAACGTGTCAAGGCTGCAGT 234

Qy 229 gccatccaaaggacccagagatgctgaaagcactgtgtctctcaaaaagcccgaggcaggg 288

Db 235 GCCATCGAGAGACCCAGAGGATGCTGAGCGGATTTGCCCCACAAAGTCTCAGCTGGG 294

Qy 289 cagatttccagtgaacgcagccgagacacccaaaattgaagtgatccagttggtgaaaaac 348

Db 295 CAGTTTCCAGCTTGCATGTCCGGAGACACCAAAATCGAGGTGGCCCAAGTTTGTAAAGGAC 354

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Db 355 CTGCTCTTACATTAAAGAAACTTTTTCGCGAGGGACGGTTCA 397

RESULT 15

A52326

LOCUS A52326 4410 bp DNA PAT 12-DEC-1997

DEFINITION Sequence 1 from Patent EP0725140.

ACCESSION A52326

VERSION A52326.1 GI:2851987

KEYWORDS

SOURCE unidentified.

ORGANISM unidentified.

REFERENCE 1 (bases 1 to 4410)

AUTHORS Legoux,R., Maldonado,P. and Salome,M.

TITLE Process of extraction of periplasmic proteins from prokaryotic microorganisms in the presence of arginine

JOURNAL Patent: EP 0725140-A 1 07-AUG-1996;

COMMENT SANOFI SA (FR)

Other publication SK 10696 960904

Other publication CZ 9600290 960814

Other publication JP 8242879 960924

Other publication FI 960427 960801

Other publication PL 312543 960805

Other publication NO 960396 960801

Other publication FR 2729972 960802

Other publication CA 2168382 960801

Other publication AU 4224496 960808.

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source Location/Qualifiers

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/note="SEQUENCE CODANT POUR LE PRECURSEUR DE L'IL-13"

terminator 763. .812

terminator 813. .1012

/note="TERMINATEUR DU GENE 10 DU PHAGE T7"

terminator 1013. .1253

/note="TERMINATEUR DU PHAGE FD"

misc\_RNA 1254. .2505

/note="GENE CODANT POUR LE REPRESSEUR DE L'OPERON LACTOSE"

misc\_RNA 2506. .4410

/note="SEQUENCE DE PBR 327"

BASE COUNT 1078 a 1142 c 1096 g 1094 t

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Query Match 51.5%; Score 202.2; DB 9; Length 4410;

Best Local Similarity 76.4%; Pred. No. 5.6e-42;

Matches 262; Conservative 0; Mismatches 78; Indels 3; Gaps 1;

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Qy 112 aacatcacccagaatc---aggcatccctctgcaaacggcgagcatggtgtgagcgtcaac 168

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Qy 229 gccatccaaaggacccagagatgctgaaagcactgtgtctctcaaaaagcccgaggcaggg 288

Db 572 GCCATCGAGAGACCCAGAGGATGCTGAGCGGATTTGCCCCACAAAGTCTCAGCTGGG 631

Qy 289 cagatttccagtgaacgcagccgagacacccaaaattgaagtgatccagttggtgaaaaac 348

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QY 349 ctgctcacctatgttaaggggagttttatcgcccatggaaaatttca 391  
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Db 692 CTGCTCTTACATTTAAAGAAACTTTTCGCGAGGGACGGTTCA 734

Search completed: May 13, 2001, 14:20:33  
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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 13, 2001, 14:29:52 ; Search time 472.02 Seconds  
(without alignments)  
486.052 Million cell updates/sec

Title: US-09-451-527-94  
Perfect score: 393  
Sequence: 1 atggcgctctgttgactgt.....atcgccatggaatttcaga 393

Scoring table: IDENTITY\_NUC  
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Searched: 678276 seqs, 291890651 residues

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	393	100.0	393	21	Canine interleukin
C 2	393	100.0	393	21	Canine interleukin
3	393	100.0	1302	21	Canine interleukin
C 4	393	100.0	1302	21	Canine interleukin
5	377	95.9	390	21	Canine interleukin
C 6	377	95.9	390	21	Canine interleukin
7	377	95.9	1269	21	Canine interleukin
C 8	377	95.9	1269	21	Canine interleukin
9	333	84.7	333	21	Canine mature inte
C 10	333	84.7	333	21	Canine mature inte
11	317	80.7	330	21	Canine mature inte

c	12	317	80.7	330	21	Z55566	Canine mature inte
	13	278	70.7	278	21	Z55554	Canine interleukin
	14	272	69.2	272	21	Z55553	Canine interleukin
	15	246.8	62.8	1270	21	F21334	Human low adenosin
	16	246.8	62.8	1270	21	A35212	Human low adenosin
	17	246.8	62.8	1282	21	F21332	Human low adenosin
	18	246.8	62.8	1282	21	A35210	Human adenosine re
	19	246.8	62.8	1290	15	Q56692	Sequence encoding
	20	246.8	62.8	6952	21	F21333	Human low adenosin
	21	246.8	62.8	6952	21	A35211	Human adenosine re
	22	246.8	62.8	14978	21	F21338	Human low adenosin
	23	246.8	62.8	14978	21	A35216	Human adenosine re
	24	245.2	62.4	1297	13	Q28947	Cytokine NC30. Q
	25	203.4	51.8	336	13	Q28944	Gly41-Cytokine cod
	26	201.8	51.3	336	13	Q28943	Asp41-Cytokine cod
	27	159.2	40.5	1212	15	Q56693	Sequence encoding
	28	101.8	25.9	5670	21	F21331	Human low adenosin
	29	101.8	25.9	5670	21	F21337	Human low adenosin
	30	101.8	25.9	5670	21	A35209	Human adenosine re
	31	101.8	25.9	5670	21	A35215	Human adenosine re
	32	99	25.2	166	21	Z55552	Canine interleukin
	33	44.6	11.3	60	13	Q28942	Cytokine signal se
	34	44.6	11.3	102	13	Q28941	Cytokine signal se
	35	40.8	10.4	2460	11	Q06086	Plasmid pZPC13 enc
	36	37.2	9.5	66	20	Z32227	Human interleukin
	37	35.8	9.1	2249	18	T74283	Cellulose binding
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	39	35.8	9.1	3187	17	T10922	Laccase gene. Myc
	40	35.8	9.1	3192	18	T72106	Myceliophthora the
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	43	34.4	8.8	772	19	V48405	Dominant-negative
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ALIGNMENTS

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ID	Z55557 standard; CDNA; 393 BP.
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AC	Z55557;
XX	
DT	14-MAR-2000 (first entry)
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DE	Canine interleukin-13 (IL-13) clone 80 cDNA coding region.
XX	
KW	Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;
KW	immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
XX	
OS	Canis familiaris.
XX	
PN	WO9961618-A2.
XX	
PD	02-DEC-1999.
XX	
PF	28-MAY-1999; 99WO-US11942.
XX	
PR	29-MAY-1998; 98US-0087306.
XX	
PA	(HESK-) HESKA CORP.
XX	
PI	Sim G, Yang S, Dreitz MJ, Wonderling RS;
XX	
DR	WPI; 2000-072623/06.
DR	P-PSDB; Y58221.
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PT	Nucleic acids encoding immunoregulatory proteins from cats or dogs,
PT	useful for treating or preventing e.g. tumors or autoimmune disease
XX	
PS	Claim li; Page 232-233; 264pp; English.

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XX Sequences Z55552-Z55560 and Z55561-Z55566 represent cDNA
CC sequences encoding canine interleukin-13 (IL-13) clones 80
CC and 78 respectively. The invention relates to canine
CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage
CC colony-stimulating factor (GMCSF), and nucleotides which encode these
CC immunoregulatory proteins. The proteins, their associated
CC nucleic acids, specific antibodies and inhibitors may be used as
CC vaccines for therapeutic or prophylactic regulation of an immune
CC response in animals (particularly cats, dogs, horses and humans).
CC They may be used to treat autoimmune or infectious diseases including
CC allergies, tumours, inflammation and graft rejection, and to increase
CC the response from a co-administered antigen. The nucleotide sequences
CC can also be used for the recombinant production of a protein, while
CC nucleotide fragments are useful as probes, as amplification primers and
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
CC The proteins may be used to raise antibodies and to screen for
CC modulators of activity, while the antibodies may be used in detection,
CC and in drug targetting.
XX
SQ Sequence 393 BP; 93 A; 118 C; 100 G; 82 T; 0 other;

Query Match      100.0%; Score 393; DB 21; Length 393;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
Matches 393; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 agccctgtgactccctctgcaacggcagcagtggtgtgagcgtcaacctgaccgcggc 120
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Db 61 agccctgtgactccctctgcaacggcagcagtggtgtgagcgtcaacctgaccgcggc 120

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   |||||
Db 121 cagaatcaggatccctctgcaacggcagcagtggtgtgagcgtcaacctgaccgcggc 180

QY 181 atgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgccatccaaagg 240
   |||||
Db 181 atgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgccatccaaagg 240

QY 241 acccagaggatgctgaaagcactgtgctctcaaaaagcccgcgagcagatttccagt 300
   |||||
Db 241 acccagaggatgctgaaagcactgtgctctcaaaaagcccgcgagcagatttccagt 300

QY 301 gaacgcagcgagacaccaaaattgaagtgtatccagttggtgaaaaaacctgtcacctat 360
   |||||
Db 301 gaacgcagcgagacaccaaaattgaagtgtatccagttggtgaaaaaacctgtcacctat 360

QY 361 gtaaggggagtttatcgccatggaaatttcaga 393
   |||||
Db 361 gtaaggggagtttatcgccatggaaatttcaga 393

RESULT 2
Z55558/c
ID Z55558 standard; cDNA; 393 BP.
XX
AC Z55558;
XX
DT 14-MAR-2000 (first entry)
XX
DE Canine interleukin-13 (IL-13) clone 80 cDNA coding region complement.
XX
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
XX
OS Canis familiaris.
XX
```

```

PN WO9961618-A2.
XX
PD 02-DEC-1999.
XX
PF 28-MAY-1999; 99WO-US11942.
XX
PR 29-MAY-1998; 98US-0087306.
XX
PA (HESK-) HESKA CORP.
XX
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;
XX
XX WPI; 2000-072623/06.
DR P-PSDB; Y58221.
DR
XX
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,
XX useful for treating or preventing e.g. tumors or autoimmune disease -
PS Claim 1i; Page 233; 264pp; English.
XX
CC Sequences Z55552-Z55560 and Z55561-Z55566 represent cDNA
CC sequences encoding canine interleukin-13 (IL-13) clones 80
CC and 78 respectively. The invention relates to canine
CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage
CC colony-stimulating factor (GMCSF), and nucleotides which encode these
CC immunoregulatory proteins. The proteins, their associated
CC nucleic acids, specific antibodies and inhibitors may be used as
CC vaccines for therapeutic or prophylactic regulation of an immune
CC response in animals (particularly cats, dogs, horses and humans).
CC They may be used to treat autoimmune or infectious diseases including
CC allergies, tumours, inflammation and graft rejection, and to increase
CC the response from a co-administered antigen. The nucleotide sequences
CC can also be used for the recombinant production of a protein, while
CC nucleotide fragments are useful as probes, as amplification primers and
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
CC The proteins may be used to raise antibodies and to screen for
CC modulators of activity, while the antibodies may be used in detection,
CC and in drug targetting.
XX
SQ Sequence 393 BP; 82 A; 100 C; 118 G; 93 T; 0 other;

Query Match      100.0%; Score 393; DB 21; Length 393;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
Matches 393; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atggcgctctggtgactgtggtcattgctctcacctgcctcgtggtggccttgcctccccg 60
   |||||
Db 393 ATGGCGCTCTGTTGACTGTGGTCATTGCTCTCACCTGCTCGGTGGCCTTGCCCTCCCCG 334

QY 61 agccctgtgactccctctgcaacggcagcagtggtgtgagcgtggtggtcaacatcacc 120
   |||||
Db 333 AGCCCTGTGACTCCCTCCCAACCCCTCAAGGAGCTCATTTGAGGAGCTGGTCAACATCACC 274

QY 121 cagaatcaggatccctctgcaacggcagcagtggtgtgagcgtcaacctgaccgcggc 180
   |||||
Db 273 CAGAATCAGGCATCCCTCTGCAACGGCAGCATGGTGTGGAGCGTCAACCTGACCGCCGCG 214

QY 181 atgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgccatccaaagg 240
   |||||
Db 213 ATGTACTGCGCAGCTCTAGAAATCTCTGATCAATGTCTCCGACTGCAGCGCCATCCAAAGG 154

QY 241 acccagaggatgctgaaagcactgtgctctcaaaaagcccgcgagcagatttccagt 300
   |||||
Db 153 ACCCAGAGGATGCTGAAGCAGCTGTGCTCTCAAAAGCCCCGCGGAGGGCAGATTTTCCAGT 94

QY 301 gaacgcagcgagacaccaaaattgaagtgtatccagttggtgaaaaaacctgtcacctat 360
   |||||
Db 93 GAACGCAGCCGAGACACCAAATTTGAAGTGATCCAGTTGGTGAAAAAACCTGTCTACCTAT 34

QY 361 gtaaggggagtttatcgccatggaaatttcaga 393
```

||||| 33 GTAAGGGGAGTTTATCGCCCATGGAATTCAGA 1

Db 33 GTAAGGGGAGTTTATCGCCCATGGAATTCAGA 1

RESULT 3

Z55555

ID Z55555 standard; cDNA; 1302 BP.

XX Z55555;

AC Z55555;

DT 14-MAR-2000 (first entry)

XX Canine interleukin-13 (IL-13) clone 80 cDNA.

DE Canine interleukin-13 (IL-13) clone 80 cDNA.

XX Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;

KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.

XX Canis familiaris.

OS Canis familiaris.

XX Key Location/Qualifiers

FT CDS 52..447

FT /\*tag= a

FT /product= "Canine IL-13 clone 80"

XX WO9961618-A2.

PN 02-DEC-1999.

XX 28-MAY-1999; 99WO-US11942.

PF 29-MAY-1998; 98US-0087306.

PR (HESK-) HESKA CORP.

XX Sim G, Yang S, Dreitz MJ, Wonderling RS;

PI WPI; 2000-072623/06.

XX P-PSDB; Y58221.

DR Nucleic acids encoding immunoregulatory proteins from cats or dogs,

XX useful for treating or preventing e.g. tumors or autoimmune disease

PS Claim 1i; Page 229-230; 264pp; English.

XX Sequences Z55552-Z55560 and Z55561-Z55566 represent cDNA

CC sequences encoding canine interleukin-13 (IL-13) clones 80

CC and 78 respectively. The invention relates to canine

CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or

CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline

CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage

CC colony-stimulating factor (GM-CSF), and nucleotides which encode these

CC immunoregulatory proteins. The proteins, their associated

CC nucleic acids, specific antibodies and inhibitors may be used as

CC vaccines for therapeutic or prophylactic regulation of an immune

CC response in animals (particularly cats, dogs, horses and humans).

CC They may be used to treat autoimmune or infectious diseases including

CC allergies, tumours, inflammation and graft rejection, and to increase

CC the response from a co-administered antigen. The nucleotide sequences

CC can also be used for the recombinant production of a protein, while

CC nucleotide fragments are useful as probes, as amplification primers and

CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).

CC The proteins may be used to raise antibodies and to screen for

CC modulators of activity, while the antibodies may be used in detection,

CC and in drug targeting.

XX Sequence 1302 BP; 337 A; 318 C; 340 G; 307 T; 0 other;

SQ

Query Match 100.0%; Score 393; DB 21; Length 1302;

Best Local Similarity 100.0%; Pred. NO. 4.9e-103;

Matches 393; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atggcgctctgtgactgtgttcattgtctcaccctgcctcggtgccttgcctccccg 60

||||| 52 atggcgctctgtgactgtgttcattgtctcaccctgcctcggtgccttgcctccccg 111

Db 52 atggcgctctgtgactgtgttcattgtctcaccctgcctcggtgccttgcctccccg 111

QY 61 agccctgtgactccctcccaaccctcaaggagctcattgaggagctggtcaacatcacc 120

XX 112 agccctgtgactccctcccaaccctcaaggagctcattgaggagctggtcaacatcacc 171

Db 121 cagaatcaggcatccctctgcaacggcagcatggtgtgagcgtaacctgaccgcgcgc 180

XX 172 cagaatcaggcatccctctgcaacggcagcatggtgtgagcgtaacctgaccgcgcgc 231

Db 181 atgtactgcgcagctctagaatctctgatcaatgtctcgcactgcagcgcctccaaagg 240

XX 232 atgtactgcgcagctctagaatctctgatcaatgtctcgcactgcagcgcctccaaagg 291

Db 241 acccagaggtgctgaaaagcactgtgctctcaaaaagcccgcggcaggcagatttccagt 300

XX 292 acccagaggtgctgaaaagcactgtgctctcaaaaagcccgcggcaggcagatttccagt 351

QY 301 gaacgcagccgagacacacaaaattgaagtgtccagttggtgaaaaaacctgtcacctat 360

XX 352 gaacgcagccgagacacacaaaattgaagtgtccagttggtgaaaaaacctgtcacctat 411

Db 361 gtaaggggagtttatcgccatggaaaatttcaga 393

XX 412 gtaaggggagtttatcgccatggaaaatttcaga 444

RESULT 4

Z55556/c

ID Z55556 standard; cDNA; 1302 BP.

XX Z55556;

AC Z55556;

DT 14-MAR-2000 (first entry)

XX Canine interleukin-13 (IL-13) clone 80 cDNA complement.

DE Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;

KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.

XX Canis familiaris.

OS Canis familiaris.

XX Key Location/Qualifiers

FT CDS complement (856..1251)

FT /\*tag= a

FT /product= "Canine IL-13 clone 80"

XX WO9961618-A2.

PN 02-DEC-1999.

XX 28-MAY-1999; 99WO-US11942.

PR 29-MAY-1998; 98US-0087306.

XX (HESK-) HESKA CORP.

XX Sim G, Yang S, Dreitz MJ, Wonderling RS;

PI WPI; 2000-072623/06.

XX P-PSDB; Y58221.

DR Nucleic acids encoding immunoregulatory proteins from cats or dogs,

XX useful for treating or preventing e.g. tumors or autoimmune disease

PS Claim 1i; Page 231-232; 264pp; English.

XX Sequences Z55552-Z55560 and Z55561-Z55566 represent cDNA

CC sequences encoding canine interleukin-13 (IL-13) clones 80

CC and 78 respectively. The invention relates to canine

CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or

CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline



interferon-alpha (IFN-alpha) and feline granulocyte macrophage colony-stimulating factor (GM-CSF), and nucleotides which encode these immunoregulatory proteins. The proteins, their associated nucleic acids, specific antibodies and inhibitors may be used as vaccines for therapeutic or prophylactic regulation of an immune response in animals (particularly cats, dogs, horses and humans). They may be used to treat autoimmune or infectious diseases including allergies, tumours, inflammation and graft rejection, and to increase the response from a co-administered antigen. The nucleotide sequences can also be used for the recombinant production of a protein, while nucleotide fragments are useful as probes, as amplification primers and as sources of inhibitory therapeutics (e.g., antisense oligonucleotides). The proteins may be used to raise antibodies and to screen for modulators of activity, while the antibodies may be used in detection, and in drug targeting.

29-MAY-1998; 98US-0087306.  
(HESK-) HESKA CORP.  
Sim G, Yang S, Dreitz MJ, Wonderling RS;  
WPI; 2000-072623/06.  
P-PSDB; Y58223.  
Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
useful for treating or preventing e.g. tumors or autoimmune disease  
Claim 1i; Page 238-239; 264pp; English.  
Sequences 255552-255560 and 255561-255566 represent cDNA  
sequences encoding canine interleukin-13 (IL-13) clones 80  
and 78 respectively. The invention relates to canine  
IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or  
feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline  
interferon-alpha (IFN-alpha) and feline granulocyte macrophage  
colony-stimulating factor (GM-CSF), and nucleotides which encode these  
immunoregulatory proteins. The proteins, their associated  
nucleic acids, specific antibodies and inhibitors may be used as  
vaccines for therapeutic or prophylactic regulation of an immune  
response in animals (particularly cats, dogs, horses and humans).  
They may be used to treat autoimmune or infectious diseases including  
allergies, tumours, inflammation and graft rejection, and to increase  
the response from a co-administered antigen. The nucleotide sequences  
can also be used for the recombinant production of a protein, while  
nucleotide fragments are useful as probes, as amplification primers and  
as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
The proteins may be used to raise antibodies and to screen for  
modulators of activity, while the antibodies may be used in detection,  
and in drug targeting.  
Sequence 390 BP; 92A; 117 C; 99 G; 82 T; 0 other;



ID 255564 standard; cDNA; 390 BP.  
XX  
AC 255564;  
DT 14-MAR-2000 (first entry)  
XX  
DE Canine interleukin-13 (IL-13) clone 78 cDNA coding region complement.  
XX  
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;  
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.  
XX  
OS Canis familiaris.  
XX  
PN WO9961618-A2.  
XX  
PD 02-DEC-1999.  
XX  
PF 28-MAY-1999; 99WO-US11942.  
XX  
PR 29-MAY-1998; 98US-0087306.  
XX  
PA (HESK-) HESKA CORP.  
XX  
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;  
XX  
DR WPI; 2000-072623/06.  
DR P-PSDB; Y58223.  
XX  
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
PT useful for treating or preventing e.g. tumors or autoimmune disease  
XX  
PS Claim 1i; Page 239; 264pp; English.  
XX  
CC Sequences 255552-255560 and 255561-255566 represent cDNA  
CC sequences encoding canine interleukin-13 (IL-13) clones 80  
CC and 78 respectively. The invention relates to canine  
CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or  
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline  
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage  
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these  
CC immunoregulatory proteins. The proteins, their associated  
CC nucleic acids, specific antibodies and inhibitors may be used as  
CC vaccines for therapeutic or prophylactic regulation of an immune  
CC response in animals (particularly cats, dogs, horses and humans).  
CC They may be used to treat autoimmune or infectious diseases including  
CC allergies, tumours, inflammation and graft rejection, and to increase  
CC the response from a co-administered antigen. The nucleotide sequences  
CC can also be used for the recombinant production of a protein, while  
CC nucleotide fragments are useful as probes, as amplification primers and  
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
CC The proteins may be used to raise antibodies and to screen for  
CC modulators of activity, while the antibodies may be used in detection,  
CC and in drug targeting.  
XX  
SQ Sequence 390 BP; 82 A; 99 C; 117 G; 92 T; 0 other;

Query Match 95.9%; Score 377; DB 21; Length 390;  
Best Local Similarity 99.2%; Pred. No. 1.2e-98;  
Matches 390; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 1 atggcgctctggtgactgtggtcattgtctcaccctgcctcggtgacctgacctccccg 60  
|||||  
Db 390 ATGGCGCTCTGGTTGACTGTGGTCAATTGCTCTCACCTGCCTCGGTGGCTTGCCTCCCCG 331  
|||||  
QY 61 agccctgtgactccctcccaaccctcaaggagctcattgaggagctggtcaacatcacc 120  
|||||  
Db 330 AGCCCTGTGACTCCCTCCCAACCCCTCAAGGAGCTCATTTGAGGAGCTGGTCAACATCACC 271  
|||||  
QY 121 cagaatcaggcatccctctgcaacgcagcagcatggtgtgagcgtcaacctgacctccggc 180  
|||||  
Db 270 CAGAATCAGGCATCCCTCTGTCAACGGCAGCATGGTGTGGAGCGTCAACCTGACCGCGGC 211  
|||||

QY 181 atgtactgcgcagctctagaatctctgatcaatgtctcgcagctgcagcgccatccaaagg 240  
|||||  
Db 210 ATGTACTGCGCAGCTCTAGAAATCTCTGATCAATGTCTCCGACTGCAGCGCCATCCAAAGG 151  
|||||  
QY 241 acccagaggatgctgaaagcactgtgctctctcaaaagcccgccgagggcagatttccagt 300  
|||||  
Db 150 ACCCAGAGGATGCTGAAAGCACTGTGCTCTCAAAAGCCCGCGCAGG---GATTTCAGT 94  
|||||  
QY 301 gaacgcagccgagacacacaaatgaagtgtccagttggtgaaaaacctgctcacctat 360  
|||||  
Db 93 GAACGCAGCCGAGACACCAAAATGAAGTGATCCAGTTGGTGAANAACCTGCTCACCTAT 34  
|||||  
QY 361 gtaaggggagtttatcgccatggaaatttcaga 393  
|||||  
Db 33 GTAAGGGGAGTTTATCGCCCATGGAATTTTCAGA 1  
|||||  
RESULT 7  
Z55561  
ID Z55561 standard; cDNA; 1269 BP.  
XX  
AC Z55561;  
XX  
DT 14-MAR-2000 (first entry)  
XX  
DE Canine interleukin-13 (IL-13) clone 78 cDNA.  
XX  
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;  
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.  
XX  
OS Canis familiaris.  
XX  
FH Key Location/Qualifiers  
FT CDS 57..449  
FT /\*tag= a  
FT /product= "Canine IL-13 clone 78"  
XX  
PN WO9961618-A2.  
XX  
PD 02-DEC-1999.  
XX  
PF 28-MAY-1999; 99WO-US11942.  
XX  
PR 29-MAY-1998; 98US-0087306.  
XX  
PA (HESK-) HESKA CORP.  
XX  
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;  
XX  
DR WPI; 2000-072623/06.  
DR P-PSDB; Y58223.  
XX  
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
PT useful for treating or preventing e.g. tumors or autoimmune disease  
XX  
PS Claim 1i; Page 235-236; 264pp; English.  
XX  
CC Sequences 255552-255560 and 255561-255566 represent cDNA  
CC sequences encoding canine interleukin-13 (IL-13) clones 80  
CC and 78 respectively. The invention relates to canine  
CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or  
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline  
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage  
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these  
CC immunoregulatory proteins. The proteins, their associated  
CC nucleic acids, specific antibodies and inhibitors may be used as  
CC vaccines for therapeutic or prophylactic regulation of an immune  
CC response in animals (particularly cats, dogs, horses and humans).  
CC They may be used to treat autoimmune or infectious diseases including  
CC allergies, tumours, inflammation and graft rejection, and to increase  
CC the response from a co-administered antigen. The nucleotide sequences  
CC can also be used for the recombinant production of a protein, while  
CC nucleotide fragments are useful as probes, as amplification primers and

CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
CC The proteins may be used to raise antibodies and to screen for  
CC modulators of activity, while the antibodies may be used in detection,  
CC and in drug targetting.

XX Sequence 1269 BP; 302 A; 320 C; 340 G; 307 T; 0 other;

Query Match 95.9%; Score 377; DB 21; Length 1269;  
Best Local Similarity 99.2%; Pred. No. 1.8e-98;  
Matches 390; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 1 atggcgctctgtgactgtggtcattgtctcactgcctcggtggtgctgctccccc 60  
Db 57 atggcgctctgtgactgtggtcattgtctcactgcctcggtggtgctgctccccc 116  
QY 61 agccctgtgactccctcccaaccctcaaggagctcattgaggagctggtcaacatcacc 120  
Db 117 agccctgtgactccctcccaaccctcaaggagctcattgaggagctggtcaacatcacc 176  
QY 121 cagaatcaggcatccctctgcaacggcagcatggtgtgagcgtcaacacctgaccgcccgc 180  
Db 177 cagaatcaggcatccctctgcaacggcagcatggtgtgagcgtcaacacctgaccgcccgc 236  
QY 181 atgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgccatccaaagg 240  
Db 237 atgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgccatccaaagg 296  
QY 241 accagaggatgctgaaagcactgtgctctcaaaagcccgcgagggcagatttccagt 300  
Db 297 accagaggatgctgaaagcactgtgctctcaaaagcccgcgagggcagatttccagt 353  
QY 301 gaacgcagccgagacaccacaaattgaagtgtccagttggtgaaacacctgctcacctat 360  
Db 354 gaacgcagccgagacaccacaaattgaagtgtccagttggtgaaacacctgctcacctat 413  
QY 361 gtaaggggagtttatcgccatggaattttcaga 393  
Db 414 gtaaggggagtttatcgccatggaattttcaga 446

RESULT 8  
255562/c  
ID 255562 standard; cDNA; 1269 BP.  
XX  
AC 255562;  
XX  
DT 14-MAR-2000 (first entry)  
XX  
DE Canine interleukin-13 (IL-13) clone 78 cDNA complement.  
XX  
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;  
XX immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.  
OS Canis familiaris.  
XX  
FH Key Location/Qualifiers  
FT CDS complement (821..1213)  
FT /\*tag= a  
FT /product= "Canine IL-13 clone 78"

XX WO9961618-A2.  
XX  
PD 02-DEC-1999.  
XX  
PF 28-MAY-1999; 99WO-US11942.  
XX  
PR 29-MAY-1998; 98US-0087306.  
XX (HESK-) HESKA CORP.  
XX  
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;  
XX

DR WPI; 2000-072623/06.  
DR P-PSDB; Y58223.  
XX  
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
XX useful for treating or preventing e.g. tumors or autoimmune disease  
PS Claim 1i; Page 237-238; 264pp; English.  
XX

CC Sequences 255552-255560 and 255561-255566 represent cDNA  
CC sequences encoding canine interleukin-13 (IL-13) clones 80  
CC and 78 respectively. The invention relates to canine  
CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or  
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline  
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage  
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these  
CC immunoregulatory proteins. The proteins, their associated  
CC nucleic acids, specific antibodies and inhibitors may be used as  
CC vaccines for therapeutic or prophylactic regulation of an immune  
CC response in animals (particularly cats, dogs, horses and humans).  
CC They may be used to treat autoimmune or infectious diseases including  
CC allergies, tumours, inflammation and graft rejection, and to increase  
CC the response from a co-administered antigen. The nucleotide sequences  
CC can also be used for the recombinant production of a protein, while  
CC nucleotide fragments are useful as probes, as amplification primers and  
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
CC The proteins may be used to raise antibodies and to screen for  
CC modulators of activity, while the antibodies may be used in detection,  
CC and in drug targetting.

XX Sequence 1269 BP; 307 A; 340 C; 320 G; 302 T; 0 other;

Query Match 95.9%; Score 377; DB 21; Length 1269;  
Best Local Similarity 99.2%; Pred. No. 1.8e-98;  
Matches 390; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 1 atggcgctctgtgactgtggtcattgtctcactgcctcggtggtgctgctccccc 60  
Db 1213 atggcgctctgtgactgtggtcattgtctcactgcctcggtggtgctgctccccc 1154  
QY 61 agccctgtgactccctcccaaccctcaaggagctcattgaggagctggtcaacatcacc 120  
Db 1153 agccctgtgactccctcccaaccctcaaggagctcattgaggagctggtcaacatcacc 1094  
QY 121 cagaatcaggcatccctctgcaacggcagcatggtgtgagcgtcaacacctgaccgcccgc 180  
Db 1093 cagaatcaggcatccctctgcaacggcagcatggtgtgagcgtcaacacctgaccgcccgc 1034  
QY 181 atgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgccatccaaagg 240  
Db 1033 atgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgccatccaaagg 974  
QY 241 accagaggatgctgaaagcactgtgctctcaaaagcccgcgagggcagatttccagt 300  
Db 973 accagaggatgctgaaagcactgtgctctcaaaagcccgcgagggcagatttccagt 917  
QY 301 gaacgcagccgagacaccacaaattgaagtgtatccagttggtgaaacacctgctcacctat 360  
Db 916 gaacgcagccgagacaccacaaattgaagtgtatccagttggtgaaacacctgctcacctat 857  
QY 361 gtaaggggagtttatcgccatggaattttcaga 393  
Db 856 gtaaggggagtttatcgccatggaattttcaga 824

RESULT 9  
255559  
ID 255559 standard; cDNA; 333 BP.  
XX  
AC 255559;  
XX  
DT 14-MAR-2000 (first entry)  
XX

DE Canine mature interleukin-13 (IL-13) clone 80 cDNA.  
XX  
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;  
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.  
XX  
OS Canis familiaris.  
OS  
PN WO9961618-A2.  
XX  
PD 02-DEC-1999.  
XX  
PF 28-MAY-1999; 99WO-US11942.  
XX  
PR 29-MAY-1998; 98US-0087306.  
XX  
PA (HESK-) HESKA CORP.  
XX  
PI Sim G, Yang S, Drelitz MJ, Wonderling RS;  
DR WPI; 2000-072623/06.  
DR P-PSDB; Y58222.  
XX  
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
PT useful for treating or preventing e.g. tumors or autoimmune disease  
XX  
PS Claim 1i; Page 233-234; 264pp; English.  
XX  
CC Sequences 255552-255560 and 255561-255566 represent cDNA  
CC sequences encoding canine interleukin-13 (IL-13) clones 80  
CC and 78 respectively. The invention relates to canine  
CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or  
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline  
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage  
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these  
CC immunoregulatory proteins. The proteins, their associated  
CC nucleic acids, specific antibodies and inhibitors may be used as  
CC vaccines for therapeutic or prophylactic regulation of an immune  
CC response in animals (particularly cats, dogs, horses and humans).  
CC They may be used to treat autoimmune or infectious diseases including  
CC allergies, tumours, inflammation and graft rejection, and to increase  
CC the response from a co-administered antigen. The nucleotide sequences  
CC can also be used for the recombinant production of a protein, while  
CC nucleotide fragments are useful as probes, as amplification primers and  
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
CC The proteins may be used to raise antibodies and to screen for  
CC modulators of activity, while the antibodies may be used in detection,  
CC and in drug targeting.  
XX  
SQ Sequence 333 BP; 89 A; 97 C; 83 G; 64 T; 0 other;

Query Match 84.7%; Score 333; DB 21; Length 333;  
Best Local Similarity 100.0%; Pred. No. 4.4e-86;  
Matches 333; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 agccctgtgactccctcccaaccctcaaggagctcattgaggagctggtcaacatcacc 120  
|||||  
Db 1 agccctgtgactccctcccaaccctcaaggagctcattgaggagctggtcaacatcacc 60  
|||||

QY 121 cagaatcaggcatccctctgcaacggcagcatggtgtggagcgtcaacctgaccgcggc 180  
|||||  
Db 61 cagaatcaggcatccctctgcaacggcagcatggtgtggagcgtcaacctgaccgcggc 120  
|||||

QY 181 atgtactgcgcagctctagaaatctctgatcaatgtctccgactgcagcgccatccaaagg 240  
|||||  
Db 121 atgtactgcgcagctctagaaatctctgatcaatgtctccgactgcagcgccatccaaagg 180  
|||||

QY 241 acccagaggatgctgaaagcactgtgctctctcaaaagcccgccgagggcagatttccagt 300  
|||||  
Db 181 acccagaggatgctgaaagcactgtgctctctcaaaagcccgccgagggcagatttccagt 240  
|||||

QY 301 gaacgcagccgagacaccaaattgaagtgatccagttggtgaaacacctgctcacctat 360  
|||||

Db 241 gaacgcagccgagacaccaaattgaagtgatccagttggtgaaacacctgctcacctat 300  
QY 361 gtaaggggagtttatcgcccatggaaatttcaga 393  
|||||  
Db 301 gtaaggggagtttatcgcccatggaaatttcaga 333  
|||||

RESULT 10  
255560/C  
ID 255560 standard; cDNA; 333 BP.  
XX  
AC 255560;  
XX  
DT 14-MAR-2000 (first entry)  
XX  
DE Canine mature interleukin-13 (IL-13) clone 80 cDNA complement.  
XX  
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;  
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.  
XX  
OS Canis familiaris.  
XX  
PN WO9961618-A2.  
XX  
PD 02-DEC-1999.  
XX  
PF 28-MAY-1999; 99WO-US11942.  
XX  
PR 29-MAY-1998; 98US-0087306.  
XX  
PA (HESK-) HESKA CORP.  
XX  
PI Sim G, Yang S, Drelitz MJ, Wonderling RS;  
XX WPI; 2000-072623/06.  
DR P-PSDB; Y58222.  
XX  
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
PT useful for treating or preventing e.g. tumors or autoimmune disease  
XX  
PS Claim 1i; Page 235; 264pp; English.  
XX  
CC Sequences 255552-255560 and 255561-255566 represent cDNA  
CC sequences encoding canine interleukin-13 (IL-13) clones 80  
CC and 78 respectively. The invention relates to canine  
CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or  
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline  
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage  
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these  
CC immunoregulatory proteins. The proteins, their associated  
CC nucleic acids, specific antibodies and inhibitors may be used as  
CC vaccines for therapeutic or prophylactic regulation of an immune  
CC response in animals (particularly cats, dogs, horses and humans).  
CC They may be used to treat autoimmune or infectious diseases including  
CC allergies, tumours, inflammation and graft rejection, and to increase  
CC the response from a co-administered antigen. The nucleotide sequences  
CC can also be used for the recombinant production of a protein, while  
CC nucleotide fragments are useful as probes, as amplification primers and  
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
CC The proteins may be used to raise antibodies and to screen for  
CC modulators of activity, while the antibodies may be used in detection,  
CC and in drug targeting.  
XX  
SQ Sequence 333 BP; 64 A; 83 C; 97 G; 89 T; 0 other;

Query Match 84.7%; Score 333; DB 21; Length 333;  
Best Local Similarity 100.0%; Pred. No. 4.4e-86;  
Matches 333; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 agccctgtgactccctcccaaccctcaaggagctcattgaggagctggtcaacatcacc 120  
|||||  
Db 333 AGCCCTGTGACTCCCTCCCAACCCTCAAGGAGCTCATTTGAGGAGCTGGTCAACATCACC 274  
|||||

QY 121 cagaatcaggcatccctctgcaacggcagcatggtgtggagcgtcaacctgaccgcccgc 180  
|||||  
Db 273 CAGAAATCAGGCATCCCTCTGCAACGGCAGCATGGTGTGGAGCGTCAACCTGACCGCCGGC 214  
  
QY 181 atgtactgcgcagctctagaatctctgatcaaatgtctccgactgcagcgccatccaaagg 240  
|||||  
Db 213 ATGTAATGCGCAGCTCTAGAAATCTCTGATCAATGTCTCCGACTGCAGCGCCATCCAAAGG 154  
  
QY 241 acccagaggtgctgaaagcactgtgctctcaaaagcccgccgagcagatttccagt 300  
|||||  
Db 153 ACCCAGAGGATGCTGAAAGCACCTGTGCTCTCAAAAGCCCGCGGCGAGAGATTTCAGT 94  
  
QY 301 gaacgcagccgagacaccaaattgaagtgtccagttggtgaaacacctgtcacctat 360  
|||||  
Db 93 GAACGCAGCCGAGACACCAAATTTGAAGTGATCCAGTTGGTGAAACCTGCTCACCTAT 34  
  
QY 361 gtaaggggagtttatcgcccatggaatttcaga 393  
|||||  
Db 33 GTAAGGGGAGTTTATCGCCCATGGAAATTTTCAGA 1  
  
RESULT 11  
Z55565  
ID Z55565 standard; cDNA; 330 BP.  
XX  
AC Z55565;  
XX  
DT 14-MAR-2000 (first entry)  
XX  
DE Canine mature interleukin-13 (IL-13) clone 78 cDNA.  
XX  
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;  
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.  
XX  
OS Canis familiaris.  
XX  
PN WO9961618-A2.  
XX  
PD 02-DEC-1999.  
XX  
PF 28-MAY-1999; 99WO-US11942.  
XX  
PR 29-MAY-1998; 98US-0087306.  
XX  
PA (HESK-) HESKA CORP.  
XX  
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;  
XX  
KW WPI; 2000-072623/06.  
DR P-PSDB; Y58224.  
XX  
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
PT useful for treating or preventing e.g. tumors or autoimmune disease  
XX  
PS Claim 1i; Page 239-240; 264pp; English.  
XX  
CC Sequences Z55552-Z55560 and Z55561-Z55566 represent cDNA  
CC sequences encoding canine interleukin-13 (IL-13) clones 80  
CC and 78 respectively. The invention relates to canine  
CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or  
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline  
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage  
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these  
CC immunoregulatory proteins. The proteins, their associated  
CC nucleic acids, specific antibodies and inhibitors may be used as  
CC vaccines for therapeutic or prophylactic regulation of an immune  
CC response in animals (particularly cats, dogs, horses and humans).  
CC They may be used to treat autoimmune or infectious diseases including  
CC allergies, tumours, inflammation and graft rejection, and to increase  
CC the response from a co-administered antigen. The nucleotide sequences  
CC can also be used for the recombinant production of a protein, while  
CC nucleotide fragments are useful as probes, as amplification primers and

CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
CC The proteins may be used to raise antibodies and to screen for  
CC modulators of activity, while the antibodies may be used in detection,  
CC and in drug targetting.  
XX  
SQ Sequence 330 BP; 88 A; 96 C; 82 G; 64 T; 0 other;  
  
Query Match 80.7%; Score 317; DB 21; Length 330;  
Best Local Similarity 99.1%; Pred. No. 1.7e-81;  
Matches 330; Conservative 0; Mismatches 0; Indels 3; Gaps 1;  
  
QY 61 agccctgtgactccctcccaacccctcaaggagctcattgagagctgggtcaacatcacc 120  
|||||  
Db 1 agccctgtgactccctcccaacccctcaaggagctcattgagagctgggtcaacatcacc 60  
  
QY 121 cagaatcaggcatccctctgcaacggcagcatggtgtggagcgtcaacctgaccgcccgc 180  
|||||  
Db 61 cagaatcaggcatccctctgcaacggcagcatggtgtggagcgtcaacctgaccgcccgc 120  
  
QY 181 atgtactgcgcagctctagaatctctgatcaaatgtctccgactgcagcgccatccaaagg 240  
|||||  
Db 121 atgtactgcgcagctctagaatctctgatcaaatgtctccgactgcagcgccatccaaagg 180  
  
QY 241 acccagaggtgctgaaagcactgtgctctcaaaagcccgccgagcagatttccagt 300  
|||||  
Db 181 acccagaggtgctgaaagcactgtgctctcaaaagcccgccgagcagatttccagt 237  
  
QY 301 gaacgcagccgagacaccaaattgaagtgtccagttggtgaaacacctgtcacctat 360  
|||||  
Db 238 gaacgcagccgagacaccaaattgaagtgtccagttggtgaaacacctgtcacctat 297  
  
QY 361 gtaaggggagtttatcgcccatggaatttcaga 393  
|||||  
Db 298 gtaaggggagtttatcgcccatggaatttcaga 330  
  
RESULT 12  
Z55566/c  
ID Z55566 standard; cDNA; 330 BP.  
XX  
AC Z55566;  
XX  
DT 14-MAR-2000 (first entry)  
XX  
DE Canine mature interleukin-13 (IL-13) clone 78 cDNA complement.  
XX  
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;  
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.  
XX  
OS Canis familiaris.  
XX  
PN WO9961618-A2.  
XX  
PD 02-DEC-1999.  
XX  
PF 28-MAY-1999; 99WO-US11942.  
XX  
PR 29-MAY-1998; 98US-0087306.  
XX  
PA (HESK-) HESKA CORP.  
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;  
XX  
DR WPI; 2000-072623/06.  
DR P-PSDB; Y58224.  
XX  
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
PT useful for treating or preventing e.g. tumors or autoimmune disease  
XX  
PS Claim 1i; Page 241; 264pp; English.  
XX  
CC Sequences Z55552-Z55560 and Z55561-Z55566 represent cDNA



sequences encoding canine interleukin-13 (IL-13) clones 80 and 78 respectively. The invention relates to canine IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline interferon-alpha (IFN-alpha) and feline granulocyte macrophage colony-stimulating factor (GM-CSF), and nucleotides which encode these immunoregulatory proteins. The proteins, their associated nucleic acids, specific antibodies and inhibitors may be used as vaccines for therapeutic or prophylactic regulation of an immune response in animals (particularly cats, dogs, horses and humans). They may be used to treat autoimmune or infectious diseases including allergies, tumours, inflammation and graft rejection, and to increase the response from a co-administered antigen. The nucleotide sequences can also be used for the recombinant production of a protein, while nucleotide fragments are useful as probes, as amplification primers and as sources of inhibitory therapeutics (e.g., antisense oligonucleotides). The proteins may be used to raise antibodies and to screen for modulators of activity, while the antibodies may be used in detection, and in drug targeting.

Sequence 330 BP; 64 A; 82 C; 96 G; 88 T; 0 other;

Query Match 80.7%; Score 317; DB 21; Length 330; Best Local Similarity 99.1%; Pred. No. 1.7e-81; Matches 330; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 61 agccctgtgactccctcccaaccctcaaggagctcattgaggagtggtcaacatcacc 120  
|||||  
Db 330 AGCCTGTGACTCCCTCCCAACCTCAAGGAGCTCATTGAGGAGCTGGTCAACATCACC 271  
|||||  
QY 121 cagaatcaggcatccctctgcacaggcagcatggtgtggagcgtcaacctgaccgcggc 180  
|||||  
Db 270 CAGAATCAGGCATCCCTCTGCAACGGCAGCATGGTGTGGAGCGTCAACCTGACCGCGGC 211  
|||||  
QY 181 atgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgccatccaaagg 240  
|||||  
Db 210 ATGTACTGCGCAGCTCTAGAAATCTCTGATCAATGTCTCCGACTGCAGCGCCATCCAAAGG 151  
|||||  
QY 241 acccagaggatgctgaaagcactgtgctctcaaaaagccgcggcaggcagatttccagt 300  
|||||  
Db 150 ACCCAGAGGATGCTGAAAGCACTGTGCTCTCAAAAGCCCGCGGCAGG---GATTTCAGT 94  
|||||  
QY 301 gaacgcagccgagacaccaaattgaagtgtccagttggtgaaaaacctgctcacctat 360  
|||||  
Db 93 GAACGCAGCCGAGACACCAAAATTGAAGTGATCCAGTTGGTGAAAAACCTGCTCACCTAT 34  
|||||  
QY 361 gtaaggggagtttatcgcccatggaatttcaga 393  
|||||  
Db 33 GTAAGGGGAGTTTATCGCCCATGGAAATTTTCAGA 1  
|||||

RESULT 13  
Z55554  
ID 255554 standard; cDNA; 278 BP.  
XX  
AC Z55554;  
XX  
XX  
DT 14-MAR-2000 (first entry)  
XX  
DE Canine interleukin-13 (IL-13) cDNA probe.  
XX  
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;  
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.  
XX  
OS Canis familiaris.  
XX  
PN WO9961618-A2.  
XX  
PD 02-DEC-1999.  
XX  
PF 28-MAY-1999; 99WO-US11942.  
XX

29-MAY-1998; 98US-0087306.  
(HESK-) HESKA CORP.  
Slim G, Yang S, Dreitz MJ, Wonderling RS;  
WPI; 2000-072623/06.  
Nucleic acids encoding immunoregulatory proteins from cats or dogs, useful for treating or preventing e.g. tumors or autoimmune disease  
Claim 1i; Page 229; 264pp; English.  
Sequences Z55552-Z55560 and Z55561-Z55566 represent cDNA sequences encoding canine interleukin-13 (IL-13) clones 80 and 78 respectively. The invention relates to canine IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline interferon-alpha (IFN-alpha) and feline granulocyte macrophage colony-stimulating factor (GM-CSF), and nucleotides which encode these immunoregulatory proteins. The proteins, their associated nucleic acids, specific antibodies and inhibitors may be used as vaccines for therapeutic or prophylactic regulation of an immune response in animals (particularly cats, dogs, horses and humans). They may be used to treat autoimmune or infectious diseases including allergies, tumours, inflammation and graft rejection, and to increase the response from a co-administered antigen. The nucleotide sequences can also be used for the recombinant production of a protein, while nucleotide fragments are useful as probes, as amplification primers and as sources of inhibitory therapeutics (e.g., antisense oligonucleotides). The proteins may be used to raise antibodies and to screen for modulators of activity, while the antibodies may be used in detection, and in drug targeting.

Sequence 278 BP; 58 A; 93 C; 69 G; 58 T; 0 other;

Query Match 70.7%; Score 278; DB 21; Length 278; Best Local Similarity 100.0%; Pred. No. 2.2e-70; Matches 278; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atggcgctctggtgactgtggtcattgctctcacctgcctcggtggccttgccctccccg 60  
|||||  
Db 1 atggcgctctggtgactgtggtcattgctctcacctgcctcggtggccttgccctccccg 60  
|||||  
QY 61 agccctgtgactccctcccaaccctcaaggagctcatgtgaggagctggtcaacatcacc 120  
|||||  
Db 61 agccctgtgactccctcccaaccctcaaggagctcatgtgaggagctggtcaacatcacc 120  
|||||  
QY 121 cagaatcaggcatccctctgcacaggcagcatggtgtggagcgtcaacctgaccgcggc 180  
|||||  
Db 121 cagaatcaggcatccctctgcacaggcagcatggtgtggagcgtcaacctgaccgcggc 180  
|||||  
QY 181 atgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgccatccaaagg 240  
|||||  
Db 181 atgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgccatccaaagg 240  
|||||  
QY 241 acccagaggatgctgaaagcactgtgctctcaaaagcc 278  
|||||  
Db 241 acccagaggatgctgaaagcactgtgctctcaaaagcc 278  
|||||

RESULT 14  
Z55553  
ID Z55553 standard; cDNA; 272 BP.  
XX  
AC Z55553;  
XX  
DT 14-MAR-2000 (first entry)  
XX  
DE Canine interleukin-13 (IL-13) cDNA fragment nCaIL13-272.  
XX  
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;

KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.  
XX Canis familiaris.  
OS  
XX WO9961618-A2.  
PN  
XX  
PD 02-DEC-1999.  
XX  
XX 28-MAY-1999; 99WO-US11942.  
PF  
XX 29-MAY-1998; 98US-0087306.  
PR  
XX (HESK-) HESKA CORP.  
PA  
XX  
XX Sim G, Yang S, Dreitz MJ, Wonderling RS;  
PI WPI; 2000-072623/06.  
XX  
XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
PT useful for treating or preventing e.g. tumors or autoimmune disease -  
PT  
XX  
PS Claim 1i; Page 228; 264pp; English.  
XX  
CC Sequences 255552-255560 and 255561-255566 represent cDNA  
CC sequences encoding canine interleukin-13 (IL-13) clones 80  
CC and 78 respectively. The invention relates to canine  
CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or  
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline  
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage  
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these  
CC immunoregulatory proteins. The proteins, their associated  
CC nucleic acids, specific antibodies and inhibitors may be used as  
CC vaccines for therapeutic or prophylactic regulation of an immune  
CC response in animals (particularly cats, dogs, horses and humans).  
CC They may be used to treat autoimmune or infectious diseases including  
CC allergies, tumours, inflammation and graft rejection, and to increase  
CC the response from a co-administered antigen. The nucleotide sequences  
CC can also be used for the recombinant production of a protein, while  
CC nucleotide fragments are useful as probes, as amplification primers and  
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
CC The proteins may be used to raise antibodies and to screen for  
CC modulators of activity, while the antibodies may be used in detection,  
CC and in drug targeting.  
XX  
SQ Sequence 272 BP; 64 A; 91 C; 69 G; 48 T; 0 other;  
  
Query Match 69.2%; Score 272; DB 21; Length 272;  
Best Local Similarity 100.0%; Pred. No. 1.2e-68;  
Matches 272; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 45 tggccttgccctcccgagccctgtgactccctccccaacccctcaaggagctcattgagga 104  
Db 1 tggccttgccctcccgagccctgtgactccctccccaacccctcaaggagctcattgagga 60  
  
Qy 105 gctggtcaacatcacccagaatcaggcatccctctgcaacggcagcatggtgtggagcgt 164  
Db 61 gctggtcaacatcacccagaatcaggcatccctctgcaacggcagcatggtgtggagcgt 120  
  
Qy 165 caacctgaccgcgggcatgtactgcgcagctctagaaatctctgatcaatgtctccgactg 224  
Db 121 caacctgaccgcgggcatgtactgcgcagctctagaaatctctgatcaatgtctccgactg 180  
  
Qy 225 cagcgccatccaaaggaccagagatgctgaaagcactgtgctctcaaaagcccgcgcc 284  
Db 181 cagcgccatccaaaggaccagagatgctgaaagcactgtgctctcaaaagcccgcgcc 240  
  
Qy 285 agggcagatttccagtgaacgcgagacgagaca 316  
Db 241 agggcagatttccagtgaacgcgagacgagaca 272

RESULT 15

4/

F21334  
ID F21334 standard; DNA; 1270 BP.  
XX  
AC F21334;  
XX  
DT 14-MAR-2001 (first entry)  
XX  
DE Human low adenosine antisense oligonucleotide related sequence #2901.  
XX  
KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;  
KW human; airway disorder; bronchoconstriction; lung inflammation;  
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;  
KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;  
KW respiratory obstruction; pulmonary obstruction; impeded respiration;  
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;  
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;  
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;  
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;  
KW cancer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200062736-A2.  
XX  
PD 26-OCT-2000.  
XX  
PF 24-MAR-2000; 2000WO-US08020.  
XX  
XX 06-APR-1999; 99US-0127958.  
PR  
XX (UYEC-) UNIV EAST CAROLINA.  
PA (NYCE/) NYCE J W.  
XX  
PI Nyce JW;  
XX  
DR WPI; 2000-679539/66.  
XX  
PT Low adenosine (A) content antisense oligonucleotides which do not  
PT trigger adenosine receptors during metabolism, useful e.g. for treating  
PT cancers and respiratory obstructions -  
XX  
PS Disclosure; Page 1336; 1592pp; English.  
XX  
CC The present invention describes low adenosine (A) content antisense  
CC oligonucleotides and compositions (I) comprising them. In the antisense  
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.  
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,  
CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.  
CC The antisense oligonucleotides and (I) can be used to down-regulate the  
CC expression and or activity of target polypeptides associated with  
CC lung/respiratory disorders and malignancies, such as stimulating and  
CC activating peptide factors and transmitters, transcription factors,  
CC immunoglobulins and antibodies, antibody receptors, cytokines and  
CC chemokines, endogenously produced specific and non-specific enzymes,  
CC binding proteins, adhesion molecules and their receptors, cytokine and  
CC chemokine receptors, adenosine receptors, bradykinin receptors, central  
CC nervous system (CNS) and peripheral nervous and non-nervous system  
CC receptors, CNS and peripheral nervous and non-nervous system peptide  
CC transmitters, defensins, growth factors, vasoactive peptides and  
CC receptors, binding proteins and malignancy associated proteins. The  
CC antisense oligonucleotides may be used in this way to treat disorders  
CC including respiratory obstruction (especially pulmonary obstruction  
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)  
CC and/or surfactant hypoproduction which are associated with a disease or  
CC condition selected from pulmonary vasoconstriction, inflammation,  
CC allergies, asthma, impeded respiration, respiratory distress syndrome  
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary  
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),  
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,  
CC and/or cancer. F18434 to F21543 represent human polynucleotide fragments  
CC and antisense oligonucleotides used in the exemplification of the  
XX present invention.

SQ Sequence 1270 BP; 288 A; 335 C; 336 G; 311 T; 0 other;

Query Match 62.8%; Score 246.8; DB 21; Length 1270;  
Best Local Similarity 78.4%; Pred. No. 3.2e-61;  
Matches 309; Conservative 0; Mismatches 82; Indels 3; Gaps 1;

QY	1	atggcgctctggttgactgtgtgctcattgctctcacctgcctcggtggccttgccctccccg	60
Db	45	atggcgcttttgttgaccacggtgctctcacttgctctgcttgcccttgccctcccc	104
QY	61	agccctgtgactccctcccccacccctcaaggagctcattgaggagctggtcaacatcacc	120
Db	105	ggccctgtgcctccctctacagccctcaggagctcattgaggagctggtcaacatcacc	164
QY	121	cagaatc--aggcatccctctgcaacggcgagcatggtgtggagggtcaacctgaccgcc	177
Db	165	cagaaccagaaaggctccgctctgcaatggcagcatggtatggagcatcaacctgacagct	224
QY	178	ggcatgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgccatccaa	237
Db	225	ggcatgtactgtgcagccctggaatccctgatcaacgtgtcaggctgcagtgccatcgag	284
QY	238	aggacccagaggatgctgaaagcactgtgtctctcaaaagcccgaggcgagatttcc	297
Db	285	aagacccagaggatgctgagcgattctgtcccgcacaaaggtctcagctggcgagtttcc	344
QY	298	agtgaacgcagccgagacacccaaattgaaagtgatccagttgtgaaaaaacctgctcacc	357
Db	345	agcttgcatgtcccgagacacccaaatcgaggtggcccgatttgtaaaaggacctgctctta	404
QY	358	tatgtaaggggagtttatcgccatggaaatttca	391
Db	405	catttaaaagaaactttttcgcgaggggacgggttca	438

Search completed: May 13, 2001, 14:29:54  
Job time: 18309 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 13, 2001, 14:21:14 ; Search time 226.02 Seconds  
(without alignments)  
303.596 Million cell updates/sec

Title: US-09-451-527-94  
Perfect score: 393  
Sequence: 1 atggcgctctgttgactgt.....atcgccatggaatttcaga 393

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 302621 seqs, 87301344 residues

Total number of hits satisfying chosen parameters: 605242

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_NA.\*  
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2: /cgnl\_7/ptodata/1/ina/5B\_COMB.seq.\*  
3: /cgnl\_7/ptodata/1/ina/6A\_COMB.seq.\*  
4: /cgnl\_7/ptodata/1/ina/6B\_COMB.seq.\*  
5: /cgnl\_7/ptodata/1/ina/PCTUS\_COMB.seq.\*  
6: /cgnl\_7/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	246.8	62.8	1290	1 US-08-012-543-1	Sequence 1, Appli
2	246.8	62.8	1290	5 PCT-US93-07645A-1	Sequence 1, Appli
3	246.8	62.8	1290	5 PCT-US93-07645-1	Sequence 1, Appli
4	245.2	62.4	1297	1 US-08-371-121-15	Sequence 15, Appl
5	204	51.9	384	1 US-08-371-121-17	Sequence 17, Appl
6	203.4	51.8	336	1 US-08-371-121-24	Sequence 24, Appl
7	202.2	51.5	425	1 US-08-594-469-4	Sequence 4, Appli
8	202.2	51.5	425	2 US-08-906-957-4	Sequence 4, Appli
9	202.2	51.5	4410	1 US-08-594-469-1	Sequence 1, Appli
10	202.2	51.5	4410	2 US-08-906-957-1	Sequence 1, Appli
11	201.8	51.3	336	1 US-08-371-121-2	Sequence 2, Appli
12	159.2	40.5	447	1 US-08-371-121-26	Sequence 26, Appl
13	159.2	40.5	1212	1 US-08-012-543-3	Sequence 3, Appli
14	159.2	40.5	1212	5 PCT-US93-07645A-3	Sequence 3, Appli
15	159.2	40.5	1212	5 PCT-US93-07645-3	Sequence 3, Appli
16	44.6	11.3	60	1 US-08-371-121-12	Sequence 12, Appl
17	44.6	11.3	102	1 US-08-371-121-10	Sequence 10, Appl
18	39.6	10.1	54	1 US-08-371-121-11	Sequence 11, Appl
19	39.6	10.1	96	1 US-08-371-121-9	Sequence 9, Appli
20	35.8	9.1	2249	3 US-08-814-052-19	Sequence 19, Appl
21	35.8	9.1	2300	3 US-08-814-052-18	Sequence 18, Appl
22	35.8	9.1	3183	2 US-08-939-218A-1	Sequence 1, Appli
23	35.8	9.1	3187	5 PCT-US95-06815-1	Sequence 1, Appli
24	35.8	9.1	3192	1 US-08-706-037-26	Sequence 26, Appl
25	35.8	9.1	3192	1 US-08-940-661A-1	Sequence 1, Appli
26	35.8	9.1	3192	2 US-09-083-485-1	Sequence 1, Appli
27	35.8	9.1	3192	2 US-09-005-397-26	Sequence 26, Appl

28	34.4	8.8	1322	4 US-09-128-450-27	Sequence 27, Appl
29	34.4	8.8	1521	1 US-08-496-855A-3	Sequence 3, Appli
30	34.4	8.8	1521	2 US-07-938-154-9	Sequence 9, Appli
31	34.4	8.8	1521	5 PCT-US91-02311-9	Sequence 9, Appli
32	34.4	8.8	2450	2 US-08-466-589-9	Sequence 9, Appli
33	34.4	8.8	2450	2 US-08-700-636-9	Sequence 9, Appli
34	34.4	8.8	2450	3 US-08-467-574-9	Sequence 9, Appli
35	33.2	8.4	2712	3 US-09-025-691-4	Sequence 4, Appli
36	32.4	8.2	720	4 US-09-094-359-3	Sequence 3, Appli
37	32.4	8.2	720	4 US-09-094-359-7	Sequence 7, Appli
38	32.4	8.2	720	4 US-09-172-063-11	Sequence 11, Appl
39	32.4	8.2	720	4 US-09-172-063-13	Sequence 13, Appl
40	32.4	8.2	762	1 US-08-532-390-40	Sequence 40, Appl
41	32.4	8.2	762	4 US-08-717-294-40	Sequence 40, Appl
42	32.4	8.2	768	4 US-09-094-359-11	Sequence 11, Appl
43	32.4	8.2	850	4 US-09-062-102-2	Sequence 2, Appli
44	32.4	8.2	972	4 US-09-172-063-27	Sequence 27, Appl
45	32.4	8.2	972	4 US-09-172-063-29	Sequence 29, Appl

ALIGNMENTS

RESULT 1  
US-08-012-543-1  
; Sequence 1, Application US/08012543  
; Patent No. 5596072  
; GENERAL INFORMATION:  
; APPLICANT: Culpepper, Janice  
; APPLICANT: McKenzie, Andrew  
; APPLICANT: Dang, Warren  
; APPLICANT: de Waal Malefyt, Rene  
; APPLICANT: Heath, Andrew  
; APPLICANT: Aversa, Gregorio  
; APPLICANT: Briere, Francine  
; APPLICANT: Banchereau, Jacques  
; APPLICANT: de Vries, Jan  
; APPLICANT: Zurawski, Gerard  
; TITLE OF INVENTION: Human Interleukin-13  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/012,543  
; FILING DATE: 01-FEB-1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/933,416  
; FILING DATE: 21-AUG-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0302K1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-852-9196  
; TELEFAX: 415-496-1200  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1290 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA





QY	61	agccctgtgactccctcccaacccctcaaggagctcattgaggagctggtcaacatcacc	120
Db	105	GGCCCTGTGCCTCCCTCTACAGCCCTCAGGGAGCTCATTGAGGAGCTGGTCAACATCACC	164
QY	121	cagaatc---aggcatccctctgcaacggcagcatggtgtggagcgtcaacctgaccgcc	177
Db	165	CAGAACCCAGAAGGCTCCGGCTGCTCAATGGCAGCATGGTATGGAGCATCAACCTGACAGCT	224
QY	178	ggcatgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgccatccaa	237
Db	225	GGCATGTACTGTGCAGCCCTGGAATCCCTGATCAACGTGTCAGGCTGCAGTGCCATCGAG	284
QY	238	aggacccagaggtgctgaaagcacctgtgctctcaaaagcccggcagggcagatttcc	297
Db	285	AAGACCCAGAGGATGCTGAGCGGATCTGCCCCACAAAGGTCTCAGCTGGCAGTTTCC	344
QY	298	agtgaacgcgacccgagacacccaaaattgaagtgatccagttggtgaaaaaacctgctcacc	357
Db	345	AGCTTGCAATGTCGAGAGACACCAAAATCGAGGTGGCCCCAGTTTGTAAAGGACCTGCTCTTA	404
QY	358	tatgtaaggggagtttatcgccatggaaatttca	391
Db	405	CATTTAAAGAAACTTTTTCGCGAGGGACGGTTTCA	438

RESULT 4  
 US-08-371-121-15  
 ; Sequence 15, Application US/08371121  
 ; Patent No. 5652123  
 ; GENERAL INFORMATION:  
 ; APPLICANT: CAPUT, Daniel  
 ; APPLICANT: FERRARA, Pascual  
 ; APPLICANT: GUILLEMOT, Jean-Claude  
 ; APPLICANT: LEPLATOIS, Pascal  
 ; APPLICANT: MINTY, Adrian  
 ; APPLICANT: KAGHAD, Mourad  
 ; APPLICANT: LABIT-LE BOUTEILLER, Christine  
 ; APPLICANT: MAGAZIN, Marilyn  
 ; TITLE OF INVENTION: Protein having a cytokine type  
 ; TITLE OF INVENTION: activity, recombinant DNA coding for this protein,  
 ; TITLE OF INVENTION: transformed cells and microorganisms.  
 ; NUMBER OF SEQUENCES: 27  
 ; CORRESPONDENCE ADDRESSES:  
 ; ADDRESSEE: FOLEY & LARDNER  
 ; STREET: 3000 K Street, N.W., Suite 500  
 ; CITY: Washington, D.C.  
 ; COUNTRY: USA  
 ; ZIP: 20007-5109  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/371,121  
 ; FILING DATE:  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/938,161  
 ; FILING DATE: 30-NOV-1992  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/FR92/00280  
 ; FILING DATE: 27-MAR-1992  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: FR 91 00137  
 ; FILING DATE: 08-JAN-1992  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: FR 91 03904  
 ; FILING DATE: 29-MAR-1991  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: SAXE, Bernhard D.  
 ; REGISTRATION NUMBER: 28,665  
 ; REFERENCE/DOCKET NUMBER: 16781/383

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1297 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 15..452
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 117..452
;
US-08-371-121-15

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Query Match 62.4%; Score 245.2; DB 1; Length 1297;  
Best Local Similarity 78.2%; Pred. No. 3.7e-66;  
Matches 308; Conservative 0; Mismatches 83; Indels 3; Gaps 1;

[illegible]

RESULT 5  
US-08-371-121-17  
; Sequence 17, Application US/08371121  
; Patent No. 5652123  
; GENERAL INFORMATION:  
; APPLICANT: CAPUT, Daniel  
; APPLICANT: FERRARA, Pascual  
; APPLICANT: GUILLEMOT, Jean-Claude  
; APPLICANT: LEPLATOIS, Pascal  
; APPLICANT: MINTY, Adrian  
; APPLICANT: KAGHAD, Mourad  
; APPLICANT: LABIT-LE BOUTEILLER, Christine  
; APPLICANT: MAGAZIN, Marilyn  
; TITLE OF INVENTION: Protein having a cytokine type  
; TITLE OF INVENTION: activity, recombinant DNA coding for this protein,  
; TITLE OF INVENTION: transformed cells and microorganisms.  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FOLEY & LARDNER  
; STREET: 3000 K Street, N.W., Suite 500

```

CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.2.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/371,121
FILING DATE:
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
PRIORITY APPLICATION NUMBER: US 07/938,161
FILING DATE: 30-NOV-1992
PRIORITY APPLICATION DATA:
PRIORITY APPLICATION NUMBER: PCT/FR92/00280
FILING DATE: 27-MAR-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: FR 91 00137
FILING DATE: 08-JAN-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: FR 91 03904
FILING DATE: 29-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D.
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 16781/383
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 384 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-371-121-17

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Query Match	51.98;	Score 204;	DB 1;	Length 384;
Best Local Similarity	77.18;	Pred. NO. 1e-53;		
Matches 262;	Conservative 0;	Mismatches 75;	Indels 3;	Gaps 1;

Qy	55	tccccgagccctgtgactccctcccccaacccctcaaggagctcatgaggagctgggtcaac.	114
Db	16	TCCCCAGGCCCTGTGCCCTCCCTCTACGGCCCTCAGGGAGCTCATTGAGGAGCTGGTCAAC	75
Qy	115	atcacccagaatc---aggcatccctctctgcaacggcgagcatggtgtggagcgtcaacctg	171
Db	76	ATCACCCAGAACCCAGAGGCTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAACCTG	135
Qy	172	accgccggcatgtactgcgagctctagaaatctctgatcaatgtctccgactgcagcgcc	231
Db	136	ACAGCTGACATGTACTGTGCGACCCCTGGAAATCCCTGATCAACGTGTGAGGCTGCAGTGCC	195
Qy	232	atccaaaggacccagaggatgctgaaagcactgtgctctcaaaagccccgcggcagggcag	291
Db	196	ATCGAGAAGACCCAGAGGATGTCTGAGCGGATTCTGCCCCGCCACAAGGTCTCAGCTGGGCAG	255
Qy	292	atttccagtgaaacgcagccgagagacaccaaattgaaagtgtacagttggtgaaaaacctg	351
Db	256	TTTTCCAGCTTGCCATGTCCGAGACACCAAAATCGAGGTGGCCACAGTTTGTANAGGACCTG	315
Qy	352	ctcacctatgtaaagggagtttatcgccatggaaatttca	391
Db	316	CTCTTACATTTAAAGAAACTTTTTCGCGAGGGACGGTTCA	355

RESULT 6  
US-08-371-121-24

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; Sequence 24, Application US/08371121
; Patent No. 5652123
; GENERAL INFORMATION:
; APPLICANT: CAPUT, Daniel
; APPLICANT: FERRARA, Pascual
; APPLICANT: GUILLEMOT, Jean-Claude
; APPLICANT: LEPLATOIS, Pascal
; APPLICANT: MINTY, Adrian
; APPLICANT: KAGHAD, Mourad
; APPLICANT: LABIT-LE BOUTEILLER, Christine
; APPLICANT: MAGAZIN, Marilyn
; TITLE OF INVENTION: Protein having a cytokine type
; TITLE OF INVENTION: activity, recombinant DNA coding for this protein,
; TITLE OF INVENTION: transformed cells and microorganisms.
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/371,121
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/938,161
; FILING DATE: 30-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR92/00280
; FILING DATE: 27-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91 00137
; FILING DATE: 08-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91 03904
; FILING DATE: 29-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 16781/383
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 336 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
;
; US-08-371-121-24

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Query Match 51.8%; Score 203.4; DB 1; Length 336;  
Best Local Similarity 77.8%; Pred. No. 1.5e-53;  
Matches 259; Conservative 0; Mismatches 71; Indels 3; Gaps 1;

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Db	2	GCCCTGTGCCTCCCTCTACAGCCCTCAGGGAGCTCATTTGAGGAGCTGGTCAACATCACCC	61
Qy	122	agaatc---aggcatccctctgaacggcgagcatgggtggagcgtcaacctgaccgcgcg	178
Db	62	AGAACCAGAAGGCTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAACCTGACAGCTG	121
Qy	179	qcatgtactqcqcaqtctataaatctcttgatcaatgtctccgactgcagcgccatccaaa	238

||||| 122 GCATGTACTGTGCAGCCCTGGAAATCCCTGATCAACGTGTGAGGCTGCAGTGCATCGAGA 181  
QY 239 ggaccagaggtgctgaaagcactgtgctctcaaaagcccgcgagggcagatttcca 298  
Db 182 AGACCCAGAGGATGCTGAGCGGATTCTGCCGACACAAGGTCTCAGCTGGCAGTTTCCA 241  
QY 299 gtgaacgcagccgagacacacaaaatgaagtgtccagttggtgaaacacctgctcacct 358  
Db 242 GCTTGCATGTCCGAGACACCAAAATCGAGGTGGCCAGTTTGTAAAGGACCTGCTCTTAC 301  
QY 359 atgtaaggggagtttatcgcccatggaaatttca 391  
Db 302 ATTTAAAGAAACTTTTTCGCGAGGGACGGTTCA 334  
RESULT 7  
US-08-594-469-4  
; Sequence 4, Application US/08594469  
; Patent No. 5700665  
; GENERAL INFORMATION:  
; APPLICANT: LEGOUX, Richard  
; APPLICANT: MALDONADO, Paul  
; APPLICANT: SALOME, Marc  
; TITLE OF INVENTION: Method for the extraction of  
; TITLE OF INVENTION: periplasmic proteins of prokaryotic microorganisms in the  
; TITLE OF INVENTION: presence of arginine  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Bacon & Thomas  
; STREET: 625 Slaters Lane - Fourth Floor  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: USA  
; ZIP: 22314  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/594,469  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 95 01083  
; FILING DATE: 31-JAN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: FICHTER, Richard E  
; REGISTRATION NUMBER: 26,382  
; REFERENCE/DOCKET NUMBER: REF/LEGOUX  
; TELEPHONE: (703) 683-0500  
; TELEFAX: (703) 683-1080  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 425 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-594-469-4

Query Match 51.5%; Score 202.2; DB 1; Length 425;  
Best Local Similarity 76.4%; Pred. No. 3.9e-53;  
Matches 262; Conservative 0; Mismatches 78; Indels 3; Gaps 1;

QY 52 gcctcccgagccctgtgactccctcccaaccctcaaggagctcattgaggctggtc 111  
Db 55 GCCTTCGTCGCCCTGTGCTCCCACTGCCCTCAGGGAGCTCATTTGAGGAGCTGGTC 114  
QY 112 aacatcaccagaatc---aggcatccctctgtgcaacggcagcatgggtgtgagcgtcaac 168

Db 115 AACATCACCCAGAACCAAGAGGCTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAAC 174  
QY 169 ctgaccgccggcatgtactgcgagctctagaatctctgatcaatgtctccgactgcagc 228  
Db 175 CTGACAGCTGGCATGTACTGTGCAGCCCTGGAATCCCTGATCAACGTGTTCAGGCTGCAGT 234  
QY 229 gccatccaaaaggaccagaggatgctgaaagcactgtgctctcaaaagcccgcgaggg 288  
Db 235 GCCATCGAGAAGACCCAGAGGATGTGAGCGGATTCTGCCCGCACAAAGGTCTCAGCTGGG 294  
QY 289 cagatttccagtgaacgcagccgagacacacaaaattgaagtgtatccagttggtgaaaaac 348  
Db 295 CAGTTTCCAGCTTGCAATGATGCCGAGACACCAAAATCGAGGTGGCCAGTTTGTAAAGGAC 354  
QY 349 ctgctcacctatgtaaggggagtttatcgcccatggaaatttca 391  
Db 355 CTGCTCTTACATTTAAAGAAACTTTTTCGCGAGGGACGGTTCA 397

RESULT 8  
US-08-906-957-4  
; Sequence 4, Application US/08906957  
; Patent No. 5856142  
; GENERAL INFORMATION:  
; APPLICANT: LEGOUX, Richard  
; APPLICANT: MALDONADO, Paul  
; APPLICANT: SALOME, Marc  
; TITLE OF INVENTION: Method for the extraction of  
; TITLE OF INVENTION: periplasmic proteins of prokaryotic microorganisms in the  
; TITLE OF INVENTION: presence of arginine  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Bacon & Thomas  
; STREET: 625 Slaters Lane - Fourth Floor  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: USA  
; ZIP: 22314  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/906,957  
; FILING DATE: 06-AUG-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/594,469  
; FILING DATE:  
; APPLICATION NUMBER: FR 95 01083  
; FILING DATE: 31-JAN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: FICHTER, Richard E  
; REGISTRATION NUMBER: 26,382  
; REFERENCE/DOCKET NUMBER: REF/LEGOUX  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 683-0500  
; TELEFAX: (703) 683-1080  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 425 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-906-957-4

Query Match 51.5%; Score 202.2; DB 2; Length 425;  
Best Local Similarity 76.4%; Pred. No. 3.9e-53;  
Matches 262; Conservative 0; Mismatches 78; Indels 3; Gaps 1;



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QY 52 gctctcccgagccctgtgactcctcccccaaccctcaaggagctcataggagctggtc 111
   ||| | ||||| |||| | ||||| ||||| ||||| ||||| ||||| |||||
Db 55 GCCTTCGCTGGCCCTGTGCCTCCCAGTACTGCCCTCAGGGAGCTCATTTAGGAGCTGGTC 114

QY 112 aacatcacccagaatc---aggcatcccctctgcgaacgccagcatggtgtggagcgtcaac 168
   ||||| ||||| |||| | ||||| ||||| ||||| ||||| ||||| |||||
Db 115 AACATCACCCAGAACCAAGAAGGCTCCGCTCTGCAATGCGAGCATGGTATGGAGCATCAAC 174

QY 169 ctgaccgccggcatgtactgcgcagctctagaattcttgatcaaatgtctccgactgcagc 228
   |||| | ||||| ||||| |||| | |||| | |||| | |||| | |||| | ||||
Db 175 CTGACAGCTGGCATGTACTGTGCAGCCCTGGAATCCCTGATCAACGTGTACAGGCTGCAGT 234

QY 229 gccatcaaagaccagaggatgctgaaagcactgtgctctctcaaaagcccgaggcagg 288
   ||||| | ||||| ||||| |||| | ||||| ||||| |||| | |||| | ||||
Db 235 GCCATCGAAGAAGACCACGAGAGGATGCTGAGCGGATTCTGCCCGCACAAAGGTCTCAGTG 294

QY 289 cagatttccagtgaacgcagccgagacacaccaaaaattgaagtgatccagttggtgaaaaac 348
   ||| ||||| | ||||| ||||| ||||| ||||| |||| | |||| | ||||
Db 295 CAGTTTTCCAGCTTGTCATGTCCGAGACACCAAATCGAGGTGGCCCCAGTTTGTAAAGGAC 354

QY 349 ctgctcacctatgtaaggggagtttatcgccatgccaattttca 391
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Db 355 CTGCTCTTACATTTAAAGAAACTTTTTCGCGAGGACGGTTCA 397

RESULT      9
US-08-594-469-1
; Sequence 1, Application US/08594469
; Patent No. 5700665
; GENERAL INFORMATION:
; APPLICANT: LEGOUX, Richard
; APPLICANT: MALDONADO, Paul
; APPLICANT: SALOME, Marc
; TITLE OF INVENTION: Method for the extraction of
; TITLE OF INVENTION: periplasmic proteins of prokaryotic microorganisms in the
; TITLE OF INVENTION: presence of arginine
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bacon & Thomas
; STREET: 625 Slaters Lane - Fourth Floor
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/594,469
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 95 01083
; FILING DATE: 31-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FICHTER, Richard E
; REGISTRATION NUMBER: 26,382
; REFERENCE/DOCKET NUMBER: REF/LEGOUX
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 683-0500
; TELEFAX: (703) 683-1080
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4410 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-594-469-1

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Query Match          51.5%; Score 202.2; DB 1; Length 4410;
Best Local Similarity 76.4%; Pred. No. 9.1e-53;
Matches 262; Conservative 0; Mismatches 78; Indels 3; Gaps 1;

QY  52 gcctccccgagccctgtgactccctcccccaacccctcaaggagctcataggagcgtgctc 111
Db  392 GCCTTCGCTGGCCCTGTGCTCCCACTACTGCCCTCAGGAGCTCATTGAGGAGCTGGTC 451

QY  112 aacatcaccagaatc---aggcatccctctgcaacgagcagcatgggtgtggagcgtcaac 168
Db  452 AACATCACCCAGAACCCAGAAGGCTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAAC 511

QY  169 ctgaccgccggcatgtactgcgcagctctagaaatctctgatcaatgtctccgactgcagc 228
Db  512 CTGACAGCTGGCATGTACTGTGCAGCCCTGGAATCCCTGATCAACGTGTCAGGCTGCAGT 571

QY  229 gccatccaaaggaccagaggaatgctgaaagcacctgtctctcaaaaagcccgcgaggg 288
Db  572 GCCATCGAGAAGACCCAGAGGATGCTGAGCGGATTCTGCGCCGACAAAGTCTCAGCTGGG 631

QY  289 cagatttcagtgaaacgagccgagacacacaaaattgaagtgatccagtgtggtgaaaaac 348
Db  632 CAGTTTCCAGCTTGCAATGTCGAGACACCAAAATCGAGTGGCCCAAGTTTGTAAAGGAC 691

QY  349 ctgctcacctatgtaaggagagtttatcgccatggaaatttca 391
Db  692 CTGCTCTTACATTTAAAGAAACTTTTTCGCGAGGGACGGTTCA 734

RESULT 10
US-08-906-957-1
; Sequence 1, Application US/08906957
; Patent No. 5856142
; GENERAL INFORMATION:
; APPLICANT: LEGOUX, Richard
; APPLICANT: MALDONADO, Paul
; APPLICANT: SALOME, Marc
; TITLE OF INVENTION: Method for the extraction of
; TITLE OF INVENTION: periplasmic proteins of prokaryotic microorganisms in the
; TITLE OF INVENTION: presence of arginine
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bacon & Thomas
; STREET: 625 Slaters Lane - Fourth Floor
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/906,957
; FILING DATE: 06-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/594,469
; FILING DATE:
; APPLICATION NUMBER: FR 95 01083
; FILING DATE: 31-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FICHTER, Richard E
; REGISTRATION NUMBER: 26,382
; REFERENCE/DOCKET NUMBER: REF/LEGOUX
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 683-0500
; TELEFAX: (703) 683-1080
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4410 base pairs

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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-906-957-1

Query Match      51.5%; Score 202.2; DB 2; Length 4410;
Best Local Similarity 76.4%; Pred. No. 9.1e-53;
Matches 262; Conservative 0; Mismatches 78; Indels 3; Gaps 1;

QY 52 gcttcgccgagccctgtgactccctcccaacccctcaaggagctcattgagagctggtc 111
   ||||| | | ||||| | | ||||| | | ||||| | | ||||| | | ||||| | | |||||
Db 392 GCCTTCGCTGGCCCTGTGCCTCCCACTCCCACTGCTCAGGGAGCTCATTGAGGAGCTGGTC 451

QY 112 aacatcacccagaatc---aggcatccctctgcaacggcagcatggtgtggagcgtcaac 168
   ||||| | | ||||| | | ||||| | | ||||| | | ||||| | | ||||| | | |||||
Db 452 AACATCACCCAGAACCAAGAGGCTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAAC 511

QY 169 ctgaccgcccgcattgtactgcgcagctctagaatctctgatcaatgtctccgactgcagc 228
   ||||| | | ||||| | | ||||| | | ||||| | | ||||| | | ||||| | | |||||
Db 512 CTGACAGCTGGCATGTACTGTGCAGCCCTGGAATCCCTGTATCAACGCTCAGGCTGCAGT 571

QY 229 gccatcaaaaggaccagaggtgctgaaagcactgtgctctctcaaaagcccgccgaggg 288
   ||||| | | ||||| | | ||||| | | ||||| | | ||||| | | ||||| | | |||||
Db 572 GCATCGAGAAAGACCCAGAGGATGCTGAGCGGATTTCTGCCCGCACAAAGTCTCAGCTGGG 631

QY 289 cagattccagtgaaacgcagcagacacacaaaattgaagtgatccagttggtgaaaaac 348
   || | ||||| | | ||||| | | ||||| | | ||||| | | ||||| | | ||||| | | ||
Db 632 CAGTTTCCAGCTTGCAATGTCGGAGACACCAAAATCGAGGTGGCCCCAGTTGTAAAGGAC 691

QY 349 ctgctcacctatgtaaggggagtttatcgccatggaaaatttca 391
   ||||| | | ||||| | | ||||| | | ||||| | | ||||| | | ||||| | | |||||
Db 692 CTGCTCTTACATTTAAAGAAACTTTTCGCGAGGGACGGTTCA 734

RESULT 11
US-08-371-121-2
; Sequence 2, Application US/08371121
; Patent No. 5652123
; GENERAL INFORMATION:
; APPLICANT: CAPUT, Daniel
; APPLICANT: FERRARA, Pascual
; APPLICANT: GUILLEMOT, Jean-Claude
; APPLICANT: LEPLATOIS, Pascal
; APPLICANT: MINTY, Adrian
; APPLICANT: KAGHAD, Mourad
; APPLICANT: LABIT-LE BOUTEILLER, Christine
; APPLICANT: MAGAZIN, Marilyn
; TITLE OF INVENTION: Protein having a cytokine type
; TITLE OF INVENTION: activity, recombinant DNA coding for this protein,
; TITLE OF INVENTION: transformed cells and microorganisms.
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/371,121
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/938,161
; FILING DATE: 30-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR92/00280
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;
; FILING DATE: 27-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91 00137
; FILING DATE: 08-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91 03904
; FILING DATE: 29-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 16781/383
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 336 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-371-121-2

Query Match      51.3%; Score 201.8; DB 1; Length 336;
Best Local Similarity 77.5%; Pred. No. 4.7e-53;
Matches 258; Conservative 0; Mismatches 72; Indels 3; Gaps 1;

QY 62 gccctgtgactccctcccaacccctcaaggagctcattgagagctggtcaacatcaccc 121
   ||||| | | ||||| | | ||||| | | ||||| | | ||||| | | ||||| | | |||||
Db 2 GCCCTGTGCCTCCCTCTACAGCCCTCAGGGAGCTCATTTGAGGAGCTGGTCAACATCACCC 61

QY 122 agaatc---aggcatccctctgcaacggcagcatggtgtggagcgtcaacctgaccgccc 178
   ||||| | | ||||| | | ||||| | | ||||| | | ||||| | | ||||| | | |||||
Db 62 AGAACCCAGAAAGGCTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAACCTGACAGCTG 121

QY 179 gcatgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgccatccaa 238
   ||||| | | ||||| | | ||||| | | ||||| | | ||||| | | ||||| | | |||||
Db 122 ACATGTACTGTGCAGCCCTGGAATCCCTGATCAACGCTGTGAGGCTGCGCATCGAGA 181

QY 239 ggaccagaggtgctgaaagcactgtgctctcaaaagcccgccgagggcagatttcca 298
   ||||| | | ||||| | | ||||| | | ||||| | | ||||| | | ||||| | | |||||
Db 182 AGACCCAGAGGATGCTGAGCGGATTTCTGCCCGCACAAAGTCTCAGTGGGCAGTTTCCA 241

QY 299 gtgaacgcagccgcagacacaaaattgaagtgatccagttggtgataaaacctgctcacct 358
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 242 GCTTGCATGTCGAGACACCAAAATCGAGGTGGCCCCAGTTTGTAAAGGACCTGCTCTTAC 301

QY 359 atgtaagggaggtttatcgccatggaaaatttca 391
   || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 302 ATTTAAAGAAACTTTTTCGCGAGGGACGGTTCA 334

RESULT 12
US-08-371-121-26
; Sequence 26, Application US/08371121
; Patent No. 5652123
; GENERAL INFORMATION:
; APPLICANT: CAPUT, Daniel
; APPLICANT: FERRARA, Pascual
; APPLICANT: GUILLEMOT, Jean-Claude
; APPLICANT: LEPLATOIS, Pascal
; APPLICANT: MINTY, Adrian
; APPLICANT: KAGHAD, Mourad
; APPLICANT: LABIT-LE BOUTEILLER, Christine
; APPLICANT: MAGAZIN, Marilyn
; TITLE OF INVENTION: Protein having a cytokine type
; TITLE OF INVENTION: activity, recombinant DNA coding for this protein,
; TITLE OF INVENTION: transformed cells and microorganisms.
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
```

STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington, D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/371,121  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/938,161  
FILING DATE: 30-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/FR92/00280  
FILING DATE: 27-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 91 00137  
FILING DATE: 08-JAN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 91 03904  
FILING DATE: 29-MAR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: SAXE, Bernhard D.  
REGISTRATION NUMBER: 28,665  
REFERENCE/DOCKET NUMBER: 16781/383  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 447 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-371-121-26

Query Match 40.5%; Score 159.2; DB 1; Length 447;  
Best Local Similarity 66.7%; Pred. No. 6.2e-40;  
Matches 268; Conservative 0; Mismatches 113; Indels 21; Gaps 2;

QY 1 atggcgctctggtgactgtggtcattgctctcactgcctcggtggtgccttgcctccccg 60  
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Db 49 ATGGCGCTCTGGGTGACTGCAGTCCTGGCTCTTGGTGCCTTGGTGTCTCGCGGCCCA 108  
QY 61 agcc-----ctgtgactccctcccaacctcaaggagctcattgaggagctg 108  
|  
Db 109 GGGCCGGTGCCAGAGTGTGTCTCTCCCTCTGACCTTAAGGAGCTTATTGAGGAGCTG 168  
QY 109 gtcaacatcaccagaaatcaggcatccctctgcaacggcagcatggtgtggagcgtcaac 168  
|||||  
Db 169 AGCAACATCACACACAGACCACTCCCTGTGCAACGGCAGCATGGTATGGAGTGTGGAC 228  
QY 169 ctgaccgcgcggcgtactgcgcagctctagaaatctctgatcaatgtctccgactgcagc 228  
|||||  
Db 229 CTGGCCGCTGGCGGGTCTGTGTAGCCCTGGATTCCCTGACCAACATCTCCAATTGCAAT 288  
QY 229 gccatccaaaggaccagagatgctgaaagcactgtgctctcaaaagccccgcggcaggg 288  
|||||  
Db 289 GCCATCTACAGGACCAAGAGGATATTGCATGGCCTCTGTAAACCGCAAGGCC----- 339  
QY 289 cagattccagtgaaagcagccgagacacacacaaatgaagtgatccagttggtgaaaaaac 348  
|  
Db 340 CCCACTACGGTCTCCACCTCCCGATACCAAAATCGAAGTAGCCCACTTTATATACAAAA 399  
QY 349 ctgctcacctatgaaggggagtttatcgcccatggaatttc 390  
|||||

Db 400 CTGCTCAGCTACACAAAGCAACTGTTTCGCCACGGCCCTTC 441  
RESULT 13  
US-08-012-543-3  
; Sequence 3, Application US/08012543  
; Patent No. 5596072  
; GENERAL INFORMATION:  
; APPLICANT: Culpepper, Janice  
; APPLICANT: Mckenzie, Andrew  
; APPLICANT: Dang, Warren  
; APPLICANT: de Waal Malefyt, Rene  
; APPLICANT: Heath, Andrew  
; APPLICANT: Aversa, Gregorio  
; APPLICANT: Briere, Francine  
; APPLICANT: Banhereau, Jacques  
; APPLICANT: de Vries, Jan  
; APPLICANT: Zurawski, Gerard  
; TITLE OF INVENTION: Human Interleukin-13  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/012,543  
; FILING DATE: 01-FEB-1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/933,416  
; FILING DATE: 21-AUG-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0302K1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-852-9196  
; TELEFAX: 415-496-1200  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1212 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 70..465  
; US-08-012-543-3

Query Match 40.5%; Score 159.2; DB 1; Length 1212;  
Best Local Similarity 66.7%; Pred. No. 9e-40;  
Matches 268; Conservative 0; Mismatches 113; Indels 21; Gaps 2;

QY 1 atggcgctctggtgactgtggtcattgctctcactgcctcggtggtgccttgcctccccg 60  
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Db 70 ATGGCGCTCTGGGTGACTGCAGTCCTGGCTCTTGGTGCCTTGGTGTCTCGCGGCCCA 129  
QY 61 agcc-----ctgtgactccctcccaacctcaaggagctcattgaggagctg 108  
|  
Db 130 GGGCCGGTGCCAGAGTCTGTGTCTCTCCCTCTGACCCCTTAAGGAGCTTATTGAGGAGCTG 189  
QY 109 gtcaacatcaccagaaatcaggcatccctctctgcaacggcagcatggtgtggagcgtcaac 168  
|||||

Db 190 ACACAATCATACACAAGACCAGACTCCCTGTGCAACGGCAGCATGGTATGGAGTGTGGAC 249  
QY 169 ctgaccgcggcatgtactgcagctctagaaatctctgataatgtctccgactgcagc 228  
Db 250 CTGGCCGCTGGCGGGTTCTGTGTAGCCCTGGATTCCCTGACCAACATCTCCAATTGCAAT 309  
QY 229 gccatccaaaggaccagaggtgctgaaagcactgtgctctcaaaagccgcggcagg 288  
Db 310 GCCATCTACAGGACCCAGAGGATATTGCATGGCCCTCTGTAAACCGCAAGGCC----- 360  
QY 289 cagatttcagtgaaacgcagcgagacacacaaattgaagtatccagttggtgaaaaaac 348  
Db 361 CCCACTACGGTCTCCAGCCTCCCGGATACCAAAATCGAAGTAGCCCACTTTATAACAAAA 420  
QY 349 ctgctcacctatgtaagggaggtttatcgccatggaatttc 390  
Db 421 CTGCTCAGCTACACAAGCAACTGTTTCGCCACGGGCCCTTC 462

RESULT 14  
PCT-US93-07645A-3  
; Sequence 3, Application PC/TUS9307645A  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: Human Interleukin-13  
; NUMBER OF SEQUENCES: 6  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Macintosh 6.0.5  
; SOFTWARE: Microsoft Word 5.1a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US93/07645A  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/012543  
; FILING DATE: 01-FEB-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/010977  
; FILING DATE: 29-JAN-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/933416  
; FILING DATE: 21-AUG-1992  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1212 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
PCT-US93-07645A-3

Query Match 40.5%; Score 159.2; DB 5; Length 1212;  
Best Local Similarity 66.7%; Pred. No. 9e-40;  
Matches 268; Conservative 0; Mismatches 113; Indels 21; Gaps 2;  
  
QY 1 atggcgctctggtgactgtggtcattgtctctcacctgcctcggtggtgccttgcctccccg 60  
Db 70 ATGGCGCTCTGGGTGACTGCAGTCCTGGCTCTTGCTTGCCCTGGTGGTCTCGCCGCCCCA 129  
QY 61 agcc-----ctgtgactccctcccaaccctcaaggagctcattgaggagctg 108  
Db 130 GGGCCGGTGCCCAAGATCTGTGTCTCTCCCTCTGACCCCTTAAGGAGCTTATTGAGGAGCTG 189  
QY 109 gtcaacatcacccagaaatcaggcatccctctgcaacggcagcatggtgtggagcgtcaac 168  
Db 190 AGCAACATCACACAAGACCAGACTCCCTGTGCAACGGCAGCATGGTATGGAGTGTGGAC 249  
QY 169 ctgaccgcggcatgtactgcagctctagaaatctctgataatgtctccgactgcagc 228  
Db 250 CTGGCCGCTGGCGGGTTCTGTGTAGCCCTGGATTCCCTGACCAACATCTCCAATTGCAAT 309  
QY 229 gccatccaaaggaccagaggtgctgaaagcactgtgctctcaaaagccgcggcagg 288

Db 310 GCCATCTACAGGACCCAGAGGATATTGCATGGCCTCTGTAACCGCAAGGCC----- 360  
QY 289 cagatttcagtgaaacgcagcgagacacacaaattgaagtatccagttggtgaaaaaac 348  
Db 361 CCCACTACGGTCTCCAGCCTCCCGGATACCAAAATCGAAGTAGCCCACTTTATAACAAAA 420  
QY 349 ctgctcacctatgtaagggaggtttatcgccatggaatttc 390  
Db 421 CTGCTCAGCTACACAAGCAACTGTTTCGCCACGGGCCCTTC 462  
  
RESULT 15  
PCT-US93-07645-3  
; Sequence 3, Application PC/TUS9307645  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: Human Interleukin-13  
; NUMBER OF SEQUENCES: 6  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Macintosh 6.0.5  
; SOFTWARE: Microsoft Word 5.1a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US93/07645  
; FILING DATE: 19930818  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/012543  
; FILING DATE: 01-FEB-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/010977  
; FILING DATE: 29-JAN-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/933416  
; FILING DATE: 21-AUG-1992  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1212 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
PCT-US93-07645-3

Query Match 40.5%; Score 159.2; DB 5; Length 1212;  
Best Local Similarity 66.7%; Pred. No. 9e-40;  
Matches 268; Conservative 0; Mismatches 113; Indels 21; Gaps 2;  
  
QY 1 atggcgctctggtgactgtggtcattgtctctcacctgcctcggtggtgccttgcctccccg 60  
Db 70 ATGGCGCTCTGGGTGACTGCAGTCCTGGCTCTTGCTTGCCCTGGTGGTCTCGCCGCCCCA 129  
QY 61 agcc-----ctgtgactccctcccaaccctcaaggagctcattgaggagctg 108  
Db 130 GGGCCGGTGCCCAAGATCTGTGTCTCTCCCTCTGACCCCTTAAGGAGCTTATTGAGGAGCTG 189  
QY 109 gtcaacatcacccagaaatcaggcatccctctgcaacggcagcatggtgtggagcgtcaac 168  
Db 190 AGCAACATCACACAAGACCAGACTCCCTGTGCAACGGCAGCATGGTATGGAGTGTGGAC 249  
QY 169 ctgaccgcggcatgtactgcagctctagaaatctctgataatgtctccgactgcagc 228  
Db 250 CTGGCCGCTGGCGGGTTCTGTGTAGCCCTGGATTCCCTGACCAACATCTCCAATTGCAAT 309  
QY 229 gccatccaaaggaccagaggtgctgaaagcactgtgctctcaaaagccgcggcagg 288  
Db 310 GCCATCTACAGGACCCAGAGGATATTGCATGGCCTCTGTAACCGCAAGGCC----- 360  
QY 289 cagatttcagtgaaacgcagcgagacacacaaattgaagtatccagttggtgaaaaaac 348  
Db 361 CCCACTACGGTCTCCAGCCTCCCGGATACCAAAATCGAAGTAGCCCACTTTATAACAAAA 420



Search completed: May 13, 2001, 14:21:17  
Job time: 17828 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 13, 2001, 11:40:07 ; Search time 5997.24 Seconds  
(without alignments)  
572.478 Million cell updates/sec

Title: US-09-451-527-94  
Perfect score: 393  
Sequence: 1 atggcgctctgttgactgt.....atcgccatggaaatttcaga 393

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 9623517 seqs, 4368049070 residues

Total number of hits satisfying chosen parameters: 19247034

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:  
1: gb\_estl1:\*  
2: gb\_est2:\*  
3: gb\_est3:\*  
4: gb\_est4:\*  
5: gb\_est5:\*  
6: gb\_est6:\*  
7: gb\_est7:\*  
8: gb\_est8:\*  
9: gb\_est9:\*  
10: gb\_est10:\*  
11: gb\_est11:\*  
12: gb\_est12:\*  
13: gb\_est13:\*  
14: gb\_est14:\*  
15: gb\_est15:\*  
16: gb\_est16:\*  
17: gb\_est17:\*  
18: gb\_est18:\*  
19: gb\_est19:\*  
20: gb\_est20:\*  
21: gb\_est21:\*  
22: gb\_est22:\*  
23: gb\_est23:\*  
24: gb\_est24:\*  
25: gb\_est33:\*  
26: gb\_est34:\*  
27: gb\_est35:\*  
28: gb\_est36:\*  
29: gb\_est37:\*  
30: gb\_est38:\*  
31: gb\_est39:\*  
32: gb\_est40:\*  
33: em\_estba:\*  
34: em\_estfun:\*  
35: em\_esthum1:\*  
36: em\_esthum2:\*  
37: em\_esthum3:\*  
38: em\_esthum4:\*  
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189: em\_gss\_other:\*

190: em\_gss\_pln1:\*  
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192: em\_gss\_pro:\*  
193: em\_gss\_rod1:\*  
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195: em\_gss\_rod3:\*  
196: em\_gss\_rod4:\*  
197: em\_gss\_rod5:\*  
198: em\_gss\_vrt1:\*  
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228: gb\_gss28:\*  
229: gb\_gss29:\*  
230: gb\_gss30:\*  
231: gb\_gss31:\*  
232: gb\_gss32:\*  
233: gb\_gss33:\*  
234: gb\_gss34:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	43.4	11.0	581	219	AZ305110	AZ305110 1M0005P05
2	40	10.2	463	24	AI712497	AI712497 UI-R-AF1-
C 3	37.8	9.6	994	231	CNS0402X	AL300678 Tetraodon
4	37	9.4	1016	230	CNS024F6	AL180699 Tetraodon
5	36.8	9.4	576	141	BE907816	BE907816 601501924
6	36.6	9.3	329	146	BF292210	BF292210 WHE2208_A
C 7	36.6	9.3	925	229	CNS0091P	AL053013 Drosoph11
8	36.4	9.3	277	137	BE593226	BE593226 WSL_99_B0
9	36.4	9.3	411	201	AQ001086	AQ001086 CIT-HSP-2
10	36.4	9.3	537	166	BE357229	BE357229 DGL_147_B
11	36	9.2	462	143	BF039993	BF039993 BP250023B
C 12	35.8	9.1	497	20	AI444326	AI444326 fb47h12.Y
C 13	35.8	9.1	1946	119	AW729623	AW729623 GA_Ea002
14	35.6	9.1	230	167	BE498968	BE498968 WHE0969_G
C 15	35.6	9.1	537	29	AV387571	AV387571 AV387571
C 16	35.6	9.1	1070	136	BE536034	BE536034 601062471
17	35.6	9.1	2275	14	AF034173	AF034173 AF034173
18	35.4	9.0	498	150	BF606532	BF606532 273595 MA

C	19	35.2	9.0	177	103	AI909438	AI909438 IL-BT208-
	20	35.2	9.0	570	24	AI746678	AI746678 ul06b05.Y
	21	35	8.9	359	17	AI209519	AI209519 b0e07a1.f
	22	34.8	8.9	507	138	BE705147	BE705147 SC02_08f0
C	23	34.6	8.8	965	217	AZ201624	AZ201624 SP_0053_A
	24	34.4	8.8	544	13	AA880435	AA880435 vw89f07.f
	25	34.4	8.8	553	106	AU075583	AU075583 AU075583
	26	34.4	8.8	700	113	AW318852	AW318852 un08dl2.Y
	27	34.4	8.8	712	115	AW475303	AW475303 un64b04.Y
	28	34.4	8.8	1056	144	BF143984	BF143984 601791238
	29	34.2	8.7	477	151	BF625277	BF625277 HVSMEa000
	30	34.2	8.7	535	161	BE032541	BE032541 131940 MA
	31	34.2	8.7	546	161	BE032543	BE032543 131942 MA
	32	34.2	8.7	616	106	AU066538	AU066538 AU066538
	33	34.2	8.7	691	150	BF620464	BF620464 HVSMEC001
	34	34	8.7	341	163	BE127683	BE127683 DEPA1432
	35	34	8.7	370	166	BE363650	BE363650 WSI_64_G1
	36	34	8.7	562	166	BE361027	BE361027 DGI_69_A0
C	37	34	8.7	704	230	CNS02PBO	AL207789 Tetraodon
	38	34	8.7	929	143	BF037598	BF037598 601461167
	39	34	8.7	1122	141	BE889888	BE889888 601512140
	40	33.6	8.5	577	166	BE402120	BE402120 CSB004F06
	41	33.6	8.5	643	150	BF583596	BF583596 602096668
	42	33.6	8.5	714	166	BE414190	BE414190 SCU007.CO
	43	33.6	8.5	727	164	BE216356	BE216356 HV_CEB001
	44	33.6	8.5	891	151	BF685554	BF685554 602140603
	45	33.6	8.5	902	106	AL522415	AL522415 AL522415

ALIGNMENTS

```
RESULT 1
AZ305110 AZ305110 581 bp DNA GSS 29-SEP-2000
LOCUS house mouse.
DEFINITION 1M0005P05R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0005P05 R, DNA sequence.
ACCESSION AZ305110 GI:10341800
VERSION AZ305110.1
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 581)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0005 row: P column: 05
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 581.
Location/Qualifiers
1. .581
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0005P05"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
FEATURES
source
```

```
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
BASE COUNT 169 a 139 c 153 g 120 t
ORIGIN
Query Match 11.0%; Score 43.4; DB 219; Length 581;
Best Local Similarity 76.8%; Pred. No. 0.11;
Matches 53; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
QY 1 atggcgctctgttgactgtggtcattgctctcacctgcctgcgtgcctgcctcccg 60
|||||
Db 513 ATGGCGCTCTGGGTGACTGCAGTCTTGCTTGGTGGTGGTCTCGCGGCCCA 572
QY 61 agccctgtg 69
| |||
Db 573 GGGCCGGTG 581
RESULT 2
AI712497
LOCUS AI712497 463 bp mRNA EST 08-JUN-1999
DEFINITION UI-R-AF1-aap-b-12-0-UI.s1 UI-R-AF1 Rattus norvegicus cDNA clone
UI-R-AF1-aap-b-12-0-UI 3', mRNA sequence.
ACCESSION AI712497
VERSION AI712497.1 GI:5016297
KEYWORDS EST.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 463)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
COMMENT Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: clones will be available through
Research Genetics (www.resgen.com)
Seq primer: M13 Forward
POLYA=No.
Location/Qualifiers
1. .463
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
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```

/db_xref="taxon:10116"
/clone="UI-R-AF1-aap-b-12-0-UI"
/clone_lib="UI-R-AF1"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-AF1
library is a normalized library constructed from 15 dpc
rat atrioventricular (AV) canal. The tag is a string of 5
nucleotides present between the Not I site and the
oligo-dT track. The library was constructed as described
by Bonaldo, Lennon and Soares, Genome Research 6: 791-806
, 1996. Tissue provided by Jim Lin, Department of Biology,
University of Iowa.
TAG_LIB=UI-R-AF1
TAG_TISSUE=AV canal at 15 dpc
TAG_SEQ=GAAGG"

BASE COUNT      97 a 130 c  92 g 144 t
ORIGIN

Query Match      10.2%; Score 40; DB 24; Length 463;
Best Local Similarity 58.3%; Pred. No. 0.91;
Matches 70; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 23 tcattgtctcacctgcctcggtggccttgccctcccgagccctggactccctcccaa 82
      ||||| || | | | | || || || || || || || || || || || || ||
Db 255 TGATTGCTGCCACCACCCCTGTTTCTGACCTTCATGATCCCTATGACTTCTCCCTGC 314

QY 83 ccctcaaggagctcattgaggagctggtggtcaacatcacccagaatcaggcatccctctgca 142
      |||| | | | ||| ||||| || || || || || || || || || || || ||
Db 315 CCCTTAGTTTCACTCTGATGATCTGGTCTCTCAGAACACAAATATTGGCCCTGGGGCTACA 374

RESULT 3
CNS04OZX/c
LOCUS
DEFINITION
Tetraodon nigroviridis genome survey sequence T7 end of clone
125F09 of library G from Tetraodon nigroviridis, genomic survey
sequence.
AL300678
AL300678.1 GI:8177652
GSS: genome survey sequence..
Tetraodon nigroviridis.
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Eurypterygii; Ctenosquamata; Acanthomorpha; Euacanthomorpha;
Holacanthopterygii; Acanthopterygii; Percomorpha;
Tetraodontiformes; Tetraodontidae; Tetraodontidae; Tetraodon.
1 (bases 1 to 994)
Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,
Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
Weissenbach,J.
Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis
Unpublished
2 (bases 1 to 994)
Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
Human gene number estimate provided by genome wide analysis using
Tetraodon nigroviridis DNA sequence
Unpublished
3 (bases 1 to 994)
Genoscope.
Direct Submission
Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
Location/Qualifiers

FEATURES
Source
/organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="234H06"
/clone_lib="G"
/note="Genoscope sequence ID : C0AG234DD03LPI-end : T7"
http://www.genoscope.cns.fr/Tetraodon.
224 a 312 c 280 g 183 t 17 others
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source
1. .994
/organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="125F09"
/clone_lib="G"
/note="Genoscope sequence ID : C0BG125CC05LPI-end : T7"

BASE COUNT      198 a 295 c 325 g 174 t  2 others
ORIGIN

Query Match      9.6%; Score 37.8; DB 231; Length 994;
Best Local Similarity 51.5%; Pred. No. 4.6;
Matches 87; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

QY 14 tgactgtggtcattgtctcacctgcctcggtggccttgccctcccgagccctgtgactc 73
      || |||| | | | | | | | | || || || || || || || || || || ||
Db 244 TGGCTGTGCTCTTTCTTCCATCGGGACAACAAGGCCTTCGCTGCCCTCCTCAGCCGACC 185

QY 74 cctccccaaccctcaaggagctcattgaggagctggtggtcaacatcacccagaatcaggcat 133
      | ||| || || |||| | | || || || || || || || || || || || ||
Db 184 TCGGGGCAAGTCTTTCAGGAGTCTGTAGAGGACCTTGACCCACATCTGTTCATCTCCAGCTGC 125

QY 134 ccctctgcaacggcagcatggtggtgagcgtcaacctgaccgcgcggcat 182
      | || | ||||| || || || || || || || || || || || || || ||
Db 124 TCTGCTGTGATGGCAGCCCTTGTC AAGATCACCGAGCAGAGCCAGGAAAT 76

RESULT 4
CNS024F6
LOCUS
DEFINITION
Tetraodon nigroviridis genome survey sequence T7 end of clone
234H06 of library G from Tetraodon nigroviridis, genomic survey
sequence.
AL180699
AL180699.1 GI:7818756
GSS: genome survey sequence.
Tetraodon nigroviridis.
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Eurypterygii; Ctenosquamata; Acanthomorpha; Euacanthomorpha;
Holacanthopterygii; Acanthopterygii; Percomorpha;
Tetraodontiformes; Tetraodontidae; Tetraodontidae; Tetraodon.
1 (bases 1 to 1016)
Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,
Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
Weissenbach,J.
Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis
Unpublished
2 (bases 1 to 1016)
Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
Human gene number estimate provided by genome wide analysis using
Tetraodon nigroviridis DNA sequence
Unpublished
3 (bases 1 to 1016)
Genoscope.
Direct Submission
Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
Location/Qualifiers

FEATURES
Source
/organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="234H06"
/clone_lib="G"
/note="Genoscope sequence ID : C0AG234DD03LPI-end : T7"
http://www.genoscope.cns.fr/Tetraodon.
224 a 312 c 280 g 183 t 17 others
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RESULT 9  
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LOCUS  
DEFINITION  
          AQ001086          411 bp          DNA                  26-JUN-1998  
          CIT-HSP-2288N10.TR CIT-HSP Homo sapiens genomic clone 2288N10, DNA  
          sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
          human.  
REFERENCE  
AUTHORS  
          Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K.,  
          Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H.,  
          Simon,M. and Venter,J.C.  
TITLE  
JOURNAL  
COMMENT  
          Use of a random BAC End Sequence Database for Sequence-Ready Map  
          Building (1998)  
          Unpublished (1998)  
          Contact: Mark Adams  
          Department of Eukaryotic Genomics  
          The Institute for Genomic Research  
          9712 Medical Center Dr., Rockville, MD 20850, USA  
          Tel: 301 838 0200  
          Fax: 301 838 0208  
          Email: mdadams@tigr.org  
          Clones are available from Research Genetics (info@resgen.com). BAC  
          end search page:  
          http://www.tigr.org/tdb/humgen/bac\_end\_search/bac\_end\_search.html  
          Seq primer: M13 Reverse  
          Class: BAC ends.

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          /clone\_lib="CIT-HSP"  
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          HindIII"

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          120 a 100 c 101 g 90 t  
          Query Match          9.3%; Score 36.4; DB 201; Length 411;  
          Best Local Similarity 48.5%; Pred. No. 8.9;  
          Matches 100; Conservative 0; Mismatches 106; Indels 0; Gaps 0;

QY 29 ctctcacctgcctcgtggtgcctgcctccccgagccctgtgactccctccccacccctca 88  
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Db 287 CCTCGCCTGCCTGCATGGCAAGCCACCCGAGCCAGTGCCTGTCACCGCCCTCT 228  
QY 89 aggaagctcattgaggagctggtcaacatcacccagagaatcaggcatccctctgcaacggca 148  
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Db 227 CCCAGACTGGGGTCCCTGCTGGGGTGGGGCCACATGGGGTCCCTGAAAGGGCAGGGCTG 168  
QY 149 gcatggtgtggagcgtcaacctgaccgcccgcgtactgctgagcagctctagaatctctga 208  
          |  
Db 167 GTGCTGAGGGGTCTGTTCATGATGATCAGTCCCGCCTCTTCTTTTCTGCTCAGTAATCTCACA 108  
QY 209 tcaatgtctccgactgcagcgccatc 234  
          |  
Db 107 TGAGCTTTTAAAGAATCCACTTC 82

RESULT 10  
BE357229  
LOCUS  
DEFINITION  
          BE357229          537 bp          mRNA                  20-JUL-2000  
          DGI\_147\_B02.g1\_A002 Dark Grown 1 (DG1) Sorghum bicolor cDNA, mRNA  
          sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
          Sorghum bicolor  
          Sorghum  
          Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
          Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae  
          ; Andropogoneae; Sorghum.  
REFERENCE  
AUTHORS  
          1 (bases 1 to 537)  
          Cordonnier-Pratt,M.-M., Gingle,A., Marsala,C., Sudman,M. and Pratt  
          ,L.H.  
TITLE  
JOURNAL  
COMMENT  
          An EST database from Sorghum: dark-grown seedlings  
          Unpublished (2000)  
          Contact: Cordonnier-Pratt MM  
          Department of Botany  
          The University of Georgia  
          Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA  
          Tel: 706 542 1860  
          Fax: 706 542 1805  
          Email: mmpratt@uga.edu  
          Sequences have been trimmed to exclude PolyA, vector and regions  
          below Phred quality 16. The threshold for highest quality sequence  
          is 20.  
          Seq primer: PolyTMix  
          High quality sequence start: 31  
          High quality sequence stop: 514  
          POLYA=No.

FEATURES  
          source  
          1..537  
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          /db\_xref="taxon:4558"  
          /clone\_lib="Dark Grown 1 (DG1)"  
          /note="Organ: 5-day-old dark-grown seedlings; Vector:  
          Lambda Zap; Site\_1: XhoI; Site\_2: EcoRI; The library was  
          made from poly-A RNA in the cloning vector lambda Zap II.  
          Clones to be sequenced were prepared by mass excision."

BASE COUNT  
ORIGIN  
          89 a 160 c 176 g 112 t  
          Query Match          9.3%; Score 36.4; DB 166; Length 537;  
          Best Local Similarity 53.5%; Pred. No. 9.6;  
          Matches 76; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

QY 84 cctcaaggagctcattgaggagctggtcaacatcacccagagaatcaggcatccctctgcaa 143  
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Db 249 CCCCATGGAGAGGCTCGGGGAGCCCGGACATCGCGCGGTGCTCGGGTTCCTCTGCAC 308  
QY 144 cggcagcatggtgtgagcgtcaacctgaccgcccgcgtactgctgagcagctctagaatc 203  
          |||  
Db 309 CGACGCCCGCAGTGGGTCAACGGCCAGGTCAATCCGCCCAACGGCGGCTACGTGTGATG 368  
QY 204 tctgatcaatgtctccgactgc 225  
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Db 369 TCTGATCTTTAGCTTCTACAGC 390

RESULT 11  
BF039993  
LOCUS  
DEFINITION  
          BF039993          462 bp          mRNA                  10-OCT-2000  
          BP250023B10D12 Soares normalized bovine placenta Bos taurus cDNA  
          clone BP250023B10D12 5', mRNA sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
          Bos taurus  
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
          Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
          Bovidae; Bovinae; Bos.  
REFERENCE  
AUTHORS  
          1 (bases 1 to 462)  
          Lewin,H.A., Soares,M.B., Rebeiz,M., Pardinas,J., Liu,L. and Larson  
          ,J.H.









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OM nucleic - nucleic search, using sw model

Run on: May 13, 2001, 14:20:33 ; Search time 9342.78 Seconds  
(without alignments)  
525.651 Million cell updates/sec

Title: US-09-451-527-96  
Perfect score: 333  
Sequence: 1 agccctgtgactccctcccc.....atcgccatggaaatttcaga 333

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1283235 seqs, 7373929652 residues

Total number of hits satisfying chosen parameters: 2566470

Minimum DB seq length: 0  
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:\*  
1: gb\_bal:\*  
2: gb\_ba2:\*  
3: gb\_ba3:\*  
4: gb\_in1:\*  
5: gb\_in2:\*  
6: gb\_in3:\*  
7: gb\_om:\*  
8: gb\_ov:\*  
9: gb\_pat1:\*  
10: gb\_pat2:\*  
11: gb\_ph:\*  
12: gb\_pl1:\*  
13: gb\_pl2:\*  
14: gb\_pl3:\*  
15: gb\_pl4:\*  
16: em\_bal:\*  
17: em\_ba2:\*  
18: em\_fun:\*  
19: em\_htgo\_hum:\*  
20: em\_htgo\_inv:\*  
21: em\_htgo\_rod:\*  
22: em\_htg\_hum1:\*  
23: em\_htg\_hum2:\*  
24: em\_htg\_hum3:\*  
25: em\_htg\_hum4:\*  
26: em\_htg\_hum5:\*  
27: em\_htg\_hum6:\*  
28: em\_htg\_hum7:\*  
29: em\_htg\_hum8:\*  
30: em\_htg\_inv1:\*  
31: em\_htg\_inv2:\*  
32: em\_htg\_other:\*  
33: em\_htg\_rod:\*  
34: em\_hum1:\*  
35: em\_hum2:\*  
36: em\_hum3:\*  
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39: em\_hum6:\*  
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81: gb\_htg22:\*  
82: gb\_htg23:\*  
83: gb\_htg24:\*  
84: gb\_htg25:\*  
85: gb\_pr1:\*  
86: gb\_pr2:\*  
87: gb\_pr3:\*  
88: gb\_pr4:\*  
89: gb\_pr5:\*  
90: gb\_pr6:\*  
91: gb\_pr7:\*  
92: gb\_pr8:\*  
93: gb\_pr9:\*  
94: gb\_rol:\*  
95: gb\_ro2:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	333	100.0	1302	7	AF244915 Canis fam
2	203.4	61.1	336	9	A29931 Sequence co
3	203.4	61.1	336	10	I58494 Sequence 24
4	203.4	61.1	1270	93	HUMIL13A L06801 Homo sapien
5	203.4	61.1	1282	92	HSNC30 X69079 H.sapiens 1
6	203.4	61.1	1290	10	I34548 Sequence 1
7	201.8	60.6	336	9	A29930 Sequence co
8	201.8	60.6	336	10	I58481 Sequence 2
9	201.8	60.6	417	88	AF043334 Homo sapi
10	201.8	60.6	1297	9	A29948 Coding sequ
11	201.8	60.6	1297	10	I58488 Sequence 15



12	200.2	60.1	384	9	A29950	A29950 Nucleic aci
13	200.2	60.1	384	10	I58489	I58489 Sequence 17
14	198.6	59.6	425	9	AR027065	AR027065 Sequence
15	198.6	59.6	425	10	I86198	I86198 Sequence 4
16	198.6	59.6	4410	9	A52326	A52326 Sequence 1
17	198.6	59.6	4410	9	AR027062	AR027062 Sequence
18	198.6	59.6	4410	10	I86195	I86195 Sequence 1
19	179	53.8	343	7	AF072807	AF072807 Bos tauru
20	142	42.6	447	10	I58495	I58495 Sequence 26
21	142	42.6	1207	94	MUSSTCPE	M23504 Mus musculu
22	142	42.6	1212	10	I34549	I34549 Sequence 3
23	131.4	39.5	443	94	RATIL13A	L26913 Rattus Norv
24	106.2	31.9	213343	78	AF276990	AF276990 Canis fam
25	71	21.3	3714	93	HUM11DC99Z	L42080 Homo sapien
26	71	21.3	4600	93	HUMIL13B	L13029 Human inter
27	71	21.3	4740	93	HSU10307	U10307 Human inter
28	71	21.3	5670	93	HSU31120	U31120 Human inter
29	71	21.3	50282	85	AC004039	AC004039 Homo sapi
30	71	21.3	78469	75	AC074127	AC074127 Homo sapi
31	70.6	21.2	3395	93	HUM11DC98Z	L42079 Homo sapien
32	70	21.0	3520	7	BTA132441	AJ132441 Bos tauru
33	58.4	17.5	78469	75	AC074127	AC074127 Homo sapi
34	51.6	15.5	4376	94	MUSIL13A	L13028 Mouse inter
35	49.4	14.8	142732	88	AC084392	AC084392 Homo sapi
36	49.4	14.8	159500	94	AC005742	AC005742 Mus muscu
37	49.4	14.8	237823	66	AC020886	AC020886 Mus muscu
38	40.8	12.3	38390	3	SC2H12	AL359215 Streptomy
39	37	11.1	39739	3	SCD16A	AL078618 Streptomy
40	36.8	11.1	185300	2	AP000063	AP000063 Aeropyrum
41	36.6	11.0	51440	12	AB025632	AB025632 Arabidops
42	36.4	10.9	1091	94	AB015206	AB015206 Mus muscu
43	36.4	10.9	1122	94	MMU18723	Y18723 Mus musculu
44	36.4	10.9	2437	3	SAAJ3310	AJ223310 Streptomy
45	36.4	10.9	2437	3	SAU77894	U77894 Streptomyce

ALIGNMENTS

RESULT	1	
AF244915		
LOCUS	AF244915	1302 bp mRNA MAM 16-OCT-2000
DEFINITION	Canis familiaris interleukin-13 mRNA, complete cds.	
ACCESSION	AF244915	
VERSION	AF244915.1	GI:7528273
KEYWORDS		
SOURCE	dog.	
ORGANISM	Canis familiaris	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.	
AUTHORS	1 (bases 1 to 1302)	
TITLE	Yang,S., Boroughs,K.L. and McDermott,M.J.	
JOURNAL	Canine interleukin-13: molecular cloning of full-length cDNA and expression of biologically active recombinant protein	
MEDLINE	J. Interferon Cytokine Res. 20 (9), 779-785 (2000)	
PUBMED	20485146	
REFERENCE	2 (bases 1 to 1302)	
AUTHORS	Yang,S.	
TITLE	Direct Submission	
JOURNAL	Submitted (13-MAR-2000) Allergy and Immunology, Heska Corporation, 1613 Prospect Parkway, Fort Collins, CO 80525, USA	
FEATURES	Location/Qualifiers	
source	1. .1302	
	/organism="Canis familiaris"	
	/db_xref="taxon:9615"	
5'UTR	1. .51	
CDS	52. .447	
	/codon_start=1	
	/product="interleukin-13"	
	/protein_id="AAF63204.1"	
	/db_xref="GI:7528274"	
	/translation="MALWLTVVIALTCLGLASPSVTPPTLKEIIELVNITQNOA	

3'UTR						
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ORIGIN						
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Best Local Similarity	100.0%;	Pred. No. 2.2e-78;				
Matches 333;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;		
QY	1	agccctgtgactccctcccaaccctcaaggagctcattgaggagctgggtcaacatcacc	60			
Db	112	AGCCCTGTGACTCCCTCCCAACCCTCAAGGAGCTCATTTGAGGAGCTGGTCAACATCACC	171			
QY	61	cagaatcaggcatccctctgcaacggcagcatggtgtggagcgtcaaacctgaccgccggc	120			
Db	172	CAGAAATCAGGCATCCCTCTGCAACGGCAGCATGGTGTGGAGCGTCAACCTGACCCGGCGC	231			
QY	121	atgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgcattccaaagg	180			
Db	232	ATGTACTGGCAGCTCTAGAAATCTCTGATCAATGTCTCCGACTGCAGCGCCATCCAAAGG	291			
QY	181	accagaggatgctgaaagcactgtgctctcaaaagcccgccgagggcagatttccagt	240			
Db	292	ACCCAGAGGATGCTGAAAGCACTGTGCTCTCAAAAGCCCGCGAGGGCAGATTTCCAGT	351			
QY	241	gaacgcagccgagacaccaaattgaagtgtatccagttggtgaaaaacctgtcacctat	300			
Db	352	GAACGCAGCCGAGACACCAAAATTGAAGTGATCCAGTTGGTGAAAAACCTGTCTCACCTAT	411			
QY	301	gtaaggggagtttatcgccatggaatttcaga	333			
Db	412	GTAAGGGGAGTTTATCGCCATGGAATTTTTCAGA	444			

RESULT	2	
A29931		
LOCUS	A29931	336 bp DNA PAT 23-JUN-1995
DEFINITION	Sequence coding for the mature cytokine like protein.	
ACCESSION	A29931	
VERSION	A29931.1	GI:1249019
KEYWORDS	synthetic construct.	
SOURCE	synthetic construct.	
ORGANISM	artificial sequence.	
REFERENCE	1 (bases 1 to 336)	
AUTHORS	Caput,D., Ferrara,P., Guillemot,J.C., Kaghad,M., Labit-le Bouteiller,C., Leplatois,P., Magazin,M. and Minty,A.	
TITLE	Protein having cytokin type activity, recombinant DNA coding for this protein, transformed cells and microorganisms	
JOURNAL	Patent: EP 0506574-A 3 30-SEP-1992;	
FEATURES	ELF SANOFI	
source	Location/Qualifiers	
	1. .336	
	/organism="synthetic construct"	
	/db_xref="taxon:32630"	
BASE COUNT	80 a	95 c 90 g 71 t
ORIGIN		
Query Match	61.1%;	Score 203.4; DB 9; Length 336;
Best Local Similarity	77.8%;	Pred. No. 7.5e-44;
Matches 259;	Conservative 0;	Mismatches 71; Indels 3; Gaps 1;

QY	2	gccctgtgactccctcccaaccctcaaggagctcattgaggagctgggtcaacatcacc	61
Db	2	GCCCTGTGCCTCCCTCTACAGCCCTCAGGGAGCTCATTCAGGAGCTGGTCAACATCACC	61
QY	62	agaatc---aggcatccctctgcaacggcagcatggtgtggagcgtcaacctgaccgcg	118
Db	62	AGAACAGAAAGGCTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAACCTGACAGCTG	121

QY	119	gcatgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgccatccaaa	178
Db	122	GCATGTACTGTGCAGCCCTGGAAATCCCTGTATCAACGTTGACGGCTGCAGTGCCATCGAGA	181
QY	179	ggaccagaggtgctgaaagcaactgtgctctcaaaagccgcggcagggcagattcca	238
Db	182	AGACCCAGAGGATGCTGAGCGGATTCTGCCCGCACAAAGGTCTCAGCTGGGCAGTTTTC	241
QY	239	gtgaacgcagccgagacaccaaattgaagtgatccagttgggtgaaaaacctgctcacct	298
Db	242	GCTTGCAATGTCGAGACACCAAAATCGAGGTGGCCCGAGTTGTAAAGGACCTGCTCTTAC	301
QY	299	atgtaaggggagtttatcgccatggaaatttca	331
Db	302	ATTTAAGAAACTTTTTCGGAGGGACGGTTCA	334
RESULT	3		
LOCUS	I58494	336 bp	DNA
DEFINITION	Sequence 24 from patent US 5652123.	PAT	07-OCT-1997
ACCESSION	I58494		
VERSION	I58494.1	GI:2477732	
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE.	1 (bases 1 to 336)		
AUTHORS	Caput,D., Ferrara,P., Guillemot,J., Kaghad,M., Labit-Le Bouteiller,C., Leplatois,P., Magazin,M. and Minty,A.		
TITLE	Protein having interleukin 13 activity, recombinant DNA coding for this protein, transformed cells and microorganisms		
JOURNAL	Patent: US 5652123-A 24 29-JUL-1997;		
FEATURES	Location/Qualifiers		
source	1. .336		
BASE COUNT	80 a 95 c 90 g 71 t		
ORIGIN	/organism="unknown"		
Query Match	61.1%;	Score 203.4;	DB 10; Length 336;
Best Local Similarity	77.8%;	Pred. No. 7.5e-44;	
Matches	259;	Conservative 0;	Mismatches 71; Indels 3; Gaps 1;
QY	2	gccctgtgactccctcccaacccctcaaggagctcattgaggagctgggtcaacatcaccc	61
Db	2	GCCCTGTGCCTCCCTCTACAGCCCTCAGGGAGCTCATTTGAGGAGCTGGTCAACATCACCC	61
QY	62	agaatc---aggcatccctctgcaacggcagcatgggtggagcggtcaacctgacgcgcg	118
Db	62	AGAACCAAGAAGGCTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAACCTGACAGCTG	121
QY	119	gcatgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgccatccaaa	178
Db	122	GCATGTACTGTGCAGCCCTTGGAAATCCCTGTATCAACGTTGACGGCTGCAGTGCCATCGAGA	181
QY	179	ggaccagaggtgctgaaagcaactgtgctctcaaaagccgcggcagggcagattcca	238
Db	182	AGACCCAGAGGATGCTGACGGATTCTGCCCGCACAAAGGTCTCAGCTGGGCAGTTTTC	241
QY	239	gtgaacgcagccgagacaccaaattgaagtgatccagttgggtgaaaaacctgctcacct	298
Db	242	GCTTGCAATGTCGAGACACCAAAATCGAGGTGGCCCGAGTTGTAAAGGACCTGCTCTTAC	301
QY	299	atgtaaggggagtttatcgccatggaaatttca	331
Db	302	ATTTAAGAAACTTTTTCGGAGGGACGGTTCA	334
RESULT	4		
HUMIL13A			
LOCUS	HUMIL13A	1270 bp	mrna
DEFINITION	Homo sapiens interleukin 13 mRNA, complete cds.	PRI	22-JUL-1993

ACCESSION	L06801		
VERSION	L06801.1	GI:186275	
KEYWORDS	cytokine; growth factor; interleukin 13; regulatory protein.		
SOURCE	Homo sapiens cDNA to mRNA.		
ORGANISM	Homo sapiens		
REFERENCE	1 (bases 1 to 1270)		
AUTHORS	McKenzie,A.N.J., Culpepper,J.A., de Waal Malefyt,R., Briere,F., Punnonen,J., Aversa,G., Sato,A., Dang,W., Cocks,B.G., Menon,S., de Vries,J.E., Banchereau,J. and Zurawski,G.R.		
TITLE	Interleukin-13, a T cell-derived cytokine that regulates human monocyte and B cell function		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 90, 3735-3739 (1993)		
MEDLINE	93234572		
FEATURES	Location/Qualifiers		
source	1. .1270		
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CDS	45..443		
	/codon_start=1		
	/product="interleukin 13"		
	/protein_id="AAA36107.1"		
	/db_xref="GI:186276"		
	/translation="MALLLTFTVIALTCLGGFASPGVPVPPSTALRELEELVNITQNQK		
	APLCNGSMVWSINLTAGMYCAALSLINVSQCSAIEKTRMLSGFCHPKVSAGQFSSL		
	HVRDTKIEVAQFVKDLLLHLKLFREGRFN"		
polyA_site	1270.		
BASE COUNT	288 a 335 c 336 g 311 t		
ORIGIN			
Query Match	61.1%;	Score 203.4;	DB 93; Length 1270;
Best Local Similarity	77.8%;	Pred. No. 7e-44;	
Matches	259;	Conservative 0;	Mismatches 71; Indels 3; Gaps 1;
QY	2	gccctgtgactccctcccaacccctcaaggagctcattgaggagctgggtcaacatcaccc	61
Db	106	GCCCTGTGCCTCCCTCTACAGCCCTCAGGGAGCTCATTTGAGGAGCTGGTCAACATCACCC	165
QY	62	agaatc---aggcatccctctgcaacggcagcatgggtggagcggtcaacctgacgcgcg	118
Db	166	AGAACCAAGAAGGCTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAACCTGACAGCTG	225
QY	119	gcatgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgccatccaaa	178
Db	226	GCATGTACTGTGCAGCCCTGGAATCCCTGATCAACGTTGACGGCTGCAGTGCCATCGAGA	285
QY	179	ggaccagaggtgctgaaagcaactgtgctctcaaaagccgcggcagggcagattcca	238
Db	286	AGACCCAGAGGATGCTGACGGATTCTGCCCGCACAAAGGTCTCAGCTGGGCAGTTTTC	345
QY	239	gtgaacgcagccgagacaccaaattgaagtgatccagttgggtgaaaaacctgctcacct	298
Db	346	GCTTGCAATGTCGAGACACCAAAATCGAGGTGGCCCGAGTTGTAAAGGACCTGCTCTTAC	405
QY	299	atgtaaggggagtttatcgccatggaaatttca	331
Db	406	ATTTAAGAAACTTTTTCGCGAGGGACGGTTCA	438
RESULT	5		
HSNC30			
LOCUS	HSNC30	1282 bp	mrna
DEFINITION	H.sapiens interleukin-13 mRNA.	PRI	17-FEB-1997
ACCESSION	X69079		
VERSION	X69079.1	GI:297787	
KEYWORDS	lymphokine.		
SOURCE	human.		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;		
	Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1 (bases 1 to 1282)		



Db 406 ATTTAAGAAACTTTTTCGCGAGGGACGGTTCA 438

RESULT 7

A29930 LOCUS A29930 336 bp DNA PAT 23-JUN-1995

DEFINITION Sequence coding for the mature cytokine like protein.

ACCESSION A29930

VERSION A29930.1 GI:1249018

KEYWORDS synthetic construct.

SOURCE ORGANISM synthetic construct

REFERENCE 1 (bases 1 to 336) artificial sequence.

AUTHORS Caput,D., Ferrara,P., Guillemot,J.C., Kaghad,M., Labit-le Bouteiller,C., Leplatois,P., Magazin,M. and Minty,A.

TITLE Protein having cytokin type activity, recombinant DNA coding for this protein, transformed cells and microorganisms

JOURNAL Patent: EP 0506574-A 2 30-SEP-1992;

ELF SANOFI

FEATURES

Source Location/Qualifiers

1..336

/organism="synthetic construct"

/db\_xref="taxon:32630"

BASE COUNT 81 a 95 c 89 g 71 t

ORIGIN

Query Match 60.6%; Score 201.8; DB 9; Length 336;

Best Local Similarity 77.5%; Pred. No. 2e-43;

Matches 258; Conservative 0; Mismatches 72; Indels 3; Gaps 1;

QY 2 gccctgtgactccctcccaaccctcaaggagctcattgaggagctggtcaacatcaccc 61

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Db 2 GCCCTGTGCCTCCCTCTACAGCCCTCAGGGAGCTCATTGGAGGAGCTGGTCAACATCACCC 61

QY 62 agaatc---aggcatccctctgcaacgagcagcatggtgtgagcgtcaacctgaccgccg 118

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Db 62 AGAACCAGAAGGCTCCGCTCTACAGCCCTCAGGGAGCTCATTGAGGAGCTGGTCAACATCACCC 61

QY 119 gcatgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgccatccaa 178

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Db 122 ACATGTACTGTGCAGCCCTGGAATCCCTGTATGCAACGTGTCAACGTGCCATCGAGA 181

QY 179 ggaccagaggtgctgaaagcactgtgctctcaaaaagcccgagggcagatttcca 238

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Db 182 AGACCCAGAGGATGCTGAGCGGATTTCTGCCCGCACAAAGTCTCAGCTGGGACGTTTCCA 241

QY 239 gtgaacgcagccgagacacccaaattgaagtgtatccagttgtgaaaaaacctgctcacct 298

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Db 242 GCTTGCATGTCCGAGACACCAAAATCGAGGTGGCCAGTTTGTAAAGGACCTGCTCTTAC 301

QY 299 atgtaaggggagtttatcgccatggaatttca 331

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Db 302 ATTTAAGAAACTTTTTCGCGAGGGACGGTTCA 334

RESULT 8

I58481 LOCUS I58481 336 bp DNA PAT 07-OCT-1997

DEFINITION Sequence 2 from patent US 5652123.

ACCESSION I58481

VERSION I58481.1 GI:2477719

KEYWORDS Unknown..

SOURCE ORGANISM Unknown..

REFERENCE 1 (bases 1 to 336) Unclassified.

AUTHORS Caput,D., Ferrara,P., Guillemot,J., Kaghad,M., Labit-Le Bouteiller,C., Leplatois,P., Magazin,M. and Minty,A.

TITLE Protein having interleukin 13 activity, recombinant DNA coding for this protein, transformed cells and microorganisms

JOURNAL Patent: US 5652123-A 2 29-JUL-1997;

FEATURES

Source Location/Qualifiers

1..336

/organism="synthetic construct"

/db\_xref="taxon:32630"

BASE COUNT 81 a 95 c 89 g 71 t

ORIGIN

Query Match 60.6%; Score 201.8; DB 9; Length 336;

Best Local Similarity 77.5%; Pred. No. 2e-43;

Matches 258; Conservative 0; Mismatches 72; Indels 3; Gaps 1;

QY 2 gccctgtgactccctcccaaccctcaaggagctcattgaggagctggtcaacatcaccc 61

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QY 62 agaatc---aggcatccctctgcaacgagcagcatggtgtgagcgtcaacctgaccgccg 118

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Db 62 AGAACCAGAAGGCTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAACCTGACAGCTG 121

QY 119 gcatgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgccatccaa 178

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Db 122 ACATGTACTGTGCAGCCCTGGAATCCCTGTATCAACGTGTCAACGTGCCATCGAGA 181

QY 179 ggaccagaggtgctgaaagcactgtgctctcaaaaagcccgagggcagatttcca 238

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Db 182 AGACCCAGAGGATGCTGAGCGGATTTCTGCCCGCACAAAGTCTCAGCTGGGACGTTTCCA 241

QY 239 gtgaacgcagccgagacacccaaattgaagtgtatccagttgtgaaaaaacctgctcacct 298

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Db 242 GCTTGCATGTCCGAGACACCAAAATCGAGGTGGCCAGTTTGTAAAGGACCTGCTCTTAC 301

QY 299 atgtaaggggagtttatcgccatggaatttca 331

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Db 302 ATTTAAGAAACTTTTTCGCGAGGGACGGTTCA 334

FEATURES

Source Location/Qualifiers

1..336

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/cell\_type="PHA-treated peripheral blood leukocyte"

1..417

/gene="IL13"

1..24

/gene="IL13"

/note="second PCR"

/PCR\_conditions="94C-1min, 50C-1min, 72C-3min, 30 cycles;

Deltacycler II from Ericomp"

4..402

CDS

FEATURES

Source Location/Qualifiers

1..336

/organism="unknown"

BASE COUNT 81 a 95 c 89 g 71 t

ORIGIN

Query Match 60.6%; Score 201.8; DB 10; Length 336;

Best Local Similarity 77.5%; Pred. No. 2e-43;

Matches 258; Conservative 0; Mismatches 72; Indels 3; Gaps 1;

QY 2 gccctgtgactccctcccaaccctcaaggagctcattgaggagctggtcaacatcaccc 61

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Db 2 GCCCTGTGCCTCCCTCTACAGCCCTCAGGGAGCTCATTGAGGAGCTGGTCAACATCACCC 61

QY 62 agaatc---aggcatccctctgcaacgagcagcatggtgtgagcgtcaacctgaccgccg 118

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Db 62 AGAACCAGAAGGCTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAACCTGACAGCTG 121

QY 119 gcatgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgccatccaa 178

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Db 122 ACATGTACTGTGCAGCCCTGGAATCCCTGTATCAACGTGTCAACGTGCCATCGAGA 181

QY 179 ggaccagaggtgctgaaagcactgtgctctcaaaaagcccgagggcagatttcca 238

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QY 239 gtgaacgcagccgagacacccaaattgaagtgtatccagttgtgaaaaaacctgctcacct 298

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Db 242 GCTTGCATGTCCGAGACACCAAAATCGAGGTGGCCAGTTTGTAAAGGACCTGCTCTTAC 301

QY 299 atgtaaggggagtttatcgccatggaatttca 331

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Db 302 ATTTAAGAAACTTTTTCGCGAGGGACGGTTCA 334

RESULT 9

AF043334 LOCUS AF043334 417 bp mRNA PRI 21-FEB-1998

DEFINITION Homo sapiens interleukin 13 precursor (IL13) mRNA, complete cds.

ACCESSION AF043334

VERSION AF043334.1 GI:2905619

KEYWORDS human.

SOURCE ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 417)

Direct Submission

Submitted (15-JAN-1998) Protein Engineering, General Institute of Technology, Hyundai Pharm. Ind. Co., Ltd., 213 Sosa Bon 1-dong, Sosa-gu, Bucheon 422-231, Korea

Nested PCR:

1) first PCR : forward primer (5'-ctcaatcctctcctgttgga-3')

reverse primer (5'-tagtcaggtcctgtctctgc-3')

2) second PCR : forward primer (5'-ctcatggcgctttttgtgaccacg-3')

reverse primer (5'-gatgctttcgaagtgttcagttgaa-3').

FEATURES

Source Location/Qualifiers

1..417

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/cell\_type="PHA-treated peripheral blood leukocyte"

1..417

/gene="IL13"

1..24

/gene="IL13"

/note="second PCR"

/PCR\_conditions="94C-1min, 50C-1min, 72C-3min, 30 cycles;

Deltacycler II from Ericomp"

4..402

CDS



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/gene="IL13"
/codon_start=1
/product="interleukin 13 precursor"
/protein_id="AAC03535.1"
/db_xref="GI:2905620"
/translation="MALLLTIVIALTCLGGFASPGVPPSTALRELIEELVNITQNK
APLNGSMVWSINLTAGMYCAALESINLVSGCSAIEKTQRLMGGFCPHKVSAGQFSSL
HVRDTKIEVAQFVKDLLLLHLKLLFREGRFN"
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/gene="IL13"
64..399
/gene="IL13"
/product="interleukin 13"
complement(394..417)
/note="second PCR"
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sig_peptide          91 a 121 c 108 g 97 t
mat_peptide
primer_bind
BASE COUNT          91 a 121 c 108 g 97 t
ORIGIN
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Query Match 60.6%; Score 201.8; DB 88; Length 417;  
Best Local Similarity 77.5%; Pred. No. 2e-43;  
Matches 258; Conservative 0; Mismatches 72; Indels 3; Gaps 1;

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QY 2 gccctgtgactccctccccaacccctcaaggagctcattgaggagctggtcaacatcaccc 61
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Db 65 GCCCTGTGCCTCCCTCTACAGCCCTCAGGGAGCTCATTGAGGAGCTGGTCAACATCACCC 124

QY 62 agaatc---aggcatccctctgcaacggcagcatggtgtggagcgtcaaacctgaccgccg 118
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Db 125 AGAACCAAGAAGGCTCCGCTCTGCAATGGCAGCATGGTTTGGAGCATCAACCTGACAGCTG 184

QY 119 gcatgtactgcgagctctagaatctctgataatctctccgactgctccgagcgccatccaaa 178
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Db 185 GCATGTACTGTGCAGCCCTGGAATCCCTGATCAACGTGTTCAGGCTGCAGTGGCAGTTTCCA 244

QY 179 ggaccagaggtgctgaaagcactgtgctctcaaaagccgcggcaggcgagatttcca 238
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Db 245 AGACCCAGAGGATGCTGGCGGATTCTGCCGCACAAAGGTCTCAGCTGGGCAGTTTCCA 304

QY 239 gtgaacgcagccgagacaccaaattgaagtgatccagttggtgaaaaacctgctcacct 298
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Db 305 GCTTGCAATGTCGAGACACCAAAATCGAGGTGGCCAGTTTGTAAAGGACCTGCTCTTAC 364

QY 299 atgtaaggggagtttatcgccatggaaatttca 331
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Db 365 ATTTAAGAAACTTTTCGCGAGGACGGTTCA 397
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RESULT 10
A29948
LOCUS A29948 1297 bp DNA PAT 23-JUN-1995
DEFINITION Coding sequence for protein with cytokine like activity.
ACCESSION A29948
VERSION A29948.1 GI:1249028
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM artificial sequence.
REFERENCE 1 (bases 1 to 1297)
AUTHORS Caput,D., Ferrara,P., Guillemot,J.C., Kaghad,M., Labit-le
Bouteiller,C., Leplatois,P., Magazin,M. and Minty,A.
TITLE Protein having cytokin type activity, recombinant DNA coding for
this protein, transformed cells and microorganisms
JOURNAL Patent: EP 0506574-A 21 30-SEP-1992;
ELF SANOFI
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FEATURES
source Location/Qualifiers
1..1297
/organism="synthetic construct"
/db_xref="taxon:32630"
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/codon_start=1
/transl_table=11
/product="protein with cytokine like activity"
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/protein_id="CAA01982.1"
/db_xref="GI:1249029"
/translation="MHPLLNPLLLALGLMALLTTVIALTCLGGFASPGVPPSTALR
ELIEELVNITQNKAPLNGSMVWSINLTADMYCAALESINLVSGCSAIEKTQRLM
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BASE COUNT          309 a 341 c 336 g 311 t
ORIGIN
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Query Match 60.6%; Score 201.8; DB 9; Length 1297;  
Best Local Similarity 77.5%; Pred. No. 1.9e-43;  
Matches 258; Conservative 0; Mismatches 72; Indels 3; Gaps 1;

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QY 2 gccctgtgactccctccccaacccctcaaggagctcattgaggagctggtcaacatcaccc 61
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Db 118 GCCCTGTGCCTCCCTCTACAGCCCTCAGGGAGCTCATTGAGGAGCTGGTCAACATCACCC 177

QY 62 agaatc---aggcatccctctgcaacggcagcatggtgtggagcgtcaaacctgaccgccg 118
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Db 178 AGAACCAAGAAGGCTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAACCTGACAGCTG 237

QY 119 gcatgtactgcgagctctagaatctctgataatctctccgactgctccgagcgccatccaaa 178
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Db 238 ACATGTACTGTGCAGCCCTGGAATCCCTGATCAACGTGTTCAGGCTGCAGTGGCAGTTTCCA 297

QY 179 ggaccagaggtgctgaaagcactgtgctctcaaaagccgcggcaggcgagatttcca 238
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Db 298 AGACCCAGAGGATGCTGCAGCGGATTCTGCCCGCACAAAGGTCTCAGCTGGGCAGTTTCCA 357

QY 239 gtgaacgcagccgagacaccaaattgaagtgatccagttggtgaaaaacctgctcacct 298
| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 358 GCTTGCAATGTCGAGACACCAAAATCGAGGTGGCCAGTTTGTAAAGGACCTGCTCTTAC 417

QY 299 atgtaaggggagtttatcgccatggaaatttca 331
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Db 418 ATTTAAGAAACTTTTTCGCGAGGACGGTTCA 450
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RESULT 11
I58488
LOCUS I58488 1297 bp DNA PAT 07-OCT-1997
DEFINITION Sequence 15 from patent US 5652123.
ACCESSION I58488
VERSION I58488.1 GI:2477726
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1297)
AUTHORS Caput,D., Ferrara,P., Guillemot,J., Kaghad,M., Labit-Le
Bouteiller,C., Leplatois,P., Magazin,M. and Minty,A.
TITLE Protein having interleukin 13 activity, recombinant DNA coding for
this protein, transformed cells and microorganisms
JOURNAL Patent: US 5652123-A 15 29-JUL-1997;
FEATURES Location/Qualifiers
source 1..1297
/organism="unknown"
BASE COUNT          309 a 341 c 336 g 311 t
ORIGIN
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Query Match 60.6%; Score 201.8; DB 10; Length 1297;  
Best Local Similarity 77.5%; Pred. No. 1.9e-43;  
Matches 258; Conservative 0; Mismatches 72; Indels 3; Gaps 1;

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QY 2 gccctgtgactccctccccaacccctcaaggagctcattgaggagctggtcaacatcaccc 61
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Db 118 GCCCTGTGCCTCCCTCTACAGCCCTCAGGGAGCTCATTGAGGAGCTGGTCAACATCACCC 177

QY 62 agaatc---aggcatccctctgcaacggcagcatggtgtggagcgtcaaacctgaccgccg 118
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Db 178 AGAACCAAGAAGGCTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAACCTGACAGCTG 237
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QY	119	gcatgtactgcgcagctctagaatctctgalcaatgtctccgactgcagcgccatccaaa	178
Db	238	ACATGTACTGTGCAGCCCTGGAATCCCTGATCAACGTGTCAAGGCTGCAGTGCCATCGAGA	297
QY	179	ggaccagaggatgctgaaagcactgtgctctcaaaaagcccggcagggcagatttcca	238
Db	298	AGACCCAGAGGATGCTGAGCGGATTCTGCCCGCACAAAGGTCTCAGCTGGGCAGTTTCCA	357
QY	239	gtgaacgcagccgagacacacaaaattgaagtgatccagttgggtgaaaaaacctgctcacct	298
Db	358	GCTTGCAATGTCGGAGACACCAAAATCGAGGTGGCCACAGTTTGTAAAGGACCTGCTCTTAC	417
QY	299	atgtaaggggagtttatcgccatggaaaatttca	331
Db	418	ATTTAAAGAAACTTTTTCGGGAGGGACGGTTCA	450
RESULT 12			
A29950			
LOCUS	A29950	384 bp	DNA
DEFINITION	Nucleic acid fragment B.		
ACCESSION	A29950		
VERSION	A29950.1 GI:1249030		
KEYWORDS	synthetic construct.		
SOURCE	synthetic construct		
ORGANISM	artificial sequence.		
REFERENCE	1 (bases 1 to 384)		
AUTHORS	Caput,D., Ferrara,P., Guillemot,J.C., Kaghad,M., Labit-le		
TITLE	Bouteiller,C., Leplatols,P., Magazin,M. and Minty,A.		
JOURNAL	Protein having cytokin type activity, recombinant DNA coding for		
	this protein, transformed cells and microorganisms		
	Patent: EP 0506574-A 23 30-SEP-1992;		
FEATURES	ELF SANOFI		
source	Location/Qualifiers		
	1..384		
	/organism="synthetic construct"		
	/db_xref="taxon:32630"		
BASE COUNT	97 a	104 c	99 g 84 t
ORIGIN			
Query Match 60.1%; Score 200.2; DB 9; Length 384;			
Best Local Similarity 77.2%; Pred. NO. 5.3e-43;			
Matches 257; Conservative 0; Mismatches 73; Indels 3; Gaps 1;			
QY	2	gccctgtactccctcccaaacctcaaggagctcattgaggagctgggtcaacatcaccc	61
Db	23	GCCCTGTGCCTCCCTCTACGGCCCTCAGGGAGCTCATTTGAGGAGCTGGTCAACATCACCC	82
QY	62	agaatc---aggcatccctctgcaacggcgagcatgggtggagcgtcaaacctgaccgccg	118
Db	83	AGAACCAAGAGGCTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAACCTGACAGCTG	142
QY	119	gcatgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgccatccaaa	178
Db	143	ACATGTACTGTGCAGCCCTGGAATCCCTGATCAACGTGTCAAGGCTGCAGTGCCATCGAGA	202
QY	179	ggaccagaggatgctgaaagcactgtgctctcaaaaagcccggcagggcagatttcca	238
Db	203	AGACCCAGAGGATGCTGAGCGGATTCTGCCCGCACAAAGGTCTCAGCTGGGCAGTTTCCA	262
QY	239	gtgaacgcagccgagacacacaaaattgaagtgatccagttgggtgaaaaaacctgctcacct	298
Db	263	GCTTGCAATGTCGGAGACACCAAAATCGAGGTGGCCACAGTTTGTAAAGGACCTGCTCTTAC	322
QY	299	atgtaaggggagtttatcgccatggaaaatttca	331
Db	323	ATTTAAAGAAACTTTTTCGGGAGGGACGGTTCA	355
RESULT 13			
T58489			
LOCUS	T58489	425 bp	DNA
DEFINITION	Sequence 4 from patent US 5856142.		
ACCESSION	T58489		
VERSION	T58489.1 GI:5937905		
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 425)		
AUTHORS	Legoux,R., Maldonado,P. and Salome,M.		
TITLE	Method for the extraction of periplasmic proteins from prokaryotic		
JOURNAL	microorganisms in the presence of arginine		
	Patent: US 5856142-A 4 05-JAN-1999;		
FEATURES	Location/Qualifiers		
source	1..425		
	/organism="unknown"		
BASE COUNT	100 a	116 c	110 g 99 t
ORIGIN			
Query Match 59.6%; Score 198.6; DB 9; Length 425;			

LOCUS	I58489	384 bp	DNA	PAT	07-OCT-1997
DEFINITION	Sequence 17 from patent US 5652123.				
ACCESSION	I58489				
VERSION	I58489.1 GI:2477727				
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 384)				
AUTHORS	Caput,D., Ferrara,P., Guillemot,J., Kaghad,M., Labit-Le				
TITLE	Bouteiller,C., Leplatols,P., Magazin,M. and Minty,A.				
JOURNAL	Protein having interleukin 13 activity, recombinant DNA coding for				
FEATURES	this protein, transformed cells and microorganisms				
source	Patent: US 5652123-A 17 29-JUL-1997;				
BASE COUNT	97 a	104 c	99 g	84 t	
ORIGIN					
Query Match	60.1%; Score 200.2; DB 10; Length 384;				
Best Local Similarity	77.2%; Pred. No. 5.3e-43;				
Matches	257; Conservative	0; Mismatches	73; Indels	3; Gaps	1;
QY	2	gccctgtactccctcccaaacctcaaggagctcattgaggagctgggtcaacatcaccc	61		
Db	23	GCCCTGTGCCTCCCTCTACGGCCCTCAGGAGCTCATTTGAGGAGCTGGTCAACATCACCC	82		
QY	62	agaatc---aggcatccctctgcaacggcgagcatgggtggagcgtcaaacctgaccgccg	118		
Db	83	AGAACCAAGAGGCTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAACCTGACAGCTG	142		
QY	119	gcatgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgccatccaaa	178		
Db	143	ACATGTACTGTGCAGCCCTGGAAATCCCTGATCAACGTGTCAAGGCTGCAGTGCATCGAGA	202		
QY	179	ggaccagaggatgctgaaagcactgtgctctcaaaaagcccggcaggcgagatttcca	238		
Db	203	AGACCCAGAGGATGCTGAGCGGATTCTGCCCGCACAAAGGTCTCAGCTGGGCAGTTTCCA	262		
QY	239	gtgaacgcagccgagacacacaaaattgaagtgatccagttgggtgaaaaaacctgctcacct	298		
Db	263	GCTTGCAATGTCGGAGACACCAAAATCGAGGTGGCCAGTTTGTAAAGGACCTGCTCTTAC	322		
QY	299	atgtaaggggaggtttatcgccatggaaaatttca	331		
Db	323	ATTTAAAGAAACTTTTTCGGGAGGGACGGTTCA	355		
RESULT	14				
LOCUS	AR027065	425 bp	DNA	PAT	29-SEP-1999
DEFINITION	Sequence 4 from patent US 5856142.				
ACCESSION	AR027065				
VERSION	AR027065.1 GI:5937905				
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 425)				
AUTHORS	Legoux,R., Maldonado,P. and Salome,M.				
TITLE	Method for the extraction of periplasmic proteins from prokaryotic				
JOURNAL	microorganisms in the presence of arginine				
FEATURES	Patent: US 5856142-A 4 05-JAN-1999;				
source	Location/Qualifiers				
BASE COUNT	100 a	116 c	110 g	99 t	
ORIGIN					
Query Match	59.6%; Score 198.6; DB 9; Length 425;				

Best Local Similarity 76.9%; Pred. No. 1.4e-42;  
Matches 256; Conservative 0; Mismatches 74; Indels 3; Gaps 1;

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QY	62	agaatc---aggcatccctctgcaacggcagcatggtgtggagcgtcaaacctgaccgcg	118
Db	125	AGAACCAGAAGGGCTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAACCTGACAGCTG	184

QY	119	gcatgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgccatccaaa	178
Db	185	GCATGTACTGTGCAGCCCTGGAATCCCTGATCAACGTTGTGAGGCTGCAGTGCCCATCGAGA	244

QY	179	ggaccagaggtgctgaaagcactgtgctctctcaaaagcccgcggcagggcagatttcca	238
Db	245	AGACCCAGAGGATGCTGAGCGGATTCTGCCCGCACACAGGTCTCAGCTGGGCAGTTTTTCCA	304

QY	239	gtgaacgcagccgcagacaccaaattgaagtgatccagttggtgaaaaacctgctcacct	298
Db	305	GCTTGATGTCCGAGACACCAAAATCGAGGTGGCCCGAGTTGTAAAGGACCTGCTCTTAC	364

QY	299	atgtaaggggagtttatcgcccatggaaatttca	331
Db	365	ATTAAAGAAACTTTTTCGCGAGGGACGGTTCA	397

RESULT 15

I86198

LOCUS I86198 425 bp DNA PAT 10-JUN-1998

DEFINITION Sequence 4 from patent US 5700665.

ACCESSION I86198

VERSION I86198.1 GI:3205916

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 425)

AUTHORS Legoux,R., Maldonado,P. and Salome,M.

TITLE Method for the extraction of periplasmic proteins from prokaryotic microorganisms in the presence of arginine

JOURNAL Patent: US 5700665-A 4 23-DEC-1997;

FEATURES

source

1. .425

Location/Qualifiers

BASE COUNT 100 a 116 c 110 g 99 t

ORIGIN

Query Match 59.6%; Score 198.6; DB 10; Length 425;  
Best Local Similarity 76.9%; Pred. No. 1.4e-42;  
Matches 256; Conservative 0; Mismatches 74; Indels 3; Gaps 1;

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QY	62	agaatc---aggcatccctctgcaacggcagcatggtgtggagcgtcaaacctgaccgcg	118
Db	125	AGAACCAGAAGGGCTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAACCTGACAGCTG	184

QY	119	gcatgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgccatccaaa	178
Db	185	GCATGTACTGTGCAGCCCTGGAATCCCTGATCAACGTTGTGAGGCTGCAGTGCCCATCGAGA	244

QY	179	ggaccagaggtgctgaaagcactgtgctctcaaaagcccgcggcagggcagatttcca	238
Db	245	AGACCCAGAGGATGCTGAGCGGATTCTGCCCGCACACAGGTCTCAGCTGGGCAGTTTTTCCA	304

QY	239	gtgaacgcagccgcagacaccaaattgaagtgatccagttggtgaaaaacctgctcacct	298
Db	305	GCTTGATGTCCGAGACACCAAAATCGAGGTGGCCCGAGTTGTAAAGGACCTGCTCTTAC	364

QY	299	atgtaaggggagtttatcgcccatggaaatttca	331
Db	365	ATTAAAGAAACTTTTTCGCGAGGGACGGTTCA	397

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Job time: 19115 sec

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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: May 13, 2001, 14:29:54 ; Search time 472.02 Seconds  
(without alignments)  
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Perfect score: 333  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 678276 seqs, 291890651 residues

Total number of hits satisfying chosen parameters: 1356552

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	333	100.0	333	21	255559 Canine mature inte
2	333	100.0	333	21	255560 Canine mature inte
3	333	100.0	393	21	255557 Canine interleukin
4	333	100.0	393	21	255558 Canine interleukin
5	333	100.0	1302	21	255555 Canine interleukin
6	333	100.0	1302	21	255556 Canine mature inte
7	317	95.2	330	21	255565 Canine mature inte
8	317	95.2	330	21	255566 Canine mature inte
9	317	95.2	390	21	255563 Canine interleukin
10	317	95.2	390	21	255564 Canine interleukin
11	317	95.2	1269	21	255561 Canine interleukin

C	12	317	95.2	1269	21	255562	Canine interleukin
	13	256	76.9	272	21	255553	Canine interleukin
	14	218	65.5	278	21	255554	Canine interleukin
	15	203.4	61.1	336	13	Q28944	Gly41-Cytokine cod
	16	203.4	61.1	1270	21	F21334	Human low adenosin
	17	203.4	61.1	1270	21	A35212	Human adenosine re
	18	203.4	61.1	1282	21	F21332	Human low adenosin
	19	203.4	61.1	1282	21	A35210	Human adenosine re
	20	203.4	61.1	1290	15	Q56692	Sequence encoding
	21	203.4	61.1	6952	21	F21333	Human low adenosin
	22	203.4	61.1	6952	21	A35211	Human adenosine re
	23	203.4	61.1	14978	21	F21338	Human low adenosin
	24	203.4	61.1	14978	21	A35216	Human adenosine re
	25	201.8	60.6	336	13	Q28943	Asp41-Cytokine cod
	26	201.8	60.6	1297	13	Q28947	Cytokine NC30. Q
	27	142	42.6	1212	15	Q56693	Sequence encoding
	28	71	21.3	5670	21	F21331	Human low adenosin
	29	71	21.3	5670	21	F21337	Human low adenosin
	30	71	21.3	5670	21	A35209	Human adenosine re
	31	71	21.3	5670	21	A35215	Human adenosine re
	32	39	11.7	166	21	255552	Canine interleukin
	33	34	10.2	479	21	C38383	Zea mays DNA fragm
	34	34	10.2	1896	21	Z48297	S. coelicolor YesW
	35	33.4	10.0	66	20	Z32227	Human interleukin
	36	33.4	10.0	772	19	V48405	Dominant-negative
	37	32.4	9.7	717	21	A93373	Enhanced green flu
	38	32.4	9.7	717	21	A93374	Enhanced blue fluo
	39	32.4	9.7	717	21	A93375	Enhanced cyan fluo
	40	32.4	9.7	717	21	A27573	DNA encoding EGFP
	41	32.4	9.7	717	21	A27574	DNA encoding EBFP
	42	32.4	9.7	717	21	A27575	DNA encoding BCFP
	43	32.4	9.7	720	21	C62377	CDNA encoding a gr
	44	32.4	9.7	720	21	Z45642	DNA encoding the m
	45	32.4	9.7	720	21	Z45644	DNA encoding the m

ALIGNMENTS

RESULT 1  
Z55559  
ID Z55559 standard; cDNA; 333 Bp.  
XX  
AC Z55559;  
XX  
DT 14-MAR-2000 (first entry)  
XX  
DE Canine mature interleukin-13 (IL-13) clone 80 cDNA.  
DE  
XX Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;  
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.  
XX  
OS Canis familiaris.  
XX  
PN WO9961618-A2.  
XX  
PD 02-DEC-1999.  
XX  
PF 28-MAY-1999; 99WO-US11942.  
XX  
PR 29-MAY-1998; 98US-0087306.  
XX  
PA (HESK-) HESKA CORP.  
XX  
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;  
XX  
DR WPI; 2000-072623/06.  
DR P-PSDB; Y58222.  
XX  
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
PT useful for treating or preventing e.g. tumors or autoimmune disease  
XX  
PS Claim li; Page 233-234; 264pp; English.

```
XX Sequences Z55552-Z55560 and Z55561-Z55566 represent cDNA
CC sequences encoding canine interleukin-13 (IL-13) clones 80
CC and 78 respectively. The invention relates to canine
CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
CC interferon-alpha (IFN-alpha), and feline granulocyte macrophage
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these
CC immunoregulatory proteins. The proteins, their associated
CC nucleic acids, specific antibodies and inhibitors may be used as
CC vaccines for therapeutic or prophylactic regulation of an immune
CC response in animals (particularly cats, dogs, horses and humans).
CC They may be used to treat autoimmune or infectious diseases including
CC allergies, tumours, inflammation and graft rejection, and to increase
CC the response from a co-administered antigen. The nucleotide sequences
CC can also be used for the recombinant production of a protein, while
CC nucleotide fragments are useful as probes, as amplification primers and
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
CC The proteins may be used to raise antibodies and to screen for
CC modulators of activity, while the antibodies may be used in detection,
CC and in drug targetting.
XX
SQ Sequence 333 BP; 89 A; 97 C; 83 G; 64 T; 0 other;

Query Match      100.0%; Score 333; DB 21; Length 333;
Best Local Similarity 100.0%; Pred. No. 1.4e-90;
Matches 333; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agccctgtgactccctcccaaccctcaaggagctcattgaggagctggtcaacatcacc 60
Db 1 agccctgtgactccctcccaaccctcaaggagctcattgaggagctggtcaacatcacc 60

QY 61 cagaatcaggcatccctctgcaacggcagcatggtgtggagcggtcaacctgaccgccggc 120
Db 61 cagaatcaggcatccctctgcaacggcagcatggtgtggagcggtcaacctgaccgccggc 120

QY 121 atgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgccatccaaagg 180
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QY 181 acccagaggatgctgaaagcactgtgctctcaaaagcccgcgggcagagatttccagt 240
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QY 301 gtaaggggagtttatcgccatggaatttcaga 333
Db 301 gtaaggggagtttatcgccatggaatttcaga 333

RESULT 2
Z55560/c
ID Z55560 standard; cDNA; 333 BP.
XX
AC Z55560;
XX
DT 14-MAR-2000 (first entry)
DE Canine mature interleukin-13 (IL-13) clone 80 cDNA complement.
XX
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
XX
OS Canis familiaris.
XX
PN WO9961618-A2.
XX
PD 02-DEC-1999.
XX
```

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PF 28-MAY-1999; 99WO-US11942.
XX
PR 29-MAY-1998; 98US-0087306.
XX
PA (HESK-) HESKA CORP.
XX
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;
XX
DR WPI; 2000-072623/06.
DR P-PSDB; Y58222.
XX
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,
PT useful for treating or preventing e.g. tumors or autoimmune disease
XX
PS Claim 1i; Page 235; 264pp; English.
XX
CC Sequences Z55552-Z55560 and Z55561-Z55566 represent cDNA
CC sequences encoding canine interleukin-13 (IL-13) clones 80
CC and 78 respectively. The invention relates to canine
CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these
CC immunoregulatory proteins. The proteins, their associated
CC nucleic acids, specific antibodies and inhibitors may be used as
CC vaccines for therapeutic or prophylactic regulation of an immune
CC response in animals (particularly cats, dogs, horses and humans).
CC They may be used to treat autoimmune or infectious diseases including
CC allergies, tumours, inflammation and graft rejection, and to increase
CC the response from a co-administered antigen. The nucleotide sequences
CC can also be used for the recombinant production of a protein, while
CC nucleotide fragments are useful as probes, as amplification primers and
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
CC The proteins may be used to raise antibodies and to screen for
CC modulators of activity, while the antibodies may be used in detection,
CC and in drug targetting.
XX
SQ Sequence 333 BP; 64 A; 83 C; 97 G; 89 T; 0 other;

Query Match      100.0%; Score 333; DB 21; Length 333;
Best Local Similarity 100.0%; Pred. No. 1.4e-90;
Matches 333; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 cagaatcaggcatccctctgcaacggcagcatggtgtggagcggtcaacctgaccgccggc 120
Db 273 CAGAATCAGGCATCCCTCTGCAACGGCAGCATGGTGTGGAGCGTCAACCTGACCCCGCGC 214

QY 121 atgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgccatccaaagg 180
Db 213 ATGTACTGCGCAGCTCTAGAAATCTCTGATCAATGTCTCCGACTGCAGCGCCATCCAAAG 154

QY 181 acccagaggatgctgaaagcactgtgctctcaaaagcccgcgggcagagatttccagt 240
Db 153 ACCCAGAGGATGCTGAAAGCACTGTGCTCTCAAAAGCCCGCGGCGAGGTCAGATTTCAGT 94

QY 241 gaacgcagccgagacaccaaattgaagtgatccagttggtgaaacacctgctcacctat 300
Db 93 GAACGCAGCCGAGACACCAAAATTGAAGTGATCCAGTTGGTGAAAAACCTGCTCACCTAT 34

QY 301 gtaaggggagtttatcgccatggaatttcaga 333
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RESULT 3
Z55557
ID Z55557 standard; cDNA; 393 BP.
XX
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AC 255557;  
XX  
DT 14-MAR-2000 (first entry)  
XX  
DE Canine interleukin-13 (IL-13) clone 80 cDNA coding region.  
XX  
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;  
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.  
XX  
OS Canis familiaris.  
XX  
PN WO9961618-A2.  
XX  
PD 02-DEC-1999.  
XX  
PF 28-MAY-1999; 99WO-US11942.  
XX  
PR 29-MAY-1998; 98US-0087306.  
XX  
PA (HESK-) HESKA CORP.  
XX  
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;  
XX  
DR WPI; 2000-072623/06.  
DR P-PSDB; Y58221.  
XX  
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
PT useful for treating or preventing e.g. tumors or autoimmune disease  
XX  
PS Claim 11; Page 232-233; 264pp; English.  
XX  
CC Sequences 255552-255560 and 255561-255566 represent cDNA  
CC sequences encoding canine interleukin-13 (IL-13) clones 80  
CC and 78 respectively. The invention relates to canine  
CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or  
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline  
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage  
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these  
CC immunoregulatory proteins. The proteins, their associated  
CC nucleic acids, specific antibodies and inhibitors may be used as  
CC vaccines for therapeutic or prophylactic regulation of an immune  
CC response in animals (particularly cats, dogs, horses and humans).  
CC They may be used to treat autoimmune or infectious diseases including  
CC allergies, tumours, inflammation and graft rejection, and to increase  
CC the response from a co-administered antigen. The nucleotide sequences  
CC can also be used for the recombinant production of a protein, while  
CC nucleotide fragments are useful as probes, as amplification primers and  
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
CC The proteins may be used to raise antibodies and to screen for  
CC modulators of activity, while the antibodies may be used in detection,  
CC and in drug targeting.  
XX  
SQ Sequence 393 BP; 93 A; 118 C; 100 G; 82 T; 0 other;

Query Match 100.0%; Score 333; DB 21; Length 393;  
Best Local Similarity 100.0%; Pred. No. 1.5e-90;  
Matches 333; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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ID 255558 standard; cDNA; 393 BP.  
XX  
AC 255558;  
XX  
DT 14-MAR-2000 (first entry)  
XX  
DE Canine interleukin-13 (IL-13) clone 80 cDNA coding region complement.  
XX  
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;  
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.  
XX  
OS Canis familiaris.  
XX  
PN WO9961618-A2.  
XX  
PD 02-DEC-1999.  
XX  
PF 28-MAY-1999; 99WO-US11942.  
XX  
PR 29-MAY-1998; 98US-0087306.  
XX  
PA (HESK-) HESKA CORP.  
XX  
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;  
XX  
DR WPI; 2000-072623/06.  
DR P-PSDB; Y58221.  
XX  
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
PT useful for treating or preventing e.g. tumors or autoimmune disease  
XX  
PS Claim 11; Page 233; 264pp; English.  
XX  
CC Sequences 255552-255560 and 255561-255566 represent cDNA  
CC sequences encoding canine interleukin-13 (IL-13) clones 80  
CC and 78 respectively. The invention relates to canine  
CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or  
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline  
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage  
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these  
CC immunoregulatory proteins. The proteins, their associated  
CC nucleic acids, specific antibodies and inhibitors may be used as  
CC vaccines for therapeutic or prophylactic regulation of an immune  
CC response in animals (particularly cats, dogs, horses and humans).  
CC They may be used to treat autoimmune or infectious diseases including  
CC allergies, tumours, inflammation and graft rejection, and to increase  
CC the response from a co-administered antigen. The nucleotide sequences  
CC can also be used for the recombinant production of a protein, while  
CC nucleotide fragments are useful as probes, as amplification primers and  
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
CC The proteins may be used to raise antibodies and to screen for  
CC modulators of activity, while the antibodies may be used in detection,  
CC and in drug targeting.  
XX  
SQ Sequence 393 BP; 82 A; 100 C; 118 G; 93 T; 0 other;

Query Match 100.0%; Score 333; DB 21; Length 393;  
Best Local Similarity 100.0%; Pred. No. 1.5e-90;  
Matches 333; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agccctgtgactccctcccaaccctcaaggagctcaattgaggagctggtgtaacatcacc 60  
|||||  
Db 333 AGCCCTGTGACTCCCTCCCAACCCCTCAAGGAGCTCATTTGAGGAGCTGGTCAACATCACC 274  
|||||  
QY 61 cagaatcaggcatccctctgcaacggcagcatggtgtggagcgtcaacctgaccgcggc 120  
|||||  
Db 273 CAGAATCAGGCATCCCTCTGCAACGGCAGCATGGTGTGGAGCGTCAACCTGACCGCGGC 214  
|||||  
QY 121 atgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgccatccaaagg 180  
|||||  
Db 213 ATGTACTGCCGAGCTCTAGAATCTCTGATCAATGTCTCCGACTGCAGCGCCATCCAAAGG 154  
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QY 181 acccagaggatgctgaaagcactgtgctctcctcaaaagcccgcgaggcagatttccagt 240  
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Db 153 ACCCAGAGGATGCTGAAGCACTGTGCTCTCAAAAGCCCGGCGCAGGGCAGATTTCAGT 94  
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QY 241 gaacgcagccgagacacacaaattgaagtgtccagttggtgaaacacctgctcacctat 300  
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Db 93 GAACGCAGCCGAGACACCAAAATTGAAGTGATCCAGTTGGTGAAAAACCTGCTCACCTAT 34  
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QY 301 gtaaggggagtttatcgccatggaaatttcaga 333  
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Db 33 GTAAGGGGAGTTTATCGCCATGGAAATTTTCAGA 1  
|||||  
RESULT 5  
255555  
ID 255555 standard; cDNA; 1302 BP.  
XX  
AC 255555;  
XX  
DT 14-MAR-2000 (first entry)  
XX  
DE Canine interleukin-13 (IL-13) clone 80 cDNA.  
XX  
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;  
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.  
XX  
OS Canis familiaris.  
XX  
FH Key Location/Qualifiers  
FT CDS 52..447  
FT /\*tag= a  
FT /product= "Canine IL-13 clone 80"  
XX  
PN WO9961618-A2.  
XX  
PD 02-DEC-1999.  
XX  
PF 28-MAY-1999; 99WO-US11942.  
XX  
PR 29-MAY-1998; 98US-0087306.  
XX  
PA (HESK-) HESKA CORP.  
XX  
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;  
XX  
DR WPI; 2000-072623/06.  
DR P-PSDB; Y58221.  
XX  
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
PT useful for treating or preventing e.g. tumors or autoimmune disease -  
XX  
PS Claim 1i; Page 229-230; 264pp; English.  
XX  
CC Sequences 255552-255560 and 255561-255566 represent cDNA  
CC sequences encoding canine interleukin-13 (IL-13) clones 80  
CC and 78 respectively. The invention relates to canine  
CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or  
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline  
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage  
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these

CC immunoregulatory proteins. The proteins, their associated  
CC nucleic acids, specific antibodies and inhibitors may be used as  
CC vaccines for therapeutic or prophylactic regulation of an immune  
CC response in animals (particularly cats, dogs, horses and humans).  
CC They may be used to treat autoimmune or infectious diseases including  
CC allergies, tumours, inflammation and graft rejection, and to increase  
CC the response from a co-administered antigen. The nucleotide sequences  
CC can also be used for the recombinant production of a protein, while  
CC nucleotide fragments are useful as probes, as amplification primers and  
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
CC The proteins may be used to raise antibodies and to screen for  
CC modulators of activity, while the antibodies may be used in detection,  
CC and in drug targetting.  
XX  
SQ Sequence 1302 BP; 337 A; 318 C; 340 G; 307 T; 0 other;  
Query Match 100.0%; Score 333; DB 21; Length 1302;  
Best Local Similarity 100.0%; Pred. No. 2.4e-90;  
Matches 333; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 agccctgtgactccctcccaaccctcaaggagctcattgaggagctggtgtaacatcacc 60  
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Db 112 agccctgtgactccctcccaaccctcaaggagctcattgaggagctggtgtaacatcacc 171  
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QY 61 cagaatcaggcatccctctgcaacggcagcatggtgtggagcgtcaacctgaccgcggc 120  
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Db 172 cagaatcaggcatccctctgcaacggcagcatggtgtggagcgtcaacctgaccgcggc 231  
|||||  
QY 121 atgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgccatccaaagg 180  
|||||  
Db 232 atgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgccatccaaagg 291  
|||||  
QY 181 acccagaggatgctgaaagcactgtgctctcctcaaaagcccgcgaggcagatttccagt 240  
|||||  
Db 292 acccagaggatgctgaaagcactgtgctctcctcaaaagcccgcgaggcagatttccagt 351  
|||||  
QY 241 gaacgcagccgagacacacaaattgaagtgtccagttggtgaaacacctgctcacctat 300  
|||||  
Db 352 gaacgcagccgagacacacaaattgaagtgtccagttggtgaaacacctgctcacctat 411  
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QY 301 gtaaggggagtttatcgccatggaaatttcaga 333  
|||||  
Db 412 gtaaggggagtttatcgccatggaaatttcaga 444  
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RESULT 6  
255556/c  
ID 255556 standard; cDNA; 1302 BP.  
XX  
AC 255556;  
XX  
DT 14-MAR-2000 (first entry)  
XX  
DE Canine interleukin-13 (IL-13) clone 80 cDNA complement.  
XX  
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;  
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.  
XX  
OS Canis familiaris.  
XX  
FH Key Location/Qualifiers  
FT CDS complement (856..1251)  
FT /\*tag= a  
FT /product= "Canine IL-13 clone 80"  
XX  
PN WO9961618-A2.  
XX  
PD 02-DEC-1999.  
XX  
PF 28-MAY-1999; 99WO-US11942.  
XX  
PR 29-MAY-1998; 98US-0087306.





||||| 238 gaagcagcgagacacaaattgaagtgtccagttggtgaaaaacctgctcaacctat 297

QY 301 gtaaggggagtttatgccatggaatttcaga 333

Db 298 gtaaggggagtttatgccatggaatttcaga 330

RESULT 8

Z55566/c

ID 255566 standard; cDNA; 330 BP.

XX

AC 255566;

XX

DT 14-MAR-2000 (first entry)

XX

DE Canine mature interleukin-13 (IL-13) clone 78 cDNA complement.

XX

KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;

KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.

XX

OS Canis familiaris.

XX

PN WO9961618-A2.

XX

PD 02-DEC-1999.

XX

PF 28-MAY-1999; 99WO-US11942.

XX

PR 29-MAY-1998; 98US-0087306.

XX

PA (HESK-) HESKA CORP.

XX

PI Sim G, Yang S, Dreitz MJ, Wonderling RS;

XX

DR WPI; 2000-072623/06.

DR P-PSDB; Y58224.

XX

PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,

PT useful for treating or preventing e.g. tumors or autoimmune disease

XX

PS Claim 1i; Page 241; 264pp; English.

XX

CC Sequences Z55552-Z55560 and Z55561-Z55566 represent cDNA

CC sequences encoding canine interleukin-13 (IL-13) clones 80

CC and 78 respectively. The invention relates to canine

CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or

CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline

CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage

CC colony-stimulating factor (GM-CSF), and nucleotides which encode these

CC immunoregulatory proteins. The proteins, their associated

CC nucleic acids, specific antibodies and inhibitors may be used as

CC vaccines for therapeutic or prophylactic regulation of an immune

CC response in animals (particularly cats, dogs, horses and humans).

CC They may be used to treat autoimmune or infectious diseases including

CC allergies, tumours, inflammation and graft rejection, and to increase

CC the response from a co-administered antigen. The nucleotide sequences

CC can also be used for the recombinant production of a protein, while

CC nucleotide fragments are useful as probes, as amplification primers and

CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).

CC The proteins may be used to raise antibodies and to screen for

CC modulators of activity, while the antibodies may be used in detection,

CC and in drug targeting.

XX

SQ Sequence 330 BP; 64 A; 82 C; 96 G; 88 T; 0 other;

Query Match 95.2%; Score 317; DB 21; Length 330;

Best Local Similarity 99.1%; Pred. No. 9e-86;

Matches 330; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 1 agccctgtgactccctcccaacctcaaggagctcattgaggagctggtcaacatcacc 60

|||||

Db 330 AGCCCTGTGACTCCCTCCCTCCCAACCTCAAGGAGCTCATTGAGGAGCTGGTCAACATCACC 271

QY 61 cagaatcaggcatccctctgcaacggcagcatggtgtggagcgtaaacctgaccgcggc 120

|||||

Db 270 CAGAAATCAGGCATCCCTCTGCAACGGCAGCATGGTGTGGAGCGTCAACCTGACCGCGGC 211

QY 121 atgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgcacaaagg 180

|||||

Db 210 ATGTACTGCGCAGCTCTAGAACTCTGATCAATGTCTCCGACTGCGAGGCCATCCAAGG 151

QY 181 accagagagatgctgaaagcactgtgctctctcaaaagccgcggcagggcagattccagt 240

|||||

Db 150 ACCCAGAGGATGCTGAAAGCACTGTGCTCTCAAAAGCCCGCGGACG--GATTTCAGT 94

QY 241 gaacgcagccgagacacacaaattgaagtgtatccagttggtgaaaaacctgctcacctat 300

|||||

Db 93 GAACGAGCCGAGACACCAAAATTGAAGTGATCCAGTTGGTGAATAAACCCTGCTCACCTAT 34

QY 301 gtaaggggagtttatgccatggaatttcaga 333

|||||

Db 33 GTAAGGGGAGTTTATCGCCATGGAAATTTTCAGA 1

RESULT 9

Z55563

ID 255563 standard; cDNA; 390 BP.

XX

AC 255563;

XX

DT 14-MAR-2000 (first entry)

XX

DE Canine interleukin-13 (IL-13) clone 78 cDNA coding region.

XX

KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;

KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.

XX

OS Canis familiaris.

XX

PN WO9961618-A2.

XX

PD 02-DEC-1999.

XX

PF 28-MAY-1999; 99WO-US11942.

XX

PR 29-MAY-1998; 98US-0087306.

XX

PA (HESK-) HESKA CORP.

XX

PI Sim G, Yang S, Dreitz MJ, Wonderling RS;

XX

DR WPI; 2000-072623/06.

DR P-PSDB; Y58223.

XX

PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,

PT useful for treating or preventing e.g. tumors or autoimmune disease

XX

PS Claim 1i; Page 238-239; 264pp; English.

XX

CC Sequences Z55552-Z55560 and Z55561-Z55566 represent cDNA

CC sequences encoding canine interleukin-13 (IL-13) clones 80

CC and 78 respectively. The invention relates to canine

CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or

CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline

CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage

CC colony-stimulating factor (GM-CSF), and nucleotides which encode these

CC immunoregulatory proteins. The proteins, their associated

CC nucleic acids, specific antibodies and inhibitors may be used as

CC vaccines for therapeutic or prophylactic regulation of an immune

CC response in animals (particularly cats, dogs, horses and humans).

CC They may be used to treat autoimmune or infectious diseases including

CC allergies, tumours, inflammation and graft rejection, and to increase

CC the response from a co-administered antigen. The nucleotide sequences

CC can also be used for the recombinant production of a protein, while









|||||  
Db 1093 CAGAAATCAGGCATCCCTCTGCAACGGCAGCATGGTGTGGAGCGTCAACCTGACCGCGGC 1034  
QY 121 atgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgccatccaaagg 180  
Db 1033 ATGTACTGCGCAGCTCTAGAAATCTCTGATCAATGTCTCCGACTGCAGCGCCATCCAAAGG 974  
QY 181 acccagaggatgctgaaagcaactgtgctctcaaaagcccgggcagggcagatttcaggt 240  
Db 973 ACCCAGAGGATGCTGAAAGCACTGTGCTCTCAAAAGCCCGCGCAGG---GATTTCAGT 917  
QY 241 gaacgcagccgagacaccaaattgaagtgtccagttgtgtaaaacacctgtcacctat 300  
Db 916 GAACGCAGCCGAGACACCAAAATTGAAGTGATCCAGTTGGTGAAAAACCTGCTCACCTAT 857  
QY 301 gtaaggggagtttatcgccatgggaaatttcaga 333  
Db 856 GTAAGGGGAGTTTATCGCCCATGGAAATTTCAGA 824  
  
RESULT 13  
Z55553  
ID Z55553 standard; cDNA; 272 BP.  
XX AC Z55553;  
XX  
DT 14-MAR-2000 (first entry)  
XX  
DE Canine interleukin-13 (IL-13) cDNA fragment nCaILL13-272.  
XX  
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;  
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.  
OS  
OS Canis familiaris.  
XX  
XX WO9961618-A2.  
PN  
XX  
PD 02-DEC-1999.  
XX  
PF 28-MAY-1999; 99WO-US11942.  
XX  
PR 29-MAY-1998; 98US-0087306.  
XX  
XX (HESK-) HESKA CORP.  
PA  
XX  
XX Sim G, Yang S, Dreitz MJ, Wonderling RS;  
PI  
XX  
XX WPI; 2000-072623/06.  
DR  
XX  
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
PT useful for treating or preventing e.g. tumors or autoimmune disease  
XX  
XX Claim 1i; Page 228; 264pp; English.  
XX  
XX Sequences Z55552-Z55560 and Z55561-Z55566 represent cDNA  
CC sequences encoding canine interleukin-13 (IL-13) clones 80  
CC and 78 respectively. The invention relates to canine  
CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or  
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline  
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage  
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these  
CC immunoregulatory proteins. The proteins, their associated  
CC nucleic acids, specific antibodies and inhibitors may be used as  
CC vaccines for therapeutic or prophylactic regulation of an immune  
CC response in animals (particularly cats, dogs, horses and humans).  
CC They may be used to treat autoimmune or infectious diseases including  
CC allergies, tumours, inflammation and graft rejection, and to increase  
CC the response from a co-administered antigen. The nucleotide sequences  
CC can also be used for the recombinant production of a protein, while  
CC nucleotide fragments are useful as probes, as amplification primers and  
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
CC The proteins may be used to raise antibodies and to screen for  
CC modulators of activity, while the antibodies may be used in detection,

CC and in drug targeting.  
XX  
SQ Sequence 272 BP; 64 A; 91 C; 69 G; 48 T; 0 other;  
  
Query Match 76.9%; Score 256; DB 21; Length 272;  
Best Local Similarity 100.0%; Pred. No. 1.6e-67;  
Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 agccctgtgactccctcccaacccctcaaggagctcattgaggagctgggtcaacatcacc 60  
Db 17 agccctgtgactccctcccaacccctcaaggagctcattgaggagctgggtcaacatcacc 76  
QY 61 cagaatcaggcatccctctgcaacggcagcatggtgtggagcgtcaacctgaccgcccgc 120  
Db 77 cagaatcaggcatccctctgcaacggcagcatggtgtggagcgtcaacctgaccgcccgc 136  
QY 121 atgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgccatccaaagg 180  
Db 137 atgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgccatccaaagg 196  
QY 181 acccagaggatgctgaaagcaactgtgctctcaaaagcccgggcagatttcaggt 240  
Db 197 acccagaggatgctgaaagcaactgtgctctcaaaagcccgggcagatttcaggt 256  
QY 241 gaacgcagccgagaca 256  
Db 257 gaacgcagccgagaca 272  
  
RESULT 14  
Z55554  
ID Z55554 standard; cDNA; 278 BP.  
XX AC Z55554;  
XX  
DT 14-MAR-2000 (first entry)  
XX  
DE Canine interleukin-13 (IL-13) cDNA probe.  
XX  
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;  
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.  
XX  
OS Canis familiaris.  
XX  
XX WO9961618-A2.  
PN  
XX  
XX 02-DEC-1999.  
XX  
PF 28-MAY-1999; 99WO-US11942.  
XX  
PR 29-MAY-1998; 98US-0087306.  
XX  
XX (HESK-) HESKA CORP.  
PA  
XX  
XX Sim G, Yang S, Dreitz MJ, Wonderling RS;  
PI  
XX  
XX WPI; 2000-072623/06.  
DR  
XX  
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
PT useful for treating or preventing e.g. tumors or autoimmune disease  
XX  
XX Claim 1i; Page 229; 264pp; English.  
XX  
XX Sequences Z55552-Z55560 and Z55561-Z55566 represent cDNA  
CC sequences encoding canine interleukin-13 (IL-13) clones 80  
CC and 78 respectively. The invention relates to canine  
CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or  
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline  
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage  
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these  
CC immunoregulatory proteins. The proteins, their associated  
CC nucleic acids, specific antibodies and inhibitors may be used as





GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: May 13, 2001, 14:21:17 ; Search time 226.02 Seconds  
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Title: US-09-451-527-96  
Perfect score: 333  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 302621 seqs, 87301344 residues

Total number of hits satisfying chosen parameters: 605242

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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6: /cgnl\_7/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	203.4	61.1	336	1	US-08-371-121-24 Sequence 24, Appl
2	203.4	61.1	1290	1	US-08-012-543-1 Sequence 1, Appli
3	203.4	61.1	1290	5	PCT-US93-07645A-1 Sequence 1, Appli
4	203.4	61.1	1290	5	PCT-US93-07645-1 Sequence 1, Appli
5	201.8	60.6	336	1	US-08-371-121-2 Sequence 2, Appli
6	201.8	60.6	1297	1	US-08-371-121-15 Sequence 15, Appl
7	200.2	60.1	384	1	US-08-371-121-17 Sequence 17, Appl
8	198.6	59.6	425	1	US-08-594-469-4 Sequence 4, Appli
9	198.6	59.6	425	2	US-08-906-957-4 Sequence 4, Appli
10	198.6	59.6	4410	1	US-08-594-469-1 Sequence 1, Appli
11	198.6	59.6	4410	2	US-08-906-957-1 Sequence 1, Appli
12	142	42.6	447	1	US-08-371-121-26 Sequence 26, Appl
13	142	42.6	1212	1	US-08-012-543-3 Sequence 3, Appli
14	142	42.6	1212	5	PCT-US93-07645A-3 Sequence 3, Appli
15	142	42.6	1212	5	PCT-US93-07645-3 Sequence 3, Appli
16	33.4	10.0	1322	4	US-09-128-450-27 Sequence 27, Appl
17	32.4	9.7	720	4	US-09-094-359-3 Sequence 3, Appli
18	32.4	9.7	720	4	US-09-094-359-7 Sequence 7, Appli
19	32.4	9.7	720	4	US-09-172-063-11 Sequence 11, Appl
20	32.4	9.7	720	4	US-09-172-063-13 Sequence 13, Appl
21	32.4	9.7	762	1	US-08-532-390-40 Sequence 40, Appl
22	32.4	9.7	762	4	US-08-717-294-40 Sequence 40, Appl
23	32.4	9.7	768	4	US-09-094-359-11 Sequence 11, Appl
24	32.4	9.7	850	4	US-09-062-102-2 Sequence 2, Appli
25	32.4	9.7	972	4	US-09-172-063-27 Sequence 27, Appl
26	32.4	9.7	972	4	US-09-172-063-29 Sequence 29, Appl
27	32.4	9.7	1095	4	US-09-085-305-5 Sequence 5, Appli

28	32.4	9.7	1929	2	US-08-818-253-1	Sequence 1, Appli
29	32.4	9.7	1929	2	US-08-818-253-5	Sequence 5, Appli
30	32.4	9.7	1929	4	US-08-818-252-1	Sequence 1, Appli
31	32.4	9.7	1929	4	US-08-818-252-5	Sequence 5, Appli
32	32.4	9.7	1959	2	US-08-818-253-3	Sequence 3, Appli
33	32.4	9.7	1959	4	US-08-818-252-3	Sequence 3, Appli
34	32.4	9.7	1971	2	US-08-818-253-7	Sequence 7, Appli
35	32.4	9.7	1971	4	US-08-818-252-7	Sequence 7, Appli
36	32.4	9.7	7938	4	US-09-331-581-14	Sequence 14, Appl
37	32	9.6	1926	2	US-08-978-182-2	Sequence 2, Appli
38	32	9.6	1926	2	US-09-205-681-2	Sequence 2, Appli
c 39	32	9.6	3958	2	US-07-952-853-21	Sequence 21, Appl
c 40	32	9.6	3958	2	US-08-914-848-21	Sequence 21, Appl
41	31.8	9.5	4184	2	US-08-785-310A-4	Sequence 4, Appli
c 42	31.8	9.5	35081	2	US-08-752-760A-1	Sequence 1, Appli
43	31.4	9.4	398	4	US-09-060-756-630	Sequence 630, App
44	31.2	9.4	720	4	US-09-094-359-5	Sequence 5, Appli
45	31.2	9.4	720	4	US-09-094-359-9	Sequence 9, Appli

ALIGNMENTS

RESULT 1  
US-08-371-121-24  
; Sequence 24, Application US/083711121  
; Patent No. 5652123  
; GENERAL INFORMATION:  
; APPLICANT: CAPUT, Daniel  
; APPLICANT: FERRARA, Pascual  
; APPLICANT: GUILLEMOT, Jean-Claude  
; APPLICANT: LEPLATOIS, Pascal  
; APPLICANT: MINTY, Adrian  
; APPLICANT: KAGHAD, Mourad  
; APPLICANT: LABIT-LE BOUTEILLER, Christine  
; APPLICANT: MAGAZIN, Marilyn  
; TITLE OF INVENTION: Protein having a cytokine type  
; TITLE OF INVENTION: activity, recombinant DNA coding for this protein,  
; TITLE OF INVENTION: transformed cells and microorganisms.  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FOLEY & LARDNER  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington, D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/371,121  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/938,161  
; FILING DATE: 30-NOV-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/FR92/00280  
; FILING DATE: 27-MAR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 91 00137  
; FILING DATE: 08-JAN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 91 03904  
; FILING DATE: 29-MAR-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SAXE, Bernhard D.  
; REGISTRATION NUMBER: 28,665  
; REFERENCE/DOCKET NUMBER: 16781/383  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 672-5300



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;
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 336 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-371-121-24

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QY 119 gcatgtactgcgcagctctagaatctctgatcaaatgtctccgactgcagggccatccaaa 178
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QY 179 ggaccagagagtgctgaaagcactgtgctctcaaaaagcccgcgagggcagatttcca 238
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QY 239 gtgaacgcagcgagacacacaaattgaagtgtatccagttggtgaaaaacctgctcacct 298
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Db 242 GCTTGCAATGTCGAGACACCAAAATCGAGGTGGCCCGAGTTTGTAAAGGACCTGCTCTTAC 301

QY 299 atgtaaggggagtttatcgccatggaaaatttca 331
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Db 302 ATTTAAAGAAACTTTTTCGCGAGGACGGTTCA 334

RESULT 2
US-08-012-543-1
; Sequence 1, Application US/08012543
; Patent No. 5596072
; GENERAL INFORMATION:
; APPLICANT: Culpepper, Janice
; APPLICANT: McKenzie, Andrew
; APPLICANT: Dang, Warren
; APPLICANT: de Waal Malefyt, Rene
; APPLICANT: Heath, Andrew
; APPLICANT: Aversa, Gregorio
; APPLICANT: Briere, Francine
; APPLICANT: Bancheureau, Jacques
; APPLICANT: de Vries, Jan
; APPLICANT: Zurawski, Gerard
; TITLE OF INVENTION: Human Interleukin-13
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/012,543
; FILING DATE: 01-FEB-1993
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; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/933,416
; FILING DATE: 21-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0302K1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-852-9196
; TELEFAX: 415-496-1200
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1290 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 45..443
; US-08-012-543-1

Query Match          61.1%; Score 203.4; DB 1; Length 1290;
Best Local Similarity 77.8%; Pred. No. 6.3e-55;
Matches 259; Conservative 0; Mismatches 71; Indels 3; Gaps 1;

QY 2 gccctgtgactccctcccaaccctcaaggagctcattgaggagctggtcaacatcaccc 61
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Db 166 AGAACCAGAAGGCTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAACCTGACAGCTG 225

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QY 179 ggaccagagagtgctgaaagcactgtgctctcaaaaagcccgcgagggcagatttcca 238
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Db 406 ATTTAAAGAAACTTTTTCGCGAGGACGGTTCA 438

RESULT 3
PCT-US93-07645A-1
; Sequence 1, Application PC/TUS9307645A
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Human Interleukin-13
; NUMBER OF SEQUENCES: 6
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.5
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07645A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/012543
; FILING DATE: 01-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/010977
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; FILING DATE: 29-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/933416
; FILING DATE: 21-AUG-1992
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1290 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
PCT-US93-07645A-1

Query Match. 61.1%; Score 203.4; DB 5; Length 1290;
Best Local Similarity 77.8%; Pred. No. 6.3e-55;
Matches 259; Conservative 0; Mismatches 71; Indels 3; Gaps 1;

QY 2 gccctgtgactccctcccaaccctcaaggagctcattgaggagctggtcaacatcaccc 61
Db 106 GCCCTGTGCCTCCCTCTACAGCCCTCAGGGAGCTCATTTGAGGAGCTGGTCAACATCACCC 165

QY 62 agaatc---aggcatccctctgcaaacggcagcagcatggtgtagcgtcaaacctgaccgcg 118
Db 166 AGAACCAAGAAGGCTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAACCTGACAGCTG 225

QY 119 gcatgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgccatccaaa 178
Db 226 GCATGTACTGTGCAGCCCTGGAATCCCTGATCAACGCTGTCAGGCTGCAGTGCCATCGAGA 285

QY 179 ggaccagaggtgctgaaagcactgtgctctcaaaaagcccgcgagggcagagatttcca 238
Db 286 AGACCCAGAGGATGCTGAGCGGATTCTGCCCGCACAAAGTCTCAGCTGGGCAGTTTCCA 345

QY 239 gtgaacgcagccgcagacacacccaaattgaagtgtatccagttggtgaaaaaacctgctcacct 298
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QY 299 atgtaagggagtttatcgccatggaaatttca 331
Db 406 ATTTAAAGAAACTTTTTCGCGAGGGACGGTTCA 438

RESULT 4
PCT-US93-07645-1
; Sequence 1, Application PC/TUS9307645
; GENERAL INFORMATION:
; APPLICANT: Human Interleukin-13
; TITLE OF INVENTION:
; NUMBER OF SEQUENCES: 6
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.5
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07645
; FILING DATE: 19930818
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/012543
; FILING DATE: 01-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/010977
; FILING DATE: 29-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/933416
; FILING DATE: 21-AUG-1992
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1290 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
PCT-US93-07645-1
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Query Match. 61.1%; Score 203.4; DB 5; Length 1290;
Best Local Similarity 77.8%; Pred. No. 6.3e-55;
Matches 259; Conservative 0; Mismatches 71; Indels 3; Gaps 1;

QY 2 gccctgtgactccctcccaaccctcaaggagctcattgaggagctggtcaacatcaccc 61
Db 106 GCCCTGTGCCTCCCTCTACAGCCCTCAGGGAGCTCATTTGAGGAGCTGGTCAACATCACCC 165

QY 62 agaatc---aggcatccctctgcaaacggcagcagcatggtgtagcgtcaaacctgaccgcg 118
Db 166 AGAACCAAGAAGGCTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAACCTGACAGCTG 225

QY 119 gcatgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgccatccaaa 178
Db 226 GCATGTACTGTGCAGCCCTGGAATCCCTGATCAACGCTGTCAGGCTGCAGTGCCATCGAGA 285

QY 179 ggaccagaggtgctgaaagcactgtgctctcaaaaagcccgcgagggcagagatttcca 238
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QY 239 gtgaacgcagccgcagacacacccaaattgaagtgtatccagttggtgaaaaaacctgctcacct 298
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QY 299 atgtaagggagtttatcgccatggaaatttca 331
Db 406 ATTTAAAGAAACTTTTTCGCGAGGGACGGTTCA 438

RESULT 5
US-08-371-121-2
; Sequence 2, Application US/08371121
; Patent No. 5652123
; GENERAL INFORMATION:
; APPLICANT: CAPUT, Daniel
; APPLICANT: FERRARA, Pascual
; APPLICANT: GUILLEMOT, Jean-Claude
; APPLICANT: LEPLATOIS, Pascal
; APPLICANT: MINTY, Adrian
; APPLICANT: KAGHAD, Mourad
; APPLICANT: LABIT-LE BOUTEILLER, Christine
; APPLICANT: MAGAZIN, Marilyn
; TITLE OF INVENTION: protein having a cytokine type
; TITLE OF INVENTION: activity, recombinant DNA coding for this protein,
; TITLE OF INVENTION: transformed cells and microorganisms.
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/371,121
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/938,161
; FILING DATE: 30-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR92/00280
; FILING DATE: 27-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91 00137
; FILING DATE: 08-JAN-1992
; PRIOR APPLICATION DATA:
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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: May 13, 2001, 11:40:15 ; Search time 5997.24 Seconds  
(without alignments)  
485.077 Million cell updates/sec

Title: US-09-451-527-96  
Perfect score: 333  
Sequence: 1 agccctgtgactccctccc.....atcgccatggaaatttcaga 333

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 9623517 seqs, 4368049070 residues

Total number of hits satisfying chosen parameters: 19247034

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
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3	36.4	10.9	537	166	BE357229	BE357229 DGL_147_B
4	36	10.8	462	143	BF039993	BF039993 BP250023B
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8	35.4	10.6	498	150	BF606532	BF606532 273595 MA
9	34.4	10.3	507	138	BE705147	BE705147 SC02_08f0
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C 13	34.2	10.3	965	217	AZ201624	AZ201624 SP_0053_A
14	34	10.2	370	166	BE363650	BE363650 WSL_64_G1
15	34	10.2	562	166	BE361027	BE361027 DGL_69_A0
16	34	10.2	929	143	BF037598	BF037598 601461167
17	33.8	10.2	341	163	BE127683	BE127683 DEPA1432
18	33.6	10.1	577	166	BE402120	BE402120 CSB004F06







Db 233 CTGGTGGCAAGGGGGCTTCGCCGAGNTCTACAAGGCCAAGCTGAAGCAGAACACGTCT 292

QY 205 tgctctcaaaagccgcgagggcagatttcc 237

Db 293 GAGCAGTTCGAGACCGTGGCCGTCAGATCTTC 325

RESULT 5

AI444326/c

LOCUS AI444326 497 bp mRNA EST 09-MAR-1999

DEFINITION fb47h12.y1 zebrafish WashU MPIMG EST Danio rerio cDNA 5', mRNA sequence.

ACCESSION AI444326

VERSION AI444326.1 GI:4309388

KEYWORDS EST.

SOURCE zebrafish.

ORGANISM Danio rerio

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes; Cyprinidae; Rasboridae; Danio.

REFERENCE 1 (bases 1 to 497)

AUTHORS Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy ,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood ,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.

TITLE WashU Zebrafish EST Project 1998

JOURNAL Unpublished (1998)

COMMENT Contact: Stephen L. Johnson Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800 Fax: 314 286 1810 Email: zbrafish@watson.wustl.edu cDNA Library Preparation: Matthew Clark. cDNA Library Arrayed by: Matthew Clark. DNA Sequencing by: Washington University Genome Sequencing Center Clone Distribution: Genome Systems, St. Louis, Missouri (web address: www.genomesystems.com) (email contact: info@genomesystems.com) and Research Genetics, Huntsville, Alabama (web address: www.resgen.com) (email contact: info@resgen.com) and RessourcenzentrumPrimarDatenbank, Berlin, Germany (web address: www.rzpd.de)

Seq primer: T3 ET from Amersham

High quality sequence stop: 473.

FEATURES

source

1. .497

Location/Qualifiers

/organism="Danio rerio"

/db\_xref="taxon:7955"

/clone\_lib="zebrafish WashU MPIMG EST"

/sex="mixed"

/tissue\_type="26 somite embryos, adult livers, shield stage embryos"

/lab\_host="XLI-blue MRF"

/note="Vector: pSPORT1; Site\_1: NotI; Site\_2: SalI; 1st strand cDNA was primed with a Not I - oligo(dT)15 primer [5'pGACTAGTCTAGATCGGAGCGCGCCCTTTTTTT3']; double-stranded cDNA was ligated to Sal I adaptors (BRL), digested with Not I and cloned into the Not I and Sal I sites of the pSPORT1 vector (BRL). Library was constructed by Matthew Clark (Lehrach lab; ICRF, London and Max Planck Institut fuer Molekulare Genetik,Berlin). cDNAs for EST analysis were selected following oligonucleotide hybridization fingerprinting of arrayed clones from zebrafish late somitogenesis (26 ss), adult liver or embryonic shield stage (5.6 h) libraries. Fingerprint data were used to computationally cluster cDNAs, and a single cDNA from each cluster was chosen for sequencing. In some cases multiple members of the same cluster were sequenced to assess clustering parameters or single clones were sequenced additional times to assess quality control."

BASE COUNT 126 a 167 c 121 g 83 t

ORIGIN

Query Match 10.8%; Score 35.8; DB 20; Length 497;

Best Local Similarity 57.7%; Pred. No. 6.5;

Matches 64; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 184 cagaggatgctgaagcactgtgctctcaaaagccgcgagggcagatttccagtga 243

Db 422 CAGAGGATGCTGAGAGGATTCAGCTTCGCGGAGCAGCGGGGAATGGAGAGGGCTGGATGG 363

QY 244 cgcagccgagacaccaaattgaagtgtatccagttgtgtaaaaaacctgtc 294

Db 362 TTCAGACGTCGCCCACTTTTGAGTGCTCCAGTGTGTCGAGAACCAACGTC 312

RESULT 6

AW729623/c

LOCUS AW729623 1946 bp mRNA EST 16-NOV-2000

DEFINITION GA\_Ea0025J07 Gossypium arboreum 7-10 dpa fiber library Gossypium arboreum cDNA clone GA\_Ea0025J07, mRNA sequence.

ACCESSION AW729623

VERSION AW729623.1 GI:7627221

KEYWORDS EST.

SOURCE Gossypium arboreum.

ORGANISM Gossypium arboreum

Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.

REFERENCE 1 (bases 1 to 1946)

AUTHORS Wing,R.A., Frisch,D., Yu,Y., Main,D., Rambo,T., Simmons,J., Henry ,D., Wood,T.C., Leslie,A. and Wilkins,T.A.

TITLE An integrated analysis of the genetics, development, and evolution of the cotton fiber

JOURNAL Unpublished (2000)

COMMENT Contact: Wing RA Clemson University Genomics Institute Clemson University 100 Jordan Hall, Clemson, SC 29634, USA Tel: 864 656 7288 Fax: 864 656 4293 Email: rwing@clemson.edu High quality sequence stop: 1946.

FEATURES

source

1. .1946

Location/Qualifiers

/organism="Gossypium arboreum"

/strain="AKA"

/cultivar="8400"

/db\_xref="taxon:29729"

/clone="GA\_Ea0025J07"

/clone\_lib="Gossypium arboreum 7-10 dpa fiber library"

/tissue\_type="Fibers isolated from bolls harvested 7-10 dpa"

/lab\_host="E. coli"

/note="Vector: pBK-CMV; Site\_1: EcoRI; Site\_2: XhoI"

BASE COUNT 412 a 492 c 495 g 472 t 75 others

ORIGIN

Query Match 10.8%; Score 35.8; DB 119; Length 1946;

Best Local Similarity 52.8%; Pred. No. 9.5;

Matches 76; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

QY 123 gtactgcgcagctctagaatctctgatcaatgtctccgactgcagccatccaaaggac 182

Db 276 GCACTGCGGACCTCTATGTGTGATCTATGTCTCTGACTATCGAGGCACACCGCAC 217

QY 183 ccagaggatgctgaagcactgtgtctctcaaaagccgcgagggcagatttccagtga 242

Db 216 ACATAGCTAAACCAAGAACAGAGAGNTCTCGCACTCTCGTAGGCGCAGGATATGTGA 157

QY 243 acgcagccgagacaccaaattga 266













GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 13, 2001, 14:20:35 ; Search time 9342.78 Seconds  
(without alignments)  
2003.155 Million cell updates/sec

Title: US-09-451-527-99  
Perfect score: 1269  
Sequence: 1 ccagcctacgacctgcctgc.....gaaaaaaaaaaaaaaa 1269

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1283235 seqs, 7373929652 residues

Total number of hits satisfying chosen parameters: 2566470

Minimum DB seq length: 0  
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:\*  
1: gb\_bal:\*  
2: gb\_ba2:\*  
3: gb\_ba3:\*  
4: gb\_in1:\*  
5: gb\_in2:\*  
6: gb\_in3:\*  
7: gb\_om:\*  
8: gb\_ov:\*  
9: gb\_pat1:\*  
10: gb\_pat2:\*  
11: gb\_ph:\*  
12: gb\_pl1:\*  
13: gb\_pl2:\*  
14: gb\_pl3:\*  
15: gb\_pl4:\*  
16: em\_bal:\*  
17: em\_ba2:\*  
18: em\_fun:\*  
19: em\_htgo\_hum:\*  
20: em\_htgo\_inv:\*  
21: em\_htgo\_rod:\*  
22: em\_htg\_hum1:\*  
23: em\_htg\_hum2:\*  
24: em\_htg\_hum3:\*  
25: em\_htg\_hum4:\*  
26: em\_htg\_hum5:\*  
27: em\_htg\_hum6:\*  
28: em\_htg\_hum7:\*  
29: em\_htg\_hum8:\*  
30: em\_htg\_inv1:\*  
31: em\_htg\_inv2:\*  
32: em\_htg\_other:\*  
33: em\_htg\_rod:\*  
34: em\_hum1:\*  
35: em\_hum2:\*  
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41: em\_in:\*  
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44: em\_ov:\*  
45: em\_pat:\*  
46: em\_ph:\*  
47: em\_pl:\*  
48: em\_ro:\*  
49: em\_sts:\*  
50: em\_sy:\*  
51: em\_un:\*  
52: em\_vi:\*  
53: gb\_sts1:\*  
54: gb\_sts2:\*  
55: gb\_sts3:\*  
56: gb\_sy:\*  
57: gb\_un:\*  
58: gb\_vil:\*  
59: gb\_vi2:\*  
60: gb\_htg1:\*  
61: gb\_htg2:\*  
62: gb\_htg3:\*  
63: gb\_htg4:\*  
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65: gb\_htg6:\*  
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81: gb\_htg22:\*  
82: gb\_htg23:\*  
83: gb\_htg24:\*  
84: gb\_htg25:\*  
85: gb\_pr1:\*  
86: gb\_pr2:\*  
87: gb\_pr3:\*  
88: gb\_pr4:\*  
89: gb\_pr5:\*  
90: gb\_pr6:\*  
91: gb\_pr7:\*  
92: gb\_pr8:\*  
93: gb\_pr9:\*  
94: gb\_rol:\*  
95: gb\_ro2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1251	98.6	1302	7	AF244915
2	887	69.9	213343	78	AF276990
3	408.4	32.2	213343	78	AF276990
4	362	28.5	1270	93	HUMIL13A
5	362	28.5	1282	92	HSNC30
6	362	28.5	1290	10	I34548
7	360.4	28.4	1297	9	A29948
8	360.4	28.4	1297	10	I58488
9	235.6	18.6	417	88	AF043334
10	229.2	18.1	3520	7	BT132441
11	216.4	17.1	1212	10	I34549



12	208	16.4	1207	94	MUSSTCPE	M23504 Mus musculus
13	203.8	16.1	343	7	AF072807	AF072807 Bos taurus
14	193.4	15.2	384	9	A29950	A29950 Nucleic aci
15	193.4	15.2	384	10	I58489	I58489 Sequence 17
16	191.6	15.1	425	9	AR027065	AR027065 Sequence
17	191.6	15.1	425	10	I86198	I86198 Sequence 4
18	191.6	15.1	4410	9	A52326	A52326 Sequence 1
19	191.6	15.1	4410	9	AR027062	AR027062 Sequence
20	191.6	15.1	4410	10	I86195	I86195 Sequence 1
21	187.4	14.8	336	9	A29931	A29931 Sequence co
22	187.4	14.8	336	10	I58494	I58494 Sequence 24
23	185.8	14.6	336	9	A29930	A29930 Sequence co
24	185.8	14.6	336	10	I58481	I58481 Sequence 2
25	185.4	14.6	447	10	I58495	I58495 Sequence 26
c 26	169.2	13.3	3395	93	HUM11DC98Z	L42079 Homo sapien
c 27	169.2	13.3	50282	85	AC004039	AC004039 Homo sapi
28	166	13.1	4600	93	HUM1113B	L13029 Human inter
29	166	13.1	5670	93	HSU311120	U31120 Human inter
c 30	166	13.1	78469	75	AC074127	AC074127 Homo sapi
31	163.2	12.9	443	94	RAT1113A	L26913 Rattus Norv
32	125.8	9.9	827	54	G06679	G06679 human STS W
33	120.6	9.5	4740	93	HSU10307	U10307 Human inter
c 34	116.8	9.2	3714	93	HUM11DC99Z	L42080 Homo sapien
35	116.8	9.2	78469	75	AC074127	AC074127 Homo sapi
c 36	90.8	7.2	142732	88	AC084392	AC084392 Homo sapi
c 37	90.8	7.2	159500	94	AC005742	AC005742 Mus muscu
38	90.8	7.2	237823	66	AC020886	AC020886 Mus muscu
39	86.2	6.8	4376	94	MUS1113A	L13028 Mouse inter
40	59.6	4.7	102	9	A29939	A29939 Sequence co
41	59.6	4.7	102	10	I58483	I58483 Sequence 10
42	54.6	4.3	96	9	A29938	A29938 Sequence co
43	54.6	4.3	96	10	I58482	I58482 Sequence 9
c 44	48.8	3.8	1168	53	CNS06HDF	AL398857 T7 end of
45	48.2	3.8	213045	78	AL136963	AL136963 Homo sapi

ALIGNMENTS

RESULT	1
AF244915	
LOCUS	AF244915 1302 bp mRNA MAM 16-OCT-2000
DEFINITION	Canis familiaris interleukin-13 mRNA, complete cds.
ACCESSION	AF244915
VERSION	AF244915.1 GI:7528273
KEYWORDS	
SOURCE	dog.
ORGANISM	Canis familiaris
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
AUTHORS	Yang,S., Boroughs,K.L. and McDermott,M.J.
TITLE	Canine interleukin-13: molecular cloning of full-length cDNA and expression of biologically active recombinant protein
JOURNAL	J. Interferon Cytokine Res. 20 (9), 779-785 (2000)
MEDLINE	20485146
PUBMED	11032397
REFERENCE	2 (bases 1 to 1302)
AUTHORS	Yang,S.
TITLE	Direct Submission
JOURNAL	Submitted (13-MAR-2000) Allergy and Immunology, Heska Corporation, 1613 Prospect Parkway, Fort Collins, CO 80525, USA
FEATURES	Location/Qualifiers
source	1. .1302
	/organism="Canis familiaris"
	/db_xref="taxon:9615"
5'UTR	1. .51
CDS	52. .447
	/codon_start=1
	/product="interleukin-13"
	/protein_id="AAF63204.1"
	/db_xref="GI:7528274"
	/translation="MALWLTWVIALTCLGLASPSVTPSPTLKELIELVNITQNOA

3'UTR	SLONGSMVWSVNLTAGMYCAALESLINVSDCSAIQRTQMLKALCSQKPAAGQISSER
BASE COUNT	SRDTKIEVIQLVKNLLTYVRGVYRHGNER"
ORIGIN	448. .1302
	337 a 318 c 340 g 307 t
Query Match	98.6%; Score 1251; DB 7; Length 1302;
Best Local Similarity	99.8%; Pred. No. 0;
Matches 1264; Conservative	0; Mismatches 0; Indels 3; Gaps 1;
QY	6 ctacgacctgctgctcttccctcgctcctcctcgctcctgcatggtgctctgggctccatggcgctc 65
Db	1 CTACGACCTGCCTGCTCTCCCTCGCTCCTCCTGCAATGGCTTGGGCTCCATGGCGCTC 60
QY	66 tggttgactgtgtgctatgctctcacctgcctcggtgccttgcctcccccagagccctgtg 125
Db	61 TGGTTGACTGTGGTCAATTGCTCTCACCTGCCTCGGTGGCTTGCCTCCCCGAGCCCTGTG 120
QY	126 actccctcccaacccctcaaggagctcattgaggagctggtgagctgaacatcacccagaaatcag 185
Db	121 ACTCCCTCCCCAACCCCTCAAGGAGCTCATTGAGGAGCTGGTCAACATCACCCAGAAATCAG 180
QY	186 gcatccctctgcaacggcagcatggtgtggagcgtcaacctgacccgagccgcatgtactgc 245
Db	181 GCATCCCTCTGCAACGGCAGCATGGTGTGGAGCGTCAACCTGACCGCCGGCATGTACTGC 240
QY	246 gcagctctagaatctctgatcaaatgtctccgactgcagcgcccatccaaaggaccagagg 305
Db	241 GCAGCTCTAGAAATCTCTGATCAATGTCTCCGACTGCACGCCCATCCAAAGGACCCAGAGG 300
QY	306 atgctgaaagcactgtgtctctcaaaagcccgggcagg---gatttccagtgaaacgacg 362
Db	301 ATGCTGAAAGCACTGTGCTCTCAAAAGCCCGCGGAGGGGAGATTTCCAGTGAACGCGACG 360
QY	363 cgagacacccaaaaattgaagtgatccagttggtgtaaaaaacctgctcacctatgtaagggga 422
Db	361 CGAGACACCCAAAATTGAAGTGATCCAGTTGGTGTAACCAACCTGCTCACCTATGTAAAGGGA 420
QY	423 gtttatcgccatggaaaatttcagatgaagcatgaaaccttagcatccttatctgtagacc 482
Db	421 GTTTATCGCCATGGAAATTTTCAGATGAAGCATGAAACCTTAGCATCCTTATCTGTAGACC 480
QY	483 cagacctgaccttaagttccagattcatttttcttccgacgtcacaaaatttcttagg 542
Db	481 CAGACCTGACCACTTAAGTTCAGATTCATTTTCTTCCGAGGTACAAATTTCTTAGG 540
QY	543 gaggtgggggggggagaacatttccctcagctgggacctaagcctgcaccgcctgcct 602
Db	541 GAGGTGGGGGGGGGAGAACCACTTCTCAGCTGGGACCTCAGCCTGCACCCGCTGCCT 600
QY	603 ccatggagctgagccagccacccctgccttgggtgcatggggcccccagccgggtggccctc 662
Db	601 CCATGGAGCTGAGCCACGCCACCCCTGCCTTGGTGCAATGGGCCCCAGCCGGTGGCCCTC 660
QY	663 ctccgtctgcacttcatcaacgctgagggaaagcactgcacatcccatgactgtccctcct 722
Db	661 CTCCGTCTGCACCTTCATCACGCTGAGGGAAAGCACTGCATCCCATGACTGTCCCTCCT 720
QY	723 cagagcaaatgtcagcattacagtgaggagcagatatgtgtgggaggggggtctgtgtac 782
Db	721 CAGAGCAAAGTGCAGCATTACAGTGGAGGCAGATATGTGTGGAGGGGGTCTTGTGTGTAC 780
QY	783 ctgggagtggcacagacatgtttcttcttagccttatttattattgtgttattttaaac 842
Db	781 CTGGGAGTGGCACAGACATGTTTCTTCTTAGCCTTATTATTATTGTGTGTATTATAAC 840
QY	843 aagtgtctttgtttgtctgggggacagggagtggtggcttgagctggggcccgactgactcg 902
Db	841 AAGTGTCTTTGTTGTGTGGGACAGGGAGTGGCTTGGAGTGGGGGGCCAGTGACTCG 900
QY	903 ggtttagagagtcacctgggaataagcactgtgtgtgtaaaattctgtacctcactgggatac 962

Db 901 GGTTTAGAGAGTCCCTGGGAATAAGCACTGTGTGTAAAAATTCGTACCTCACTGGGATC 960

QY 963 ctggggccgacacaggggacagagaaaggtcagagatgctgtcttctgtcgcactca 1022  
|||||

Db 961 CTGGGGCCGACACAGGGGACAGGAAAGGGTCAGAGATGCTGTCTGTCTGCCACTCA 1020

QY 1023 gcagctggccctcagcccaagcaagtaattattgttttctcctgtatttaaagttaagaaa 1082  
|||||

Db 1021 GCAGCTGGCCCTCAGCCCAAGCAGTAATTATTGTTTTTCCCTGTATTTAAAGTTAAGAAA 1080

QY 1083 taaaatatgttatcaaaagagttaataatatatagaaagtagcctaaaggctgcatttg 1142  
|||||

Db 1081 TAAAAATATGTTATCAAGAGTTAATAATATATAGAAAGTAGCCTAAAGGCTGCATTG 1140

QY 1143 gtgtgtgtgcccagggcggggtg9gggggaggggtgtgtcactgaatgtgctcttt 1202  
|||||

Db 1141 GTGTGTGTGGCCAGCCGGGGGGTGGGGGGAGGGTGTGTCACTGAATGTGCTCTTT 1200

QY 1203 cactgactttgtcaaaactggaagccagaaaataaagatggtgacaaagagaaaaaaa 1262  
|||||

Db 1201 CACTGACTTTGTCAAACTGGAAGCCAGAAAATAAAGATGGTGACAAAGAGAAAAAAA 1260

QY 1263 aaaaaa 1269  
|||||

Db 1261 AAAAAA 1267

RESULT 2

AF276990/c

LOCUS

DEFINITION AF276990 213343 bp DNA HTG 29-SEP-2000

Canis familiaris chromosome 4 clone RPCI-81 390C13, \*\*\* SEQUENCING IN PROGRESS \*\*\*, 25 ordered pieces.

ACCESSION AF276990

VERSION AF276990.1 GI:9964079

KEYWORDS HTG; HTGS\_PHASE2.

SOURCE dog.

ORGANISM Canis familiaris

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

REFERENCE 1 (bases 1 to 213343)

AUTHORS Dubchak,I., Brudno,M., Loots,G.G., Pachter,L., Mayor,C., Rubin,E.M. and Frazer,K.A.

TITLE Active conservation of noncoding sequences revealed by three-way species comparisons

JOURNAL Genome Res. 10 (9), 1304-1306 (2000)

MEDLINE 20442524

PUBMED 10984448

REFERENCE 2 (bases 1 to 213343)

AUTHORS Blankespoor,C.M., Dean,W.B. and Lewis,K.D.

TITLE Direct Submission

JOURNAL Submitted (10-JUN-2000) Genome Sciences Department, Lawrence Berkeley National Laboratory, 1 Cyclotron Road, Berkeley, CA 94720, USA

COMMENT

\* NOTE: This is a 'working draft' sequence. It currently

\* consists of 25 contigs. Gaps between the contigs

\* are represented as runs of N. The order of the pieces

\* is believed to be correct as given, however the sizes

\* of the gaps between them are based on estimates that have

\* provided by the submittor.

\* This sequence will be replaced

\* by the finished sequence as soon as it is available and

\* the accession number will be preserved.

\* 1 16269: contig of 16269 bp in length

\* gap of unknown length

\* 16270 24613: contig of 8344 bp in length

\* gap of unknown length

\* 24614 28694: contig of 4081 bp in length

\* gap of unknown length

\* 28695 31694: contig of 3000 bp in length

\* gap of unknown length

\* 31695 32391: contig of 697 bp in length

\* gap of unknown length

\* 32392 36538: contig of 4147 bp in length

\* 36539 gap of unknown length

\* 39567: contig of 3029 bp in length

\* gap of unknown length

\* 41164: contig of 1597 bp in length

\* gap of unknown length

\* 56023: contig of 14859 bp in length

\* gap of unknown length

\* 69825: contig of 13802 bp in length

\* gap of unknown length

\* 71104: contig of 1279 bp in length

\* gap of unknown length

\* 72258: contig of 1154 bp in length

\* gap of unknown length

\* 73132: contig of 874 bp in length

\* gap of unknown length

\* 88901: contig of 15769 bp in length

\* gap of unknown length

\* 96587: contig of 7686 bp in length

\* gap of unknown length

\* 105542: contig of 8955 bp in length

\* gap of unknown length

\* 108418: contig of 2876 bp in length

\* gap of unknown length

\* 113668: contig of 5250 bp in length

\* gap of unknown length

\* 116446: contig of 2778 bp in length

\* gap of unknown length

\* 116447 148106: contig of 31660 bp in length

\* gap of unknown length

\* 148107 155037: contig of 6931 bp in length

\* gap of unknown length

\* 155038 170050: contig of 15013 bp in length

\* gap of unknown length

\* 170051 196830: contig of 26780 bp in length

\* gap of unknown length

\* 196831 202835: contig of 6005 bp in length

\* gap of unknown length

\* 202836 213343: contig of 10508 bp in length.

FEATURES

source

1. 213343

/organism="Canis familiaris"

/db\_xref="taxon:9615"

/chromosome="4"

/clone="RPCI-81 390C13"

BASE COUNT 60084 a 42812 c 44046 g 66392 t 9 others

ORIGIN

Query Match 69.9%; Score 887; DB 78; Length 213343;

Best Local Similarity 99.0%; Pred. No. 9.1e-226;

Matches 904; Conservative 0; Mismatches 5; Indels 4; Gaps 1;

QY 344 gatttccagtgaaacgcagccgagacacacaaaattgaagtgcattccagttggtgaaaaacct 403  
|||||

Db 112101 GATTTCAGTGAACCGACCGCAGACACCCAAAATTGAAGTGATCCAGTTGGTGAAAAACCT 112042

QY 404 gctcacctatgtaagggagtttatcgccatggaatttcagatgaagcatgaaaaactta 463  
|||||

Db 112041 GCTCACCTATGTAAGGGAGTTTATGCCATGGAATTTTCAGATGAAGCATGAAAACTTA 111982

QY 464 gcacacctatctgtagaccagacctgaccacttaagttccagattcattttctttccg 523  
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Db 111981 GCATCCTTATCTGTAGACCCAGACCTGACCACCTTAAGTTCAGATTTCATTTTCTTCCG 111922

QY 524 acgtcacaaaatttcttagggaggtg9ggggggggagaaacatttccctcagctgggacct 583  
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Db 111921 ACGTCACAAATTTCTTAGGG ---GGGGGGGGGGAAGAACCATTTCTCAGCTGGGACCT 111866

QY 584 cagcctgcaccgcctgcctccatggagctgagcccgacccctgccttggtgcatggg 643  
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Db 111865 CAGCCTGCACCGCCTGCCTCCATGGAGCTGAGCCCGAGCCACCCCTGCCTTGGTGCATGG 111806

QY 644 gccacgcccgggtggccctcctccgtctgcacttcatcaactgagggaagcactgcat 703

Db	111805	CCCCAGCCGGGTGGCCCTCCTCCGCTGCACTTCATCAACGCTGAGGGAAGCACTGCAT	111746
QY	704	cccatgactgtccctcctcagagcaaaagtcagcattacagtggaagcagatatgtgtg	763
Db	111745	CCCATGACTGTCCCCCTCCTCAGAGCAAAGTGCAGCATTACAGTGGAGGCAGATATGTGTG	111686
QY	764	ggaggggtctctgtgtacctgggagtgccacagacatgtttctcttagccttattat	823
Db	111685	GGAGGGGGTCTTGCTGTACCTGGGAGTGGCACAGACATGTTCTTCTTAGCCTTATTTAT	111626
QY	824	tattgtgttattttaacaaagtgtctttgtctgctgggacagggagtggttgag	883
Db	111625	TATTGTGTGTATTATAACAAGTGTGTTGTGTCTGGGACAGGGAGTGGCTTGGAG	111566
QY	884	ctgggggcccagtgactcgggtttagagagtcctctgggaataagcactgtgtgtaaaaatt	943
Db	111565	CTGGGGGCCCACTGACTCGGGTTTAGAGAGTCCCTCGGAATAAGCACTGTGTGTAAAAATT	111506
QY	944	ctgctacctcactgggatacctcctggggccgacacacagggggacaggaagggtcagagatgc	1003
Db	111505	CTGCTACCTCACTGGGATCCTGGGGCCGACACAGGGGACAGGAGAAAGGGTCAGAGATGC	111446
QY	1004	tgctcttgtctgccactcagcagctggccctcagccaaagcagtaattattgttttccct	1063
Db	111445	TGCTCTTGCTGCCACTCAGCAGCTGGCCCTCAGCCAAAGCAGTAATTATTGTTTTTCCT	111386
QY	1064	tgtatttaaagttaagaaaaataatgttatcaaagagttaataatatagaagagta	1123
Db	111385	TGTATTTAAAGTTAAGAAATAAAATATGTTATCAAAAGACTTAATAATATATAGAAGAGTA	111326
QY	1124	gcctaaaaggctgcatttgggtgtgtgtgccagggcggtgggtggggggggtgtt	1183
Db	111325	GCCTAAAGGCTGCATTGGTGTGTGTGGCCAGGCCGGGGGGGGGGGGGGTGT	111266
QY	1184	gtcactgaatgtgtctctttcactgactttgtcaaaactggaagccagaaaaataaagatggtg	1243
Db	111265	GTCACCTGAATGTGCTCTTTTCACTGACTTTGTCAAACTGGAAAGCCAGAAAAATAAAGATGGTG	111206
QY	1244	acaagagaaaaa 1256	
Db	111205	ACAAGAGACCTTAA 111193	

## RESULT 3

AF276990	AF276990	213343 bp	DNA	HTG	29-SEP-2000
LOCUS	Canis familiaris chromosome 4 clone RPCI-81 390C13, *** SEQUENCING				
DEFINITION	IN PROGRESS ***, 25 ordered pieces.				
ACCESSION	AF276990				
VERSION	AF276990.1	GI:9964079			
KEYWORDS	HTG; HTGS_PHASE2.				
SOURCE	dog.				
ORGANISM	Canis familiaris				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.				
REFERENCE	1 (bases 1 to 213343)				
AUTHORS	Dubchak, I., Brudno, M., Loots, G.G., Pachter, L., Mayor, C., Rubin, E.M. and Frazer, K.A.				
TITLE	Active conservation of noncoding sequences revealed by three-Way species comparisons				
JOURNAL	Genome Res. 10 (9), 1304-1306 (2000)				
MEDLINE	20442524				
PUBMED	10984448				
REFERENCE	2 (bases 1 to 213343)				
AUTHORS	Blankespoor, C.M., Dean, W.B. and Lewis, K.D.				
TITLE	Direct Submission				
JOURNAL	Submitted (10-JUN-2000) Genome Sciences Department, Lawrence Berkeley National Laboratory, 1 Cyclotron Road, Berkeley, CA 94720 USA				
COMMENT	* NOTE: This is a 'working draft' sequence. It currently consists of 25 contigs. Gaps between the contigs were represented as runs of N. The order of the pieces				





















QY 1148 tgtggccaggccggggtgtgggggggaggggtgtgtgactgaatgtgctctttcactg 1207  
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Db 3378 TGTGGACTGAGGGGG-----GTCACTGAAGAAACTGTTTCATTG 3417

QY 1208 actttgtcaaaactggaagccagaaaataaagatggtgacaagaga 1251  
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Db 3418 ACTTTGTCAAGCTGAAAGCTA-AAATAAAAATGATGACAAGAGA 3460

RESULT 11  
I34549  
LOCUS I34549 1212 bp DNA PAT 06-FEB-1997  
DEFINITION Sequence 3 from patent US 5596072.  
ACCESSION I34549  
VERSION I34549.1 GI:1825340  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1212)  
AUTHORS Culpepper,J., McKenzie,A., Dang,W. and Zurawski,G.  
TITLE Method of refolding human IL-13  
JOURNAL Patent: US 5596072-A 3 21-JAN-1997;  
FEATURES Location/Qualifiers  
source 1. .1212  
/organism="unknown"  
BASE COUNT 282 a 338 c 307 g 285 t  
ORIGIN

Query Match 17.1%; Score 216.4; DB 10; Length 1212;  
Best Local Similarity 57.2%; Pred. No. 6.6e-47;  
Matches 719; Conservative 0; Mismatches 411; Indels 126; Gaps 13;

QY 35 tctgcattggtctgggtccatggcgtctgtgtgactgtgtgactgtgtcactgtcctcactg 94  
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Db 48 TCTCTCACTGGCTCTGGGCTTTCATGGCGCTCTGGGTGACTGCAGTCCGCTCTTGCTTG 107

QY 95 cctcgtgtgacctgacctcccg-----agccctgtgactccctcccaaccct 142  
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QY 143 caaggagctcattgaggagctgtcaacatcaccagaatcaggcatccctctgcaacgg 202  
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QY 203 cagcatggtgtgagcgtcaacctgaaccggtgactgactgacgtctagaaatctct 262  
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Db 228 CAGCATGGTATGGAGTGTGGACCTGGCCGCTGGCGGTTCTGTGTAGCCCTGGATTCCCT 287

QY 263 gataaatgtctccgactgcagcgccatccaaaggacccagaggatgctgaaagcactgtg 322  
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Db 288 GACCAACATCTCCAATTGCAATGCCATCTACAGGACCCAGAGGATATTGCATGGCCTCTG 347

QY 323 ctctcaaaagcccgcgaggatttccagtgaaacgcagccagacacacaaattgaagt 382  
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QY 383 gatccagttggtgaaaaaacctgctcacctatgtaaggggagtttatcgccatggaattt 442  
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QY 443 cagatgaagcatgaaaaacttagcatccttatctgtagaccagacctgaccacttaagtt 502  
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QY 503 ccagattcatttttcttccgacgtcacaaatttcttagggaggtggggggggagaa 562  
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QY 563 ccatttccctcagctgggacctcagcctgacccgcctccatggagctgagccagcc 622  
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Db 551 GGGTTGAGGAGGAGGAGATGCCTCAGC-----TTTGGCCTCAGCCTGCA 596

QY 623 acccctgccttggtgcattggggcccgccagccgggtggccctcctcgtctgcacttcaaa 682  
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QY 683 cgctgagggaaagcactgcatcccatgactgtccctcctcagagcaaaagtgcagcatta 742  
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Db 649 -----CACCCCGCGCGCCCATCCCATCCCTACAGAAAACCTGCAGCAAGA 693

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QY 799 catgttcttcttagccttatttattattgtgtgttatttataaacaagtgtcttgtttgt 858  
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QY 859 gctggggacagggagtggtggagctggagctggggcccgagtgactcgggttttaga----- 910  
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Db 813 ATCCCGGTGGGACATGGTTGCTGCCTATGCCCTGGGGCTCCAGCATTTGAAGCAGTGG 872

QY 911 -----gagtcctcctgggaataagcactgtgtgtataaaattctgtacctcactgggacctg 965  
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Db 873 GCTCTGGGGTCCCTGGCAATATTACTGTATACATAACTCTGCTACCTCACTGTAGCCTCC 932

QY 966 ggg-----ccgacacaggggacagggagaaaggtcagagatgctccttctgtctgccac 1019  
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QY 1020 tcagcagctggccctcagccaaagcagtaatttattgttttctctgtatttaaagttaag 1079  
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QY 1080 aaataaaatatgttatcaagaggttaataatatatagaaagtagcctaaaggctgcat 1139  
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QY 1140 ttggtgtgtgtgcccagggcggtgggtgggtgggtgggtgggtgtgtcactgaaatgtgtc 1199  
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QY 1200 tttcactgactttgtcaaaactggaagccagaaaataaagatggtgacaagagaaaaa 1255  
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Db 1160 TT---CATTGACTGTCAAACTAGAAAACCGAAATAAAGATGGTGACAGATAAAAAA 1212

RESULT 12

MUSSTCPE  
LOCUS Mus musculus T cell secreted protein (P600) mRNA, complete cds.  
DEFINITION M23504  
ACCESSION M23504  
VERSION M23504.1 GI:533246  
KEYWORDS inflammatory agent; secreted T cell protein.  
SOURCE Mus musculus cDNA to mRNA.  
ORGANISM Mus musculus  
REFERENCE 1 (bases 1 to 1207)  
AUTHORS Brown,K.D., Zurawski,S.M., Mosmann,T.R. and Zurawski,G.R.  
TITLE A family of small inducible proteins secreted by leukocytes are members of a new superfamily that includes leukocyte and fibroblast-derived inflammatory agents, growth factors, and indicators of various activation processes  
JOURNAL J. Immunol. 142, 679-687 (1989)  
MEDLINE 89093958  
COMMENT On Sep 9, 1994 this sequence version replaced gi:340930.  
FEATURES Location/Qualifiers  
source 1. .1207  
/organism="Mus musculus"  
/db\_xref="taxon:10090"  
/cell\_type="T helper cell"  
mRNA 1. .1207

CDS	/note="P600" 70..465 /codon_start=1 /product="T cell secreted protein" /protein_id="AAA40149.1" /db_xref="GI:533247" /translation="MALWVTAVLALACLGGLAAGPVPFRSVSLPLTLKELIEELSNI QDQPLKNGSMVWSVDLAAGFCVALDSLTNISNCNAIYRTQRIHLGLCNRKAPTIVS SLPDTKIEVAHFITKLLSYTKQLFRHGP" 1189...1194 /note="P600" 1207 /note="P600"									
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polyA_site										
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Matches 711; Conservative	0; Mismatches 410; Indels 127; Gaps 13;									
QY	35	tctgcattgctctgggtcccatggcgctctggtgactgtggtcattgctctcacctg	94							
Db	48	TCTCTCACTGGCTCTGGGCTTCATGGCGCTCTGGGFACTGCAGTCTGGCTCTGCTTG	107							
QY	95	cctcgggtggccttgccctcccg-----agccctgtgactccctcccaaccct	142							
Db	108	CCTTGGTGGTCTCGCGCCCCCAGGGCGGTGCCAAGATCTGTCTCTCCCTCTGACCTT	167							
QY	143	caaggagctcattgaggagctggtcaacatcacccagaatcaggcatccctctgcaacgg	202							
Db	168	TAAGGAGCTTATTGAGGAGCTGAGCAACATCACACAAGACCAGACTCCCCCTGTGCAACGG	227							
QY	203	cagcatggtgtggagcgtcaaacctgaccgcggcgcgatgtactgcgcagctctagaatctct	262							
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QY	263	gatcaatgtctcgcactgcagcgccatccaaaggaccagaggatgctgaaagcactgtg	322							
Db	288	GACCAACATCTCCAATTGCAATGCCATCTACAGACCAGAGGATATTGCATGGCCTCTG	347							
QY	323	ctctcaaaagccgcggcagggatttccagtgaacgcgagccgagacacccaaaattgaagt	382							
Db	348	TAACCGCAAGGCCCCCACTACGGTCTCCA-----GCCTCCCCGATACCAAATCGAAGT	401							
QY	383	gatccagtttgtaaaaaacctgctcacctatgtaaggggagtttatcgccatggaaaattt	442							
Db	402	AGCCCACTTTATAACAAACTGCTCAGCTACACAAAGCAACTGTTTCGCCACGGCCCTT	461							
QY	443	cagatgaagcatgaaaacttagcatccttatctgtagaccacagacctgaccacttaagt	502							
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QY	623	acccctgccttggtgcatggggcccagccgggtggccctcctcctcgtctgcacttcaatcaa	682							
Db	597	CTGCCTGCCTAGTCTCAGGGTCTCAGCCTTGGCAACACCCCAACCCCAACCCCAACCC	654							
QY	683	cgctgagggaaagcactgcatacccatgactgtcccctcctcagagcaaaagtgcagcatta	742							
Db	655	-----CGCCGCCCCCATCCCATCCCTACAGAAAACTGCAGCAAGA	693							
QY	743	c-----agtggaggcagatatgtgtgggaggggtcttctgtgtacctgggagtggcacaga	798							
Db	694	CCGTGAGTCCAGCCTGTGGCCTGGTCCACACAGGGGCAACTGAGGCAGGCAGCAGCTTGAG	753							

QY	799	catgtttctcttagcccttatttattattgtgtgtatttataaacaagtgctcttgtt	858
Db	754	CACATTTCTTCTTGATCTTATTATTATGGT-TGTGTGTTATTAAATGAGTCTGTCAGT	812
QY	859	gctggggacacagggagtgcttgagcgtggggggcccgactgactcgggtttaga-----	910
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QY	911	-----gagtcctctgggaataagcactgtgtgtataaaattctgctacctcactgggatacctg	965
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QY	966	gggcgcacacaggggacaggagaaag-----ggtcagagatgctgctctgtctgtgcca	1018
Db	933	AGGTCTACCCAGGCAGGGAGATGGGAGGGAGGCCAGAGCAACACTCCTGTCTGCCAC	992
QY	1019	ctcagcagctggccctcagccaagcagtaatttattgttttctctgtattttaagttaa	1078
Db	993	GGCAGCAACCCAGCCCTCAGCCATGAATAACTTATTGTT-----TTGTTCTTATATTAA	1047
QY	1079	gaataaaaatatgttatcaaaagagttaataataatataagaagtagcctaaaaaggctgca	1138
Db	1048	AGTATTAATAGCTTAGCAAGAGTTAATAATATATATGAAGAATGGCCTGTACACTCAA	1107
QY	1139	tttgggtgtgtgcccaggccggggggtggggggggtgtgtgtcactgaatgtgct	1198
Db	1108	GGTGATGTGTAGTGAATG-----GGGGAGGGTGGTGGTTTGTCACTGAACAACT	1159
QY	1199	ctttcactgactttgtcaaaactggaagccagaaaaataaagatggtgaca	1246
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RESULT 13			
AF072807			
LOCUS	AF072807	343 bp	mRNA
DEFINITION	Bos taurus interleukin-13 precursor (IL-13) mRNA, partial cds.		
ACCESSION	AF072807		
VERSION	AF072807.1 GI:4558813		
KEYWORDS	Bos taurus		
SOURCE	Bos taurus		
ORGANISM	Bos taurus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.		
AUTHORS	1 (bases 1 to 343)		
TITLE	Trigona,W.L., Brown,W.C. and Estes,D.M.		
JOURNAL	Functional implications for signaling via the IL4R/IL13R complex on bovine cells		
MEDLINE	Vet. Immunol. Immunopathol. 72 (1-2), 73-79 (1999)		
PUBMED	20080132		
REFERENCE	10614495		
AUTHORS	2 (bases 1 to 343)		
TITLE	Trigona,W.T., Hirano,A. and Estes,D.M.		
JOURNAL	Direct Submission		
FEATURES	Submitted (16-JUN-1998) Veterinary Pathobiology, University of Missouri-Columbia, W213 Veterinary Medicine Building, Columbia, MO 65211, USA		
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CDS	/organism="Bos taurus"		
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BASE COUNT	78 a	101 c	85 g	79 t					
ORIGIN									
Query Match	16.1%; Score 203.8; DB 7; Length 343;								
Best Local Similarity	78.7%; Pred. No. 1.3e-43;								
Matches 270; Conservative	0; Mismatches 67; Indels 6; Gaps 2;								
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QY	117	agccctgtgactccctcccaaccctcaaggagctcattgaggagctggtcaacatcacc	176						
Db	61	AGCCCTGTGCCTTCTGTCTACAGCCCTCAAGGAGCTCATTTGAAGAGCTGGTTAATATCACC	120						
QY	177	cagaatc---aggcatccctctgcaacggcagcatggtgtggagcgtcaacctgaccgcc	233						
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QY	234	ggcatgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgcattccaa	293						
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QY	294	aggaccagaggatgctgaaagcactgtgtctctcaaaaagcccgccgc---agggatttcc	350						
Db	241	AGGACCAAGAGGATGCTGAATGCACTCTGTCTCCTCACAAAGCCCTCAGCTAAGCAGGTTCC	300						
QY	351	agtgaacgcagccgcgagacaccaaattgaagtgtatccagttgg	393						
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RESULT 14									
A29950									
LOCUS	A29950	384 bp	DNA	PAT	23-JUN-1995				
DEFINITION	Nucleic acid fragment B.								
ACCESSION	A29950								
VERSION	A29950.1 GI:1249030								
KEYWORDS	synthetic construct.								
SOURCE	synthetic construct.								
ORGANISM	synthetic construct.								
REFERENCE	1 (bases 1 to 384)								
AUTHORS	Caput,D., Ferrara,P., Guillemot,J.C., Kaghad,M., Labit-le								
TITLE	Bouteiller,C., Leplatols,P., Magazin,M. and Minty,A.								
JOURNAL	Protein having cytokin type activity, recombinant DNA coding for								
	this protein, transformed cells and microorganisms								
	Patent: EP 0506574-A 23 30-SEP-1992;								
FEATURES	ELF SANOFI								
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ORIGIN									
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Matches 268; Conservative	0; Mismatches 81; Indels 6; Gaps 2;								
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QY	171	atcaccagaaatc---aggcatccctctgcaacggcagcatggtgtggagcgtcaacctg	227						
Db	76	ATCACCCAGAACCCAGAGGCTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAACCTG	135						
QY	228	accgccggcatgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgc	287						



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OM nucleic - nucleic search, using sw model

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(without alignments)  
1569.464 Million cell updates/sec

Title: US-09-451-527-99  
Perfect score: 1269  
Sequence: 1 ccagcctacgacctgcctgc.....gaaaaaaaaaaaaaaa 1269

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 678276 seqs, 291890651 residues

Total number of hits satisfying chosen parameters: 1356552

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_0401:\*  
1: /cgnl\_8/gcgdata/geneseq/geneseq/NA1980.DAT:\*  
2: /cgnl\_8/gcgdata/geneseq/geneseq/NA1981.DAT:\*  
3: /cgnl\_8/gcgdata/geneseq/geneseq/NA1982.DAT:\*  
4: /cgnl\_8/gcgdata/geneseq/geneseq/NA1983.DAT:\*  
5: /cgnl\_8/gcgdata/geneseq/geneseq/NA1984.DAT:\*  
6: /cgnl\_8/gcgdata/geneseq/geneseq/NA1985.DAT:\*  
7: /cgnl\_8/gcgdata/geneseq/geneseq/NA1986.DAT:\*  
8: /cgnl\_8/gcgdata/geneseq/geneseq/NA1987.DAT:\*  
9: /cgnl\_8/gcgdata/geneseq/geneseq/NA1988.DAT:\*  
10: /cgnl\_8/gcgdata/geneseq/geneseq/NA1989.DAT:\*  
11: /cgnl\_8/gcgdata/geneseq/geneseq/NA1990.DAT:\*  
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14: /cgnl\_8/gcgdata/geneseq/geneseq/NA1993.DAT:\*  
15: /cgnl\_8/gcgdata/geneseq/geneseq/NA1994.DAT:\*  
16: /cgnl\_8/gcgdata/geneseq/geneseq/NA1995.DAT:\*  
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18: /cgnl\_8/gcgdata/geneseq/geneseq/NA1997.DAT:\*  
19: /cgnl\_8/gcgdata/geneseq/geneseq/NA1998.DAT:\*  
20: /cgnl\_8/gcgdata/geneseq/geneseq/NA1999.DAT:\*  
21: /cgnl\_8/gcgdata/geneseq/geneseq/NA2000.DAT:\*  
22: /cgnl\_8/gcgdata/geneseq/geneseq/NA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1269	100.0	1269	21	255561 Canine interleukin
2	1269	100.0	1269	21	255562 Canine interleukin
3	1251	98.6	1302	21	255555 Canine interleukin
4	1251	98.6	1302	21	255556 Canine interleukin
5	390	30.7	390	21	255563 Canine interleukin
6	390	30.7	390	21	255564 Canine interleukin
7	377	29.7	393	21	255557 Canine interleukin
8	377	29.7	393	21	255558 Canine interleukin
9	362	28.5	1270	21	F21334 Human low adenosin
10	362	28.5	1270	21	A35212 Human adenosine re
11	362	28.5	1282	21	F21332 Human low adenosin

12	362	28.5	1282	21	A35210 Human adenosine re
13	362	28.5	1290	15	Q56692 Sequence encoding
14	362	28.5	6952	21	F21333 Human low adenosin
15	362	28.5	6952	21	A35211 Human adenosine re
16	362	28.5	14978	21	F21338 Human low adenosin
17	362	28.5	14978	21	A35216 Human adenosine re
18	358.8	28.3	1297	13	Q28947 Cytokine NC30. Q
19	330	26.0	330	21	255565 Canine mature inte
20	330	26.0	330	21	255566 Canine mature inte
21	317	25.0	333	21	255559 Canine mature inte
22	317	25.0	333	21	255560 Canine mature inte
23	278	21.9	278	21	255554 Canine interleukin
24	256	20.2	272	21	255553 Canine interleukin
25	216.4	17.1	1212	15	Q56693 Sequence encoding
26	187.4	14.8	336	13	Q28944 Gly41-Cytokine cod
27	185.8	14.6	336	13	Q28943 Asp41-Cytokine cod
28	166	13.1	5670	21	F21331 Human low adenosin
29	166	13.1	5670	21	F21337 Human low adenosin
30	166	13.1	5670	21	A35209 Human adenosine re
31	166	13.1	5670	21	A35215 Human adenosine re
32	155	12.2	166	21	255552 Canine interleukin
33	60.4	4.8	255	19	X11363 Human biallelic po
34	60.4	4.8	255	19	X11365 Human biallelic po
35	60.4	4.8	255	19	X11367 Human biallelic po
36	60.4	4.8	255	19	X11369 Human biallelic po
37	60.4	4.8	255	19	X11371 Human biallelic po
38	59.6	4.7	102	13	Q28941 Cytokine signal se
39	58.4	4.6	251	19	X11362 Human biallelic po
40	58.4	4.6	251	19	X11364 Human biallelic po
41	58.4	4.6	251	19	X11366 Human biallelic po
42	58.4	4.6	251	19	X11368 Human biallelic po
43	58.4	4.6	251	19	X11370 Human biallelic po
44	44.6	3.5	60	13	Q28942 Cytokine signal se
45	40.8	3.2	2460	11	Q06086 Plasmid p2PC13 enc

ALIGNMENTS

RESULT 1  
Z55561  
ID Z55561 standard; cDNA; 1269 BP.  
XX  
AC Z55561;  
XX  
DT 14-MAR-2000 (first entry)  
XX  
DE Canine interleukin-13 (IL-13) clone 78 cDNA.  
XX  
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;  
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.  
XX  
OS Canis familiaris.  
XX  
FH Key Location/Qualifiers  
FT CDS 57..449  
FT /\*tag= a  
FT /product= "Canine IL-13 clone 78"  
XX  
PN WO9961618-A2.  
XX  
PD 02-DEC-1999.  
XX  
PF 28-MAY-1999; 99WO-US11942.  
XX  
PR 29-MAY-1998; 98US-0087306.  
XX  
PA (HESK-) HESKA CORP.  
XX  
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;  
XX  
DR WPI; 2000-072623/06.  
DR P-PSDB; Y58223.

XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
PT useful for treating or preventing e.g. tumors or autoimmune disease  
XX  
PS Claim 1i; Page 235-236; 264pp; English.  
XX  
CC Sequences 255552-255560 and 255561-255566 represent cDNA  
CC sequences encoding canine interleukin-13 (IL-13) clones 80  
CC and 78 respectively. The invention relates to canine  
CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or  
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline  
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage  
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these  
CC immunoregulatory proteins. The proteins, their associated  
CC nucleic acids, specific antibodies and inhibitors may be used as  
CC vaccines for therapeutic or prophylactic regulation of an immune  
CC response in animals (particularly cats, dogs, horses and humans).  
CC They may be used to treat autoimmune or infectious diseases including  
CC allergies, tumours, inflammation and graft rejection, and to increase  
CC the response from a co-administered antigen. The nucleotide sequences  
CC can also be used for the recombinant production of a protein, while  
CC nucleotide fragments are useful as probes, as amplification primers and  
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
CC The proteins may be used to raise antibodies and to screen for  
CC modulators of activity, while the antibodies may be used in detection,  
CC and in drug targetting.  
XX  
SQ Sequence 1269 BP; 302 A; 320 C; 340 G; 307 T; 0 other;

Query Match 100.0%; Score 1269; DB 21; Length 1269;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1269; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ccagcctagacactgcctgtctcttccctcgctcctcctgctgattggctcgggtccatgg 60  
Db 1 ccagcctagacactgcctgtctcttccctcgctcctcctgctgattggctcgggtccatgg 60  
QY 61 cgctctggtgactgtggtcattggtctcactgcctcgctggtgacctgctcccgagcc 120  
Db 61 cgctctggtgactgtggtcattggtctcactgcctcgctggtgacctgctcccgagcc 120  
QY 121 ctgtgactcctcccccaccctcaaggagctcattgaggagctggtcaacatcacccaga 180  
Db 121 ctgtgactcctcccccaccctcaaggagctcattgaggagctggtcaacatcacccaga 180  
QY 181 atcaggcatccctctgcaacggcagcatggtgtgagcgtcaacctgacctgacggcatgt 240  
Db 181 atcaggcatccctctgcaacggcagcatggtgtgagcgtcaacctgacctgacggcatgt 240  
QY 241 actgcgcagctctagaatctctgtatcaatgtctccgactgcagcgccatccaaaggaccc 300  
Db 241 actgcgcagctctagaatctctgtatcaatgtctccgactgcagcgccatccaaaggaccc 300  
QY 301 agaggatgctgaaagcactgtgctctcaaaaagcccgcgaggatttccagtgaacgca 360  
Db 301 agaggatgctgaaagcactgtgctctcaaaaagcccgcgaggatttccagtgaacgca 360  
QY 361 gccgagacacccaaaattgaagtgtatccagttggtgaaaaacctgctcacctatgtaagg 420  
Db 361 gccgagacacccaaaattgaagtgtatccagttggtgaaaaacctgctcacctatgtaagg 420  
QY 421 gagtttatcgccatggaaaatttcagatgaagcatgaaaacttagcatccttatctgtaga 480  
Db 421 gagtttatcgccatggaaaatttcagatgaagcatgaaaacttagcatccttatctgtaga 480  
QY 481 cccagacctgaccttaagttccagattcattttcttccgacgtcacaaatttctta 540  
Db 481 cccagacctgaccttaagttccagattcattttcttccgacgtcacaaatttctta 540  
QY 541 gggaggtgggggggggggagaaacatttctcctcagctgggacctcagctgcaccgcctgc 600  
Db 541 gggaggtgggggggggggggagaaacatttctcctcagctgggacctcagctgcaccgcctgc 600

QY 601 ctccatggagctgagccagccacccctgccttggtgcatggggccagccgggtgccc 660  
Db 601 ctccatggagctgagccagccacccctgccttggtgcatggggccagccgggtgccc 660  
QY 661 tcctcgtctgcacttcattcaacgctgagggaaagcactgcacccatgactgtccctc 720  
Db 661 tcctcgtctgcacttcattcaacgctgagggaaagcactgcacccatgactgtccctc 720  
QY 721 ctccagagcaaaagtcagcattacagtgaggagcagatatgttgaggagggtcttctgt 780  
Db 721 ctccagagcaaaagtcagcattacagtgaggagcagatatgttgaggagggtcttctgt 780  
QY 781 acctgggagtggcacagacatgtttcttcttagccttattattattgtgttatttaa 840  
Db 781 acctgggagtggcacagacatgtttcttcttagccttattattattgtgttatttaa 840  
QY 841 acaagtgtctttgttctgctgggacagggagtggtgagctggggccagtgact 900  
Db 841 acaagtgtctttgttctgctgggacagggagtggtgagctggggccagtgact 900  
QY 901 cgggttagagagtcctcctgggaataagcactgtgtgtaaaaattctgtacctcactggga 960  
Db 901 cgggttagagagtcctcctgggaataagcactgtgtgtaaaaattctgtacctcactggga 960  
QY 961 tcctggggccgacacaggggacagggagaaagggtcagagatgctgtcttctgtccact 1020  
Db 961 tcctggggccgacacaggggacagggagaaagggtcagagatgctgtcttctgtccact 1020  
QY 1021 cagcagctggccctcagccaaagcagtaatttattgttttcttctgtatttaaagttaaga 1080  
Db 1021 cagcagctggccctcagccaaagcagtaatttattgttttcttctgtatttaaagttaaga 1080  
QY 1081 aataaaatatgttatcaaaagagtttaataatatatagaagagtagcctaaaaggctgcatt 1140  
Db 1081 aataaaatatgttatcaaaagagtttaataatatatagaagagtagcctaaaaggctgcatt 1140  
QY 1141 tgggtgtgtggtgccaggccggcggtgggggaggggtgtgtgtcactgaatgtgctct 1200  
Db 1141 tgggtgtgtggtgccaggccggcggtgggggaggggtgtgtgtcactgaatgtgctct 1200  
QY 1201 ttcactgactttgtcaaaactggaagccagaaataaagatggtgacaagagaaaaaaa 1260  
Db 1201 ttcactgactttgtcaaaactggaagccagaaataaagatggtgacaagagaaaaaaa 1260  
QY 1261 aaaaaaaaa 1269  
Db 1261 aaaaaaaaa 1269

RESULT 2  
Z55562/C  
ID Z55562 standard; cDNA; 1269 BP.  
XX  
AC Z55562;  
XX  
DT 14-MAR-2000 (first entry)  
XX  
DE Canine interleukin-13 (IL-13) clone 78 cDNA complement.  
XX  
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;  
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.  
XX  
OS Canis familiaris.  
XX  
FH Key Location/Qualifiers  
FT CDS complement (821..1213)  
FT /\*tag= a  
FT /product= "Canine IL-13 clone 78"  
XX  
PN W09961618-A2.  
XX  
PD 02-DEC-1999.





XX OS Canis familiaris.  
XX FH Key Location/Qualifiers  
FT CDS 52..447  
FT /\*tag= a  
FT /product= "Canine IL-13 clone 80"

XX WO9961618-A2.  
PN  
XX 02-DEC-1999.  
XX 28-MAY-1999; 99WO-US11942.  
XX 29-MAY-1998; 98US-0087306.  
PR (HESK-) HESKA CORP.

XX PA  
XX PI Sim G, Yang S, Dreitz MJ, Wonderling RS;  
XX WPI; 2000-072623/06.  
DR P-PSDB; Y58221.

XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
PT useful for treating or preventing e.g. tumors or autoimmune disease  
XX  
PS Claim 11; Page 229-230; 264pp; English.

XX Sequences 255552-255560 and 255561-255566 represent cDNA  
CC sequences encoding canine interleukin-13 (IL-13) clones 80  
CC and 78 respectively. The invention relates to canine  
CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or  
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline  
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage  
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these  
CC immunoregulatory proteins. The proteins, their associated  
CC nucleic acids, specific antibodies and inhibitors may be used as  
CC vaccines for therapeutic or prophylactic regulation of an immune  
CC response in animals (particularly cats, dogs, horses and humans).  
CC They may be used to treat autoimmune or infectious diseases including  
CC allergies, tumours, inflammation and graft rejection, and to increase  
CC the response from a co-administered antigen. The nucleotide sequences  
CC can also be used for the recombinant production of a protein, while  
CC nucleotide fragments are useful as probes, as amplification primers and  
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
CC The proteins may be used to raise antibodies and to screen for  
CC modulators of activity, while the antibodies may be used in detection,  
CC and in drug targeting.

XX SQ Sequence 1302 BP; 337 A; 318 C; 340 G; 307 T; 0 other;

Query Match 98.6%; Score 1251; DB 21; Length 1302;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1264; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 6 ctacgacctgcctgctcttccctcgctcctcctgcattggctctgggtccatggcgctc 65  
Db 1 ctacgacctgcctgctcttccctcgctcctcctgcattggctctgggtccatggcgctc 60  
QY 66 tgggtgactgtggtcattgtctcactgcctcggtggccttgcctcccgagccctgtg 125  
Db 61 tgggtgactgtggtcattgtctcactgcctcggtggccttgcctcccgagccctgtg 120  
QY 126 actccctcccaaccctcaaggagctcattgagagctggtcaacatcacccagaatcag 185  
Db 121 actccctcccaaccctcaaggagctcattgagagctggtcaacatcacccagaatcag 180  
QY 186 gcatccctctgcaacggcagcatggtgtggagcgtcaacctgaccgcccgcattgtactgc 245  
Db 181 gcatccctctgcaacggcagcatggtgtggagcgtcaacctgaccgcccgcattgtactgc 240  
QY 246 gcagctctagaatctctgatcaatgtctccgactgcagcgccatccaaaaggaccagagg 305







CC vaccines for therapeutic or prophylactic regulation of an immune  
CC response in animals (particularly cats, dogs, horses and humans).  
CC They may be used to treat autoimmune or infectious diseases including  
CC allergies, tumours, inflammation and graft rejection, and to increase  
CC the response from a co-administered antigen. The nucleotide sequences  
CC can also be used for the recombinant production of a protein, while  
CC nucleotide fragments are useful as probes, as amplification primers and  
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
CC The proteins may be used to raise antibodies and to screen for  
CC modulators of activity, while the antibodies may be used in detection,  
CC and in drug targeting.

XX Sequence 390 BP; 82 A; 99 C; 117 G; 92 T; 0 other;

Query Match 30.7%; Score 390; DB 21; Length 390;  
Best Local Similarity 100.0%; Pred. No. 3.3e-97;  
Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 57 atggcgctctggtgactgtggtcattgtctcaccctgcctcgggtggtgccttgcctccccc 116  
|||||  
Db 390 ATGGCGCTCTGGTTGACTGTGGTCAATTGCTCTCACCTGCCCTCGGTGGCCCTTGGCTCCCG 331  
|||||  
QY 117 agccctgactccctcccaaccctcaaggagctcattgaggagctggtgtaacatcacc 176  
|||||  
Db 330 AGCCCTGTGACTCCCTCCCAACCCCTCAAGGAGCTCATTTGAGGAGCTGGTCAACATCACC 271  
|||||  
QY 177 cagaatcaggcatccctctgcaacggcagcatggtgtgagcgtcaacctgaccgcccgc 236  
|||||  
Db 270 CAGAATCAGGCATCCCTCTGCAACGGCAGCATGGTGTGGAGCGTCAACCTGACCGCCGGC 211  
|||||  
QY 237 atgtactgcgcagctctagaaatctctgatcaatgtctccgactgcagcgccatccaaaagg 296  
|||||  
Db 210 ATGTACTGCGCAGCTCTAGAAATCTCTGATCAATGTCTCCGACTGCAGCGCCATCCAAAGG 151  
|||||  
QY 297 acccagaggatgctgaaagcactgtgctctcaaaagcccgccgagggattccagtga 356  
|||||  
Db 150 ACCCAGAGGATGCTGAAAGCACTGTGCTCTCAAAAGCCCGCGCAGGGATTCCAGTGAA 91  
|||||  
QY 357 cgcagccgagacacccaaattgaagtgtatccagttggtgaaaaacctgctcacctatgta 416  
|||||  
Db 90 CGCAGCGGAGACACCAAAATTGAAGTGATCCAGTTGGTGAAAAACCTGCTCACCTATGTA 31  
|||||  
QY 417 aggggagtttatcgccatggaaaatttcaga 446  
|||||  
Db 30 AGGGGAGTTTATCGCCATGGAAATTTTCAGA 1  
|||||

RESULT 7  
Z55557

ID Z55557 standard; cDNA; 393 BP.

XX AC Z55557;

XX 14-MAR-2000 (first entry)

DE Canine interleukin-13 (IL-13) clone 80 cDNA coding region.

XX Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;  
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.

OS Canis familiaris.

XX WO9961618-A2.

XX 02-DEC-1999.

PF 28-MAY-1999; 99WO-US11942.

XX 29-MAY-1998; 98US-0087306.

XX (HESK-) HESKA CORP.

XX

PI

XX Sim G, Yang S, Dreitz MJ, Wonderling RS;

DR WPI; 2000-072623/06.

DR P-PSDB; Y58221.

XX

PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
XX useful for treating or preventing e.g. tumors or autoimmune disease.

PS Claim 11; Page 232-233; 264pp; English.

XX

CC Sequences Z55552-Z55560 and Z55561-Z55566 represent cDNA  
CC sequences encoding canine interleukin-13 (IL-13) clones 80  
CC and 78 respectively. The invention relates to canine

CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or  
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline  
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage  
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these

CC immunoregulatory proteins. The proteins, their associated  
CC nucleic acids, specific antibodies and inhibitors may be used as  
CC vaccines for therapeutic or prophylactic regulation of an immune

CC response in animals (particularly cats, dogs, horses and humans).  
CC They may be used to treat autoimmune or infectious diseases including  
CC allergies, tumours, inflammation and graft rejection, and to increase  
CC the response from a co-administered antigen. The nucleotide sequences  
CC can also be used for the recombinant production of a protein, while

CC nucleotide fragments are useful as probes, as amplification primers and  
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
CC The proteins may be used to raise antibodies and to screen for  
CC modulators of activity, while the antibodies may be used in detection,  
CC and in drug targeting.

XX

SQ Sequence 393 BP; 93 A; 118 C; 100 G; 82 T; 0 other;

Query Match 29.7%; Score 377; DB 21; Length 393;  
Best Local Similarity 99.2%; Pred. No. 1.2e-93;  
Matches 390; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 57 atggcgctctggtgactgtggtcattgtctcaccctgcctcgggtggtgccttgcctccccc 116  
|||||  
Db 1 atggcgctctggtgactgtggtcattgtctcaccctgcctcgggtggtgccttgcctccccc 60  
|||||

QY 117 agccctgactccctcccaaccctcaaggagctcattgaggagctggtgtaacatcacc 176  
|||||  
Db 61 agccctgactccctcccaaccctcaaggagctcattgaggagctggtgtaacatcacc 120  
|||||

QY 177 cagaatcaggcatccctctgcaacggcagcatggtgtgagcgtcaacctgaccgcccgc 236  
|||||  
Db 121 cagaatcaggcatccctctgcaacggcagcatggtgtgagcgtcaacctgaccgcccgc 180  
|||||

QY 237 atgtactgcgcagctctagaaatctctgatcaatgtctccgactgcagcgccatccaaaagg 296  
|||||  
Db 181 atgtactgcgcagctctagaaatctctgatcaatgtctccgactgcagcgccatccaaaagg 240  
|||||

QY 297 acccagaggatgctgaaagcactgtgctctcaaaagcccgccgaggg--gatttccagt 353  
|||||  
Db 241 acccagaggatgctgaaagcactgtgctctcaaaagcccgccgagggcagatttccagt 300  
|||||

QY 354 gaacgcagccgagacacccaaattgaagtgtatccagttggtgaaaaacctgctcacctat 413  
|||||  
Db 301 gaacgcagccgagacacccaaattgaagtgtatccagttggtgaaaaacctgctcacctat 360  
|||||

QY 414 gtaaggggagtttatcgccatggaaaatttcaga 446  
|||||

Db 361 gtaaggggagtttatcgccatggaaaatttcaga 393  
|||||

RESULT 8

Z55558/c

ID Z55558 standard; cDNA; 393 BP.

XX

AC Z55558;

XX







nucleic acids involved in bronchoconstriction, allergies, and/or inflammation. The ON can have antiinflammatory, antiallergic, antiasthmatic, cytostatic and analgesic activities. The compositions are useful for the treatment of diseases associated with inflammation, impaired airways, including lung disease and diseases whose secondary effects afflict the lungs of a subject. They can be used for treating e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), and cancers such as leukaemias, lymphomas, carcinomas, and cancers which may metastasise to the lungs, including breast and prostate cancer. The reduction of the adenosine content of the ONs reduces side effects. The A-containing ONs break down with the release of deoxyadenosine which activates adenosine receptors causing bronchoconstriction and inflammation. A32313 to A35312 represent the nucleotide sequences given in the sequence listing from the present invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185 sequences are also called SEQ ID NO:1 to 185, but the sequences differ from the previously named sequences. SEQ ID NO:11 to 1680 (A32323 to A33992) are specifically claimed ONs from the present invention. N.B. Sequences given in the disclosure of the present invention do not match up with their corresponding SEQ ID NO: sequences given in the sequence listing.

Sequence 1270 BP; 288 A; 335 C; 336 G; 311 T; 0 other;

Query Match	28.5%;	Score 362;	DB 21;	Length 1270;
Best Local Similarity	66.0%;	Pred. NO. 3e-89;		
Matches 777;	Conservative	0;	Mismatches 290;	Indels 111; Gaps 13;

QY	26	cctcgcctcctcctgcattggctgtctgggctccatggcgctctgttgactgtggtcattgc	85
Db	14	cctcaatcctctcctgttggcactggcctcatggcgctttgttgaccacggtcattgc	73
QY	86	tctcacctgcctcgtggtgccttggctccccgagccctgtgactccctcccccaaccctcaa	145
Db	74	tctcacttgcccttgcggtcttgccctccccagggccctgtgcctccctctacagccctcag	133
QY	146	ggagctcattgaggagctggtcaacatcacccagaaac---aggcatccctctgcaacgg	202
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QY	203	cagcatggtgtggagcgtcaacctgaccgcccgcctgtactgcgcagctctagaaatctct	262
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QY	263	gatcaatgtctccgactgcagcgccatccaaaggacccagaggtatgctgaaagcactgtg	322
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Db	374	ggtggcccgatttgttaaaggacctgctcttacctttaaaagaaactttttcgcgagggacg	433
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QY	499	agttccagattcatttttcttccgacgtcacaaaattcttagggaggtggggggg-----	553
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QY	554	---gggggagaaccatttctcagctgggacctcagcctgcacggcctgcctccatggag	610
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KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;  
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;  
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;  
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;  
KW cancer; ss.  
XX  
OS Homo sapiens.  
XX WO200062736-A2.  
PN  
XX 26-OCT-2000.  
PD  
XX  
PF 24-MAR-2000; 2000WO-US08020.  
XX  
XX  
PR 06-APR-1999; 99US-0127958.  
XX  
PA (UYEC-) UNIV EAST CAROLINA.  
PA (NYCE/) NYCE J W.  
XX  
PI Nyce JW;  
XX  
XX WPI; 2000-679539/66.  
DR  
XX  
XX  
PT Low adenosine (A) content antisense oligonucleotides which do not  
PT trigger adenosine receptors during metabolism, useful e.g. for treating  
PT cancers and respiratory obstructions -  
XX  
PS Disclosure; Page 1334-1335; 1592pp; English.  
XX  
CC The present invention describes low adenosine (A) content antisense  
CC oligonucleotides and compositions (I) comprising them. In the antisense  
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.  
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,  
CC immunosuppressive, antialsthmatic, hypotensive and cytostatic activities.  
CC The antisense oligonucleotides and (I) can be used to down-regulate the  
CC expression and or activity of target polypeptides associated with  
CC lung/respiratory disorders and malignancies, such as stimulating and  
CC activating peptide factors and transmitters, transcription factors,  
CC immunoglobulins and antibodies, antibody receptors, cytokines and  
CC chemokines, endogenously produced specific and non-specific enzymes,  
CC binding proteins, adhesion molecules and their receptors, cytokine and  
CC chemokine receptors, adenosine receptors, bradykinin receptors, central  
CC nervous system (CNS) and peripheral nervous and non-nervous system  
CC receptors, CNS and peripheral nervous and non-nervous system peptide  
CC transmitters, defensins, growth factors, vasoactive peptides and  
CC receptors, binding proteins and malignancy associated proteins. The  
CC antisense oligonucleotides may be used in this way to treat disorders  
CC including respiratory obstruction (especially pulmonary obstruction  
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)  
CC and/or surfactant hypoproduction which are associated with a disease or  
CC condition selected from pulmonary vasoconstriction, inflammation,  
CC allergies, asthma, impeded respiration, respiratory distress syndrome  
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary  
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),  
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,  
CC and/or cancer. F18434 to F21543 represent human polynucleotide fragments  
CC and antisense oligonucleotides used in the exemplification of the  
CC present invention.  
XX  
SQ Sequence 6952 BP; 1536 A; 2017 C; 1919 G; 1480 T; 0 other;

Query Match 28.5%; Score 362; DB 21; Length 6952;  
Best Local Similarity 66.0%; Pred. No. 7.5e-89;  
Matches 777; Conservative 0; Mismatches 290; Indels 111; Gaps 13;  
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Db 5756 tctcacttgcccttgccggcttgcctcccgagccctgtgctcctcctctacagccctcag 5815







Db 6707 cctggggcctcgagcctcatccgaggcagggtcaggagaggggcagaaacagccgctcct 6766  
QY 1011 gtctgccactcagcagctggccctcagccaagcagtaatttatgtttttccttgatatt 1070  
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QY 1071 aaagttaagaaaaataatatgttatcaaaagagttaata 1108  
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Db 6827 aa-----atattaaatatgttagcaaaagagttaata 6857

Search completed: May 13, 2001, 14:30:23  
Job time: 18338 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 13, 2001, 14:21:21 ; Search time 226.02 Seconds  
(without alignments)  
980.315 Million cell updates/sec

Title: US-09-451-527-99  
Perfect score: 1269  
Sequence: 1 ccagcctacgacctgcctgc.....gaaaaaaaaaaaaaaaaaa 1269

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 302621 seqs, 87301344 residues

Total number of hits satisfying chosen parameters: 605242

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_NA:\*  
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2: /cgnl\_7/ptodata/1/ina/5B\_COMB.seq:\*  
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6: /cgnl\_7/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	362	28.5	1290	1	US-08-012-543-1
2	362	28.5	1290	5	PCT-US93-07645A-1
3	362	28.5	1290	5	PCT-US93-07645-1
4	360.4	28.4	1297	1	US-08-371-121-15
5	216.4	17.1	1212	1	US-08-012-543-3
6	216.4	17.1	1212	5	PCT-US93-07645A-3
7	216.4	17.1	1212	5	PCT-US93-07645-3
8	193.4	15.2	384	1	US-08-371-121-17
9	191.6	15.1	425	1	US-08-594-469-4
10	191.6	15.1	425	2	US-08-906-957-4
11	191.6	15.1	4410	1	US-08-594-469-1
12	191.6	15.1	4410	2	US-08-906-957-1
13	187.4	14.8	336	1	US-08-371-121-24
14	185.8	14.6	336	1	US-08-371-121-2
15	185.4	14.6	447	1	US-08-371-121-26
16	59.6	4.7	102	1	US-08-371-121-10
17	54.6	4.3	96	1	US-08-371-121-9
18	46.2	3.6	7218	1	US-08-232-463-14
19	44.6	3.5	60	1	US-08-371-121-12
20	39.6	3.1	54	1	US-08-371-121-11
21	39.4	3.1	7218	1	US-08-232-463-14
22	38.8	3.1	1576	2	US-09-197-378-1
23	36	2.8	740	2	US-08-713-000-8
24	36	2.8	740	2	US-08-975-316-8
25	36	2.8	740	4	US-09-211-710-8
26	36	2.8	741	2	US-08-975-316-58
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29	35.8	2.8	2249	3	US-08-814-052-19	Sequence 19, Appl
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32	35.8	2.8	3187	5	PCT-US95-06815-1	Sequence 1, Appli
33	35.8	2.8	3192	1	US-08-706-037-26	Sequence 26, Appl
34	35.8	2.8	3192	1	US-08-940-661A-1	Sequence 1, Appli
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37	34.8	2.7	1858	2	US-08-909-965C-11	Sequence 11, Appl
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39	34.8	2.7	3036	1	US-08-306-691B-52	Sequence 52, Appl
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41	34.8	2.7	3036	5	PCT-US92-02320A-1	Sequence 1, Appli
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44	34.4	2.7	1521	1	US-08-496-855A-3	Sequence 3, Appli
45	34.4	2.7	1521	5	PCT-US91-02311-9	Sequence 9, Appli

ALIGNMENTS

RESULT 1  
US-08-012-543-1  
; Sequence 1, Application US/08012543  
; Patent No. 5596072  
; GENERAL INFORMATION:  
; APPLICANT: Culpepper, Janice  
; APPLICANT: McKenzie, Andrew  
; APPLICANT: Dang, Warren  
; APPLICANT: de Waal Malefyt, Rene  
; APPLICANT: Heath, Andrew  
; APPLICANT: Aversa, Gregorio  
; APPLICANT: Briere, Francine  
; APPLICANT: Banchereau, Jacques  
; APPLICANT: de Vries, Jan  
; APPLICANT: Zurawski, Gerard  
; TITLE OF INVENTION: Human Interleukin-13  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/012,543  
; FILING DATE: 01-FEB-1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/933,416  
; FILING DATE: 21-AUG-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0302K1  
; TELEPHONE: 415-852-9196  
; TELEFAX: 415-496-1200  
; INFORMATION FOR SEQ ID NO: 1:  
; .SEQUENCE CHARACTERISTICS:  
; LENGTH: 1290 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA

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; NAME/KEY: CDS
; LOCATION: 45..443
US-08-012-543-1

Query Match      28.5%; Score 362; DB 1; Length 1290;
Best Local Similarity 66.0%; Pred. No. 2.1e-98;
Matches 777; Conservative 0; Mismatches 290; Indels 111; Gaps 13;

Qy 26 cctcgctcctcctgcatggctctgggctccatggcgctctggttgactgtggtcattgc 85
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Qy 263 gatcaatgtctccgactgcagcgcctccatccaaaggaccagaggatgctgaaagcactgtg 322
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Qy 323 ctctcaaaaagccccgggcagg---gatttccagtgaacgcagccgagacacccaaaattga 379
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Qy 726 agcaaaagtgcagcattacagtggagg-----cagatatgtgtgggaggggg----- 771
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RESULT 2
PCT-US93-07645A-1
; Sequence 1, Application PC/TUS9307645A
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Human Interleukin-13
; NUMBER OF SEQUENCES: 6
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.5
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07645A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/012543
; FILING DATE: 01-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/010977
; FILING DATE: 29-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/933416
; FILING DATE: 21-AUG-1992
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1290 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
PCT-US93-07645A-1
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Query Match 28.5%; Score 362; DB 5; Length 1290;  
Best Local Similarity 66.0%; Pred. No. 2.1e-98;  
Matches 777; Conservative 0; Mismatches 290; Indels 111; Gaps 13;

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Qy 26 cctcgctcctcctgcatggctctgggctccatggcgctctggttgactgtggtcattgc 85
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Qy 263 gatcaatgtctccgactgcagcgcctccatccaaaggaccagaggatgctgaaagcactgtg 322
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Db 314 CCCGCACAAGGTCTCAGCTGGCGAGTTTCCAGCTTGCCAGATGCTCCGAGACACCAAAATCGA 373
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QY 440 ttccagatgaagcatgaaaaacttagcatccttatctgtagaccca-gacctgaccactta 498
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Db 785 CACTTCACACACAGGCAACTGAGGCACAGACAGCAGCTCAGGCACACTTCTTCTTGGTCTTA 844
QY 819 ttattattgtgtgtatttaaacaaagtgtctttgtttgtgctggggagcagggagtg--- 875
Db 845 TTATTATTGTGTGTTATTAAATGAGTGTGTTGTCAACCGTTGGGGATTGGGGAAGACT 904
QY 876 -----gcttgagctggtggggcccaagtgactcgggtttaga----- 910
Db 905 GTGGCTGTGGCACTTGGAGCCACAGGGTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGT 964
QY 911 -----gagtccttgggaataagcactgtgtgtataaattctgtcactcactgggat 961
Db 965 GGACCCCAAGGAGTCCCTGGTAATAGTACTGTGTACAGAAATCTGCTACCTCACTGGGGT 1024
QY 962 cctgggggccc-----gacacaggggacagggagagaaaggtcagagatgctgctctt 1010
Db 1025 CCTGGGGCCTCGGAGCCTCATCCGAGGCAGGGTTCAGGAGAGGGGCAGACAGCCGCTCCT 1084
QY 1011 gtctgccactcagcagctgcccctcagccaaagcagtaatttattgttttctccttgattt 1070
Db 1085 GTCTGCCAGCCAGCAGCCAGCTCTCAGCCCAACGAGTAATTTATTGTTTTCCTCGTATT 1144
QY 1071 aaagttaagaaataaaatatgttatcaaaagagttaata 1108
Db 1145 AA-----ATATTAAATATGTTAGCAAAAGAGTTAATA 1175
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RESULT 3

PCT-US93-07645-1

; Sequence 1, Application PC/TUS9307645

; GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION: Human Interleukin-13

; NUMBER OF SEQUENCES: 6

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Apple Macintosh

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; OPERATING SYSTEM: Macintosh 6.0.5
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07645
; FILING DATE: 19930818
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/012543
; FILING DATE: 01-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/010977
; FILING DATE: 29-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/933416
; FILING DATE: 21-AUG-1992
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1290 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; PCT-US93-07645-1
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Query Match 28.5%; Score 362; DB 5; Length 1290;

Best Local Similarity 66.0%; Pred. No. 2.1e-98;

Matches 777; Conservative 0; Mismatches 290; Indels 111; Gaps 13;

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QY 26 cctcgctcctcctgcattggctctgggtcccatggcgctctggtgactgtggtcattgc 85
Db 14 CCTCAATCCTCTCCTGTTGGCACTGGGCCCTCATGGCGCTTTTGTTCACCACGGTCAATTGC 73
QY 86 tctaacctgcctcggtggccttgctcctcccgagccctgtgactcctcccaaccctcaa 145
Db 74 TCTCACTTGCCTTGGCGGCTTTGCTCCCGAGGCCCTGTGCCCTCCTCTACAGCCCTCAG 133
QY 146 ggaqctcattgaggagctggtcaacatcacccagaaac---aggcatcctctgcaacgg 202
Db 134 GGAGCTCATTTGAGGAGCTGGTCAACATCACCCAGAACCCAGAGGCTCCGCTCTGCAATGG 193
QY 203 cagcatggtgtggagcgtcaacctgaccgcccggcatgtactggcagctctagaatctct 262
Db 194 CAGCATGGTATGGAGCATCAACTGACAGCTGGCATGTACTGTGCAGCCCTGGAATCCCT 253
QY 263 gatcaatgtctccgactgcagcgccatccaaaaggacccagagagatgctgaaagcactgtg 322
Db 254 GATCAACGTGTCAGGCTGCAGTGCCTATCGAGAAGACCCAGAGGATGCTGAGCGGATTCTG 313
QY 323 ctctcaaaagcccgcggcagg---gatttcagtgaaacgcagccgagacacccaaattga 379
Db 314 CCCGCACAAGGTCTCAGCTGGCGAGTTTCCAGCTTTCAGCTTGCCAGACACCAAAATCGA 373
QY 380 agtgatccagttggtgaaaaacctgctcacctatgtaaagggagtttatcgccatggaaa 439
Db 374 GGTGGCCCAAGTTGTAAAGGACCTGCTCTTACATTTAAAGAAACTTTTTCGCGAGGGACG 433
QY 440 ttccagatgaagcatgaaaaacttagcatccttatctgtagaccca-gacctgaccactta 498
Db 434 GTTCAACTGAAACTTCGAA---AGCATCATTTATTTGCAGAGACAGGACCTGACTATTGA 489
QY 499 agttccagattcatttttcttccagcgtcaacaaattcttagggaggtggggggg----- 553
Db 490 AGTGCAGATTCAATTTCTTCTGATGTCAAAAATGTCTTGGGTAGGCGGGAAGGAGGG 549
QY 554 ---gggggagaaccatttctcagctgggacccagcctgcacccgctgcctccatggag 610
Db 550 TTAGGGAGGGGTAAATTCCTTAGCTTAGACCTCAGCCTGTGCTGCCGCTCTTCAGCCT- 608
QY 611 ctgagccagccacccctgccttggtgcatggggcccccagcggggtggccctcctccgtc- 669
Db 609 ----AGCCGACCTCAGCCTTCCCCCTTGGCCAGGGCTCAGCCTGGTGGGCTCTCTGTCTCC 664
QY 670 ----tgcacttcatcaacgctgagggaaagcactgcatcccatgactgtccccctctcag 725
Db 665 AGGCCCCGTGAGCTCGGTGGACCCAGGGATGACATGTCCCTACACCCCTCCCTGCCCCCTAG 724
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Db 665 AGGGCCCTGAGCTCGGTGGACCCAGGGATGACATGTCCCTACACCCCTCCCTGCCCTAG 724  
Qy 726 agcaaaagtcagcattacagtgagg-----cagatatgtgtggagggg----- 771  
Db 725 AGCACACTGTAGCATACAGTGGTGCCCTGCGCCCTGCGCAGACATGTGGTGGACAGGACC 784  
Qy 772 -----tcttgctgtacacctgggagtgccacagacatgtttcttcttagcctta 818  
Db 785 CACTTCACACACAGCAACTGAGGCAGACAGCAGCTCAGGCACACTTCTTCTTGCTCTTA 844  
Qy 819 ttattattgtgtatttaaaagaagtgctctttgtttgtgctggtgggacagggagtg--- 875  
Db 845 TTTATTATTGTGTGTTATTAAATGAGTGTGTTTGTACCCGTTGGGGATTGGGGAAGACT 904  
Qy 876 -----gctggagctgggggcccagtgactcgggttaga----- 910  
Db 905 GTGGCTGTGGCACTTGGAGCCCAAGGTTTCAGAGACTCAGGGCCCCCAGCACTAAAGCAGT 964  
Qy 911 -----gagtcctgggaataagcactgtgtgtataaaattctgtacctcactgggat 961  
Db 965 GGACCCCAAGGAGTCCCTGGTAATAAGTACTGTGTACAGAAATTCTGTACTCACTGGGGT 1024  
Qy 962 cctggggcc-----gacacaggggacagggagaaaggtcagagatgctgctctt 1010  
Db 1025 CCTGGGGCCTCGGAGCCTCATCCGAGGCAGGGTCAGGAGAGGGGCAGAACAGCGCTCCT 1084  
Qy 1011 gtctgccactcagcagctggccctcagcccaagcagtaatttattgttttctctgtattt 1070  
Db 1085 GTCTGCCAGCCAGCAGCCAGCTCTCAGCCCAACGAGTAATTATTGTTTTCCTCGTATT 1144  
Qy 1071 aaagttaagaaataaaatatgtttatcaaaagagttaata 1108  
Db 1145 AA-----ATATTAAATATGTTAGCAAAGAGTTAATA 1175

RESULT 4  
US-08-371-121-15  
; Sequence 15, Application US/08371121  
; Patent No. 5652123  
; GENERAL INFORMATION:  
; APPLICANT: CAPUT, Daniel  
; APPLICANT: FERRARA, Pascual  
; APPLICANT: GUILLEMOT, Jean-Claude  
; APPLICANT: LEPLATOIS, Pascal  
; APPLICANT: MINTY, Adrian  
; APPLICANT: KAGHAD, Mourad  
; APPLICANT: LABIT-LE BOUTEILLER, Christine  
; APPLICANT: MAGAZIN, Marilyn  
; TITLE OF INVENTION: Protein having a cytokine type  
; TITLE OF INVENTION: activity, recombinant DNA coding for this protein,  
; TITLE OF INVENTION: activity, recombinant DNA coding for this protein,  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FOLEY & LARDNER  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington, D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/371,121  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/938,161  
; FILING DATE: 30-NOV-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/FR92/00280  
; FILING DATE: 27-MAR-1992

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 91 00137  
; FILING DATE: 08-JAN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 91 03904  
; FILING DATE: 29-MAR-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SAXE, Bernhard D.  
; REGISTRATION NUMBER: 28,665  
; REFERENCE/DOCKET NUMBER: 16781/383  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 672-5300  
; TELEFAX: (202) 672-5399  
; TELEX: 904136  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1297 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 15..452  
; FEATURE:  
; NAME/KEY: mat\_peptide  
; LOCATION: 117..452  
; US-08-371-121-15

Query Match 28.4%; Score 360.4; DB 1; Length 1297;  
Best Local Similarity 65.9%; Pred. No. 6.2e-98;  
Matches 776; Conservative 0; Mismatches 291; Indels 111; Gaps 13;  
Qy 26 cctcgctcctcctgcattggctctgggctccatggcgctctgtgtgactgtgtgctattgc 85  
Db 26 CCTCAATCCTCTCCTGTTGGCACTGGCCCTCATGGCGCTTTTGTGTACACACGGTCAATGC 85  
Qy 86 tctcacctgcctcggtggccttgccctccccagccctgtgactccctccccacccctcaa 145  
Db 86 TCTCACTTGCCTTGGCGGCTTGGCTCCCCAGGCCCTGTGCCCTCCCTCTACAGCCCTCAG 145  
Qy 146 gtagctcattgaggagctgtcaacatcacccacagaatc---aggcatccctctgcaacgg 202  
Db 146 GGAGCTCATTGAGGAGCTGGTCAACATCACCCAGAACCCAGAGGCTCCGCTCTGCAATGG 205  
Qy 203 cagcatggtgtggagcgtcaacctgaccgcccggcatgtactgagcagctctagaatctct 262  
Db 206 CAGCATGGTATGGAGCATCAACCTGACAGCTGACATGTACTGTGAGCCCTGGAATCCCT 265  
Qy 263 gatcaatgtctccgactgcagcgcacatccaaaggacccagagagatgctgaaagcactgtg 322  
Db 266 GATCAACGTTGTCAGGCTGCAGTSCCATCGAGAAGACCCAGAGGATGCTGAGCGATTCTG 325  
Qy 323 ctctcaaaagccccgcggcagg---gatttccagtgaaacgcagccgagacacccaaattga 379  
Db 326 CCCGCACAAGGTCTCAGCTGGGCAGTGTTCAGCTTGCATGTCCGAGACACCAAAATCGA 385  
Qy 380 agtgcattccagttggtgaaaaaacctgctcacctatgtaaggaggagtttatcgccatgaaa 439  
Db 386 GGTGCCCCAGTTTGTAAAGGACGTGCTCTTACATTTAAAGAAACTTTTTCGCGAGGACG 445  
Qy 440 ttccagatgaagcatgaaacttagcatccttatctgttagacca-gacctgaccactta 498  
Db 446 GTTCAACTGAAACTTCGAA---AGCATCATTATTGTCAGAGACAGGACCTGACTATTGA 501  
Qy 499 agttccagattcatttttcttccgacgtcacaaaatttcttagggagggtggggg--- 553  
Db 502 AGTTCAGATTTCATTTTCTTCTGTGATGTCAAAAATGTCTTGGTAGGCGGGAAGGAGGG 561  
Qy 554 ---gggggagaaccatttctcagctgggacctcagcctgacccgcctgcctccatggag 610  
Db 562 TTAGGGAGGGGTAAATTCCTTAGCTTAGACCTCAGCCTGCTGCTGCCCGTCTTTCAGCCT- 620



QY	683	cgctgagggaaagcactgcatacccacatgactgtccccctcctcagagcaaaagtcagcatta	742
DB	649	-----CACCCCGCGCCCATCCCATCCCTACAGAAAACTGCAGCAAGA	693
QY	743	c---agtgaggcagatatgtgtgggaggggtcttgctgtacctggggagtggcacaga	798
DB	694	CCGTGAGTCCAGCCTGTGGCTGGTCCACACACAGGGCAACTGAGGCAGGCAGCAGCTTGAG	753
QY	799	catgtttctcttagccttatttattattgtgtgttattttaaacaaagtgtctttgttgt	858
DB	754	CACATTTCTTCTTGATCCTTATTTATTTATGGT-TGTGTGTTATTAAATGAGTCTGTCAGT	812
QY	859	gctggggacagggagtggcctggagctggggcccagtgactcgggtttaga-----	910
DB	813	ATCCCGGTGGGACATGGTTGCTGCCCTATGCCCTGGGGCTCCAGCATTGAAGCAGTGG	872
QY	911	----gagtcctcgggaataagcactgtgtgtataaaattctgtacctcactcgggatcctg	965
DB	873	GCTCTGGGGTCCCTGGCAATATTACTGTATACATAACTCTGCTACCTCACTGTAGCCTCC	932
QY	966	ggg-----ccgacacagggggacaggagagaaaggtcagagatgctgtcttctgtctgccac	1019
DB	933	AGGTCTCACCCCGCAGGAGATGGGAGGGGAGGCCAGAGCAACACTCCTGTCTGCCACG	992
QY	1020	tcagcagctgcccctcagcccaagcagtaattattgttttcccttgatatttaaagttaag	1079
DB	993	GCAGCAACCAGCCCTCAGCCATGAAATAACTTATTGTT-----TTGTTCTTATATTAAA	1047
QY	1080	aaataaaatatgttatcaagaggttaataatatataagaagtagcctaaaaagctgcat	1139
DB	1048	GTATTAAATAGCTTAGCAAAAGAGTTAATAATATATGGAAGAATGGCCTGTTACACTCAAG	1107
QY	1140	tttgtgtgtgtggcccgccgggcggtgggggggaggggtgttgtcactgaatgtgctc	1199
DB	1108	GTGATGTGTAGTGAATG-----GGGGGAGGGTGGTGGGTTTGTCACTGAACAAACTT	1159
QY	1200	tttcactgacttttgtcaaaactggaagccagaaaaataaagatggtgacaaagagaaaaa	1255
DB	1160	TTT--CATTGACTGTCAAACTAGAAAACCGGAAATAAAGATGGTGACAGATAAAAAA	1212

## RESULT 6

PCT-US93-07645A-3

: Sequence 3, Application PC/TUS9307645A

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: Human Interleukin-13

NUMBER OF SEQUENCES: 6

; NUMBER OF SEQUENCES: 0  
; COMPUTER READABLE FORM:

COMPUTER READABLE FORM.  
MEDIUM TYPE: Floppy disk

COMPUTER: Apple Macintosh

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/ COMPIER:  apple macintosh
: OPERATING SYSTEM:  Macintosh 6.0.5

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SOFTWARE: Microsoft Word 5.1a

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; CURRENT APPLICATION DATA:

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APPLICATION NUMBER: PCT/US93/07645A

FILING DATE:

PRIOR APPLICATION DATA:

APPLCATION NUMBER: US 08/012543

APPLICATION NUMBER: US 0  
FILING DATE: 01-FEB-1993

: PENDING DATE: VI EED  
: PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/010977

; AFFILIATION NUMBER: 03 0  
 ; FILING DATE: 29-JAN-1993

FILING DATE: 29-JAN-80  
PRIOR APPLICATION DATA:

APPLICANT NUMBER: IIS 07/9333416

APPLICATION NUMBER: US 0  
FILING DATE: 21-AUG-1992

FILED DATE: 21-AUG-1992  
INFORMATION FOR SEO ID NO: 3:

; INFORMATION FOR SEQ ID NO: 1  
; SEQUENCE CHARACTERISTICS:

SEQUENCE CHARACTERISTICS:  
LENGTH: 1212 base pairs

LENGTH: 1717 base  
TYPE: nucleic acid

TYPE: nucleic acid  
: STRANDEDNESS: double

STRANDEDNESS: DO  
 TOPOLOGY: linear

PCT-US93-07645A-3

Query Match	17.1%	Score 216.4;	DB 5;	Length 1212;
Best Local Similarity	57.2%	Pred. NO. 6.8e-55;		
Matches 719; Conservative	0;	Mismatches 411;	Indels 126;	Gaps 13;

Qy	35	tcttgcattggctctgggctccatggcgctctgttgactgtggtcaattgctctcacctg	94
Db	48	TCCTCACTGGCTCTGGGCTTTCATGGCGCTCTGGGTGACTGCAGTCTGGCTCTTGCTTG	107
Qy	95	ccctgggtggccttgccctcccg-----agccctgtgactccctcccaacccct	142
Db	108	CCTTGGTGGTCTCGCCGCCCCAGGGCGGTGCCAAGATCTGTGTCTCTCCCTCTGACCCCT	167
Qy	143	caaggagctcattgaggagctggtcaacatcaccagaaatcaggcatccctctgcaacgg	202
Db	168	TAAGGAGCTTATTGAGGAGCTGAGCAACATCACACAAGACCAGACTCCCCCTGTGCAACGG	227
Qy	203	cagcatggtgtggagcgtcaaacctgaccgcggcatgtactgcagactctagaatctct	262
Db	228	CAGCATGGTATGGAGTGTGGACCTGGCGCTGGCGGGTTCTGTGTAGCCCTGGATTCCCT	287
Qy	263	gatcaatgtctccgactgcagcgccatccaaaggacccagaggaatgctgaaagcactgtg	322
Db	288	GACCAACATCTCCAATTGCAATGCCATCTACAGGACCCAGAGGATATTGCATGGCCTCTG	347
Qy	323	ctctcaaaagccgcggcagggaatttccagtgaaacgcagcgcagacacacaaattgaagt	382
Db	348	TAACCGCAAGCCCCCCTACTACGGTCTCCA-----GCCTCCCGGATACCAAAATCGAAGT	401
Qy	383	gatcagttggtgaaaaacctgctcacctatgtaaggggagtatttatcgccatggaaaattt	442
Db	402	AGCCCACTTTATAACAAAACCTGCTCAGCTACACAAAGCAACTGTTTCGCCACGGCCCCCTT	461
Qy	443	cagatgaagcatgaaaacttagcatccttatctgtagaccacagacatgaccacttaagtt	502
Db	462	CTAATGAGGAGAGA-----CCATCCCTGGGCATCTCAGCT	496
Qy	503	ccagattcatttttcttccgacgtcacaaaatttcttagggaggtggggggggagaaa	562
Db	497	GTGGACTCATTTTCCTTCTCACATCAGACTTTGCT-----GGGAGAGGCAGGGAGGA	550
Qy	563	ccatttcctcagctgggacctcagcctgcaccgcctgcctccatggagctgagccccagcc	622
Db	551	GGGTGAGGAGGAAGGGAGATGCCCTCAGC-----TTTGGCCTCAGCCTGCA	596
Qy	623	acccctgccttgggtgcattggggccagccgggtggccctcctcgtctgcacttcatcaa	682
Db	597	CTGCCTGCCTAGTGCTCAGGGTCTCAGCCTGGCAACACCCCAACCCCAACCCCAACCC	648
Qy	683	cgtgagggaaagcactgcataccatgactgtccctcctcagagcaaaagtcagacatta	742
Db	649	-----CACCCCGCGCGCCCATCCCATCCCTACAGAAAACCTGCAGCAAGA	693
Qy	743	c-----agtgaggcagatatgtgtggagggggtcttctgtgtacctgggagtggcacaga	798
Db	694	CCGTGAGTCCAGCCTGTGGCCTGTGTCACACAGGGCAACTGAGGAGGCAGCAGCTTGAG	753
Qy	799	catgtttctcttagcccttattattattgtgttattttaacaagtgctttgtttgt	858
Db	754	CACATTCTCTTGATCTTATTATTATATGGT-TGTGTGTTATTATAATGAGTCTGTCTCAGT	812
Qy	859	gctggggacaggagtggtgtgagctggggggccagtgactcggggttttaga-----	910
Db	813	ATCCCGTGGGACATGGTTTGTCTGCCTATGCCCTGGGGGCTCCAGCATTTGAAGCAGTGG	872
Qy	911	-----gagtccttggaataagcactgtgtgtaaaaattctgtacctcactgggatoctg	965
Db	873	GCTCTGGGGTCCCTGGCAATATTACTGTATACATAACTCTGTCTACCTCACTGTAGCCTCC	932
Qy	966	ggg-----ccgacacaggggacaggagaaaaggtcagagatgctgctctgtctgcccac	1019
Db	933	AGGTCTCACCCAGGCAGGAGATGGGAGGGGGAGGCCAGAGCAACACTCCTGTCTGCCACG	992



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QY 1020 tcagcagctggccctcagccaagcagtaattattgttttttcccttgatttataaaagttaag 1079
    ||||| | ||||| ||||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 993 GCAGCAACCAGCCCTCAGCCATGAATAACTTATTGTT-----TTGTTCTTATATTAAA 1047

QY 1080 aaataaataatgttatcaaaagagtttaataatatagaagagtagccctaaaggctgcat 1139
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1048 GTATTAAATAGCTTAGCAAGAGTTAATAATATATGGAAGAATGCCCTGTTACACTCAAG 1107

QY 1140 ttggtgtgtggtgcccagggccggggtgggggggaggtgtgtgtcactgaatgtgctc 1199
    || ||||| | | ||||| | | ||||| | | ||||| | | ||||| | | ||||| | | |||||
Db 1108 GTGATGTGTAGTGAATG-----GGGGGAGGGTGGTGGGTTGTCACTGAACAACTT 1159

QY 1200 ttctcactgactttgtcaaaactggaagccagagaaataaagatggtgacaaagagaaaa 1255
    || | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1160 TT---CATTGACTGTCAAACTAGAAACCGGAATAAAGATGGTGACAGATAAAAAA 1212

RESULT 7
PCT-US93-07645-3
; Sequence 3, Application PC/TUS9307645
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Human Interleukin-13
; NUMBER OF SEQUENCES: 6
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.5
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07645
; FILING DATE: 19930818
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/012543
; FILING DATE: 01-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/010977
; FILING DATE: 29-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/933416
; FILING DATE: 21-AUG-1992
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1212 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
PCT-US93-07645-3

Query Match 17.1%; Score 216.4; DB 5; Length 1212;
Best Local Similarity 57.2%; Pred. No. 6.8e-55;
Matches 719; Conservative 0; Mismatches 411; Indels 126; Gaps 13;

QY 35 tcoctgcatggctctggtctccatggcgctctggttgactgtggtcattgctctcacctg 94
    || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 48 TCTCTCACTGGCTCTGGGCTTCATGGCGCTCTGGGTGACTGCAGTCTCGGCTCTTGCTTG 107

QY 95 cctcgtgtgcttgcctccccg-----agccctgtgactccccccccccccct 142
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 108 CCTTGGTGGTCTCGCCGCCCCAGGGCGGTGCCAAGATCTGTGTCTCTCCCTCTGACCCT 167

QY 143 caaggagctcattgagagctggtcaacatcacccagaatcaggcatccctctgcaacgg 202
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 168 TAAGGAGCTTATTGAGGAGCTGAGCAACATCACAAAGACCAGACTCCCCCTGTGCAACGG 227

QY 203 cagcatggtgtggagcgtcaacctgaccgcccagctactgctgagcgtctagaaatctct 262
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 228 CAGCATGGTATGACTGTGGACCTGGCCCGTGGCGGGTTCGTGTAGCCCTGGATTCCCT 287

QY 263 gatcaatgtctccgactgcagcgcccatccaaaggagggagggatgctgaaagcactgtg 322
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 288 GACCAACATCTCCAATTGCAATGCCATCTACAGAGCCACAGAGGATATTGCATGGCCTCTG 347
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QY 323 ctctcaaaagccccgcggcagggattttccagtgaaacgcagccgagacacacaaattgaagt 382
    ||||| | ||||| | | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 348 TAACCGCAAGGCCCCCACTACGGTCTCCA-----GCCTCCCGATACCAAAATCGAAGT 401

QY 383 gatccagttggtgaaaaaacctgctcacctatgtaaagggtttatcgccatggaattt 442
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 402 AGCCCACTTTATAACAAAACTGCTCAGCTACACAAAAGCAAACTGTTTCGCCACGGCCCTT 461

QY 443 cagatgaagcatgaaaaacttagcatcctctatctgtagaccagacctgaccacttaagt 502
    || ||||| | | ||||| | | ||||| | | ||||| | | ||||| | | ||||| | | |||||
Db 462 CTAATGAGGAGAGA-----CCATCCCTGGGCATCTCAGCT 496

QY 503 ccagattcattttcttctccgacgtcacaaaatttcttagggaggtgggggggggagaaa 562
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 497 GTGGACTCATTTTCCTTCTCACATCAGACTTGTCT-----GGGGAGAGCGGAGGA 550

QY 563 ccatttctcagctgggacctcagcctgacccgcctgacctccatgagctgagccccagcc 622
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Db 551 GGGTTGAGGAGGAAGGAGATGCCTCAGC-----TTTGGCCTCAGCCTGCA 596

QY 623 accctgccttgggtgcatgggccccagcgggtggccctcctcctcctcctcctcatcaa 682
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Db 597 CTGCCTGCCTAGTGTCTCAGGGTCTCAGCCTGCTCAGCCTGCAACACCCCAACCCCAACCC 648

QY 683 cgctgagggaaagcactgcatcccccatgactgtccccctcctcagagcaaaagtgcagcat 742
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Db 649 -----CACCCCGCCCGCCCATCCCATCCCATCCCATCCCATCCCATCCCATCCCATCC 693

QY 743 c----agtgagggcagatatgtgtgggaggggtgtgtgtacctgggagtggtggcacaga 798
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Db 694 CCGTGAGTCCAGCCTGTGGCCTGGTCCACACAGGGCAACTGAGGCGGCGGAGGAGCTTGAG 753

QY 799 catgtttctttagccttattattattgtgtgtttattttaaacaagtgtcttgttgt 858
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 754 CACATTTCTTCTTGATCTTATTATTATGGT-TGTGTGTTATTATAATGAGTGTGTGAGT 812

QY 859 gctgggacagggagtggtgtggagctgggggggggggggactgactcgggtttaga----- 910
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 813 ATCCCGGTGGGACATGTTTGTGCTGCCTATGCTTATGCTGGGCTCCAGCATTTGAAGCAGTGG 872

QY 911 ----gagtcctcctgggaataaagcactgtgtgtataaaattctgtacctcactcgggacatc 965
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 873 GCTCTGGGTCCCTGGCAATATTACTGTATACATAACTCTGTCTACCTCAGTGTAGCCTCC 932

QY 966 ggg-----ccgacacaggggacagggaggaaggggtcagagatgctgctctgtctgccac 1019
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Db 933 AGGTCTCACCCAGGAGAGATGGGAGGGGAGGCGGAGGCAACACTCCTGTGTGCCACG 992

QY 1020 tcagcagctggccctcagccaagcagtaattattgttttctctgtattttaaagttaag 1079
    ||||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 993 GCAGCAACCAGCCCTCAGCCATGAATAACTTATTGTT-----TTGTTCTTATATTAAA 1047

QY 1080 aaataaataatgttatcaaaagagtttaataatatatagaagtagccctaaaggctgcat 1139
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Db 1048 GTATTAAATAGCTTAGCAAGAGTTAATAATATATATGGAAGAATGGCCCTGTACACTCAAG 1107

QY 1140 ttggtgtgtgtgcccagggccggggtgggggggaggtgtgtgtcactgaatgtgctc 1199
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Db 1108 GTGATGTGTAGTGAATG-----GGGGGAGGGTGGTGGGTTTGTCACTGAACAACTT 1159

QY 1200 ttctcactgactttgtcaaaactggaagccagaaataaagatggtgacaaagagaaaaa 1255
    || | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1160 TT---CATTGACTGTCAAACTAGAAACCGGAATAAAGATGGTGACAGATAAAAAA 1212
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RESULT 8  
US-08-371-121-17  
; Sequence 17, Application US/08371121  
; Patent No. 5652123  
; GENERAL INFORMATION:  
; APPLICANT: CAPUT, Daniel  
; APPLICANT: FERRARA, Pascual



APPLICANT: GUILLEMOT, Jean-Claude  
APPLICANT: LEPLATOIS, Pascal  
APPLICANT: MINTY, Adrian  
APPLICANT: KAGHAD, Mourad  
APPLICANT: LABIT-LE BOUTEILLER, Christine  
APPLICANT: MAGAZIN, Marilyn  
TITLE OF INVENTION: protein having a cytokine type  
TITLE OF INVENTION: activity, recombinant DNA coding for this protein,  
TITLE OF INVENTION: transformed cells and microorganisms.  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FOLEY & LARDNER  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington, D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/371,121  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/938,161  
FILING DATE: 30-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/FR92/00280  
FILING DATE: 27-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 91 00137  
FILING DATE: 08-JAN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 91 03904  
FILING DATE: 29-MAR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: SAXE, Bernhard D.  
REGISTRATION NUMBER: 28,665  
REFERENCE/DOCKET NUMBER: 16781/383  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 384 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-371-121-17  
  
Query Match 15.2%; Score 193.4; DB 1; Length 384;  
Best Local Similarity 75.5%; Pred. No. 2.4e-48;  
Matches 268; Conservative 0; Mismatches 81; Indels 6; Gaps 2;  
  
QY 111 tccccgagccctgtgactccctcccaacccctcaaggagctcattgaggagctgggtcaac 170  
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Db 16 TCCCCAGGCCCTGTGCTTCCCTCTACGGCCCTCAGGGAGCTCATTGAGGAGCTGGTCAAC 75  
  
QY 171 atcaccaccagaatc---aggcatccctctgtcaaacggcagcatgggtgtggagcgtcaacctg 227  
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Db 76 ATCACCACAGAACCCAGAGGCTCCGCTCTGTGCAATGCCAGCATGGTATGGAGCATCAACCTG 135  
  
QY 228 accgcccgcagtactgcgcagctctagaaatctctgataatgtctccgactgcagcgc 287  
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Db 136 ACAGCTGACATGTACTGTGACGCCCTTGGAAATCCCTGATCAACGTGTGAGGCTGCACTGCC 195  
  
QY 288 atccaaaggacccagagctgctgaaagcactgtgctctcaaaagcccgccgagc---g 344  
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Db 196 ATCGAGAAGACCCAGAGGATGCTGAGCGGATTCTGCCCGCACAAAGGTCTCAGCTGGGCAG 255  
  
QY 345 atttcagtgaaacgcagccgagacacacaaattgaagtgtatccagttggtgaaaaacctg 404  
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Db 256 TTTTCCAGCTTGCATGTCGAGACACCAAATCGAGGTGGCCCGAGTTTGTAAAGGACCTG 315  
  
QY 405 ctcacctatgaaggaggagtttatcgcccatggaatttcagatgaagcatgaaaa 459  
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Db 316 CTCTTACATTAAAGAAACTTTTTCGCGGAGGACGGTTCAACTGAAACTTCGAAA 370  
  
RESULT 9  
US-08-594-469-4  
; Sequence 4, Application US/08594469  
; Patent No. 5700665  
; GENERAL INFORMATION:  
; APPLICANT: LEGOUX, Richard  
; APPLICANT: MALDONADO, Paul  
; APPLICANT: SALOME, Marc  
; TITLE OF INVENTION: Method for the extraction of  
; TITLE OF INVENTION: periplasmic proteins of prokaryotic microorganisms in the  
; TITLE OF INVENTION: presence of arginine  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Bacon & Thomas  
; STREET: 625 Slaters Lane - Fourth Floor  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: USA  
; ZIP: 22314  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/594,469  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 95 01083  
; FILING DATE: 31-JAN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: FICHTER, Richard E  
; REGISTRATION NUMBER: 26,382  
; REFERENCE/DOCKET NUMBER: REF/LEGOUX  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 683-0500  
; TELEFAX: (703) 683-1080  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 425 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-594-469-4  
  
Query Match 15.1%; Score 191.6; DB 1; Length 425;  
Best Local Similarity 74.9%; Pred. No. 9e-48;  
Matches 268; Conservative 0; Mismatches 84; Indels 6; Gaps 2;  
  
QY 108 gcctcccgagccctgtgactccctcccaacccctcaaggagctcattgaggagctggtc 167  
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Db 55 GCCTTCGCTGGCCCTGTGCTCCCTCCAGTACTGCCCTCAGGGAGCTCATGAGGAGCTGGTC 114  
  
QY 168 aacatacccagaatc---aggcatccctctgcaacggcagcatggtgtggagcgtcaac 224  
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Db 115 AACATCACCAGAACCCAGAGGCTCCGCTCTGCAATGGCAGCATGTGTATGGAGCATCAAC 174  
  
QY 225 ctgacccgcccgcagtactgcgcagctctagaaatctctgatcaatgtctccgactgcagc 284  
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Db 175 CTGACAGCTGGCATGTACTGTGCAGCCCTGGAATCCCTGATCAACGTGTCAGGCTGCAGT 234  
QY 285 gccatccaaaggaccagaggtgctgaaagcactgtgctctctcaaaagcccgcggcagg- 343  
Db 235 GCCATCGAGAAGACCCAGAGGATGCTGAGCGGATTCTGCCCGCACAAAGTCTCAGCTGGG 294  
QY 344 --gatttccagtgaaagcgagccgagacacacaaattgaagtgtatccagttggtgaaaaa 401  
Db 295 CAGTTTCCAGCTTGTCATGTCCGAGACACCAAAATCGAGGTGGCCCAAGTTTGTAAAGGAC 354  
QY 402 ctgctcacctatgtaaggagggtttatcgccatggaatttcagatgaagcatgaaaa 459  
Db 355 CTGCTCTTACATTAAAGAAACTTTTTCGCGAGGACGGTTCAACTGAAACTTCGAAA 412  
RESULT 10  
US-08-906-957-4  
; Sequence 4, Application US/08906957  
; Patent No. 5856142  
; GENERAL INFORMATION:  
; APPLICANT: LEGOUX, Richard  
; APPLICANT: MALDONADO, Paul  
; APPLICANT: SALOME, Marc  
; TITLE OF INVENTION: Method for the extraction of  
; TITLE OF INVENTION: periplasmic proteins of prokaryotic microorganisms in the  
; TITLE OF INVENTION: presence of arginine  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Bacon & Thomas  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: USA  
; ZIP: 22314  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/906,957  
; FILING DATE: 06-AUG-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/594,469  
; FILING DATE:  
; APPLICATION NUMBER: FR 95 01083  
; FILING DATE: 31-JAN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: FICHTER, Richard E  
; REGISTRATION NUMBER: 26,382  
; REFERENCE/DOCKET NUMBER: REF/LEGOUX  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 683-0500  
; TELEFAX: (703) 683-1080  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 425 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-906-957-4

Query Match 15.1%; Score 191.6; DB 2; Length 425;  
Best Local Similarity 74.9%; Pred. No. 9e-48;  
Matches 268; Conservative 0; Mismatches 84; Indels 6; Gaps 2;

QY 108 gccctcccgagccctgtgactccctcccaaccctcaaggagctcatgaggagctggtc 167  
Db 55 GCCCTCGCTGGCCCTGTGCCTCCCACTACTGCCCTCAGGGAGCTCATTGAGGAGCTGGTC 114

QY 168 aacatcacccagaatc---aggcatccctctgcaacggcgagcatggtgtggagcgtcaac 224  
Db 115 AACATCACCCAGAACCCAGAGGCTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAAC 174  
QY 225 ctgaccgcccgcagtgtactgctgagcagctctagaatctctgtatcaatgtctccgactgcgc 284  
Db 175 CTGACAGCTGGCATGTACTGTGCAGCCCTGGAATCCCTGATCAACGTGTCAGGCTGCAGT 234  
QY 285 gccatccaaaggaccagaggtgctgaaagcactgtgctctcaaaagcccgcggcagg- 343  
Db 235 GCCATCGAGAAGACCCAGAGGATGCTGAGCGGATTCTGCCCGCACAAAGTCTCAGCTGGG 294  
QY 344 --gatttccagtgaaagcgagccgagacacacaaattgaagtgtatccagttggtgaaaaa 401  
Db 295 CAGTTTCCAGCTTGTCATGTCCGAGACACCAAAATCGAGGTGGCCCAAGTTTGTAAAGGAC 354  
QY 402 ctgctcacctatgtaaggagggtttatcgccatggaatttcagatgaagcatgaaaa 459  
Db 355 CTGCTCTTACATTAAAGAAACTTTTTCGCGAGGACGGTTCAACTGAAACTTCGAAA 412  
RESULT 11  
US-08-594-469-1  
; Sequence 1, Application US/08594469  
; Patent No. 5700665  
; GENERAL INFORMATION:  
; APPLICANT: LEGOUX, Richard  
; APPLICANT: MALDONADO, Paul  
; APPLICANT: SALOME, Marc  
; TITLE OF INVENTION: Method for the extraction of  
; TITLE OF INVENTION: periplasmic proteins of prokaryotic microorganisms in the  
; TITLE OF INVENTION: presence of arginine  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Bacon & Thomas  
; STREET: 625 Slaters Lane - Fourth Floor  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: USA  
; ZIP: 22314  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/594,469  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 95 01083  
; FILING DATE: 31-JAN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: FICHTER, Richard E  
; REGISTRATION NUMBER: 26,382  
; REFERENCE/DOCKET NUMBER: REF/LEGOUX  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 683-0500  
; TELEFAX: (703) 683-1080  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4410 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-594-469-1

Query Match 15.1%; Score 191.6; DB 1; Length 4410;  
Best Local Similarity 74.9%; Pred. No. 4.1e-47;  
Matches 268; Conservative 0; Mismatches 84; Indels 6; Gaps 2;

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QY 108 gctctcccgagccctgtgactccctccctcccaacccctcaaggagctcattgaggagctggtc 167
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Db 392 GCCTTCGCTGGCCCTGTGCCTCCAGTACTGCCCTCAGGAGCTCATTGAGGAGCTGGTC 451

QY 168 aacatcacccagaatc---aggcatccctctgcaacgagcagcatggtgtggagcgtaaac 224
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Db 452 AACATCACCCAGAACCCAGAAAGGCTCCGGCTCTGCAATGGCAGCATGGTATGGAGCATCAAC 511

QY 225 ctgaccgcccgcgcattactgcgcagctctagaatctctgatcaaatgtctccgactgcagc 284
    ||||| || ||||| ||||| ||||| || ||||| ||||| ||||| ||||| ||||| |||||
Db 512 CTGACAGCTGGCATGTACTGTGACGCCCTGGAATCCCTGATCAACGTGTCAGGCTGCAGT 571

QY 285 gccatccaaaggaccagagggatgctgaaagcactgtgctctctcaaaagccccgcggcagg- 343
    ||||| | | ||||| ||||| ||||| | ||||| ||||| ||||| ||||| ||||| |||||
Db 572 GCCATCGAGAAGACCCAGAGGATGCTGAGCGGATTCTGCCCGCACAAAGGTCTCAGCTGG 631

QY 344 --gattccagtgaaacgagccgagacacacacaaattgaagtgatccagttggtgaaaaac 401
    | ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 632 CAGTTTTCAGCTTGTCATGCTCCGAGACACCAAAATCGAGGTGGCCCAAGTTTGTAAAGGAC 691

QY 402 ctgctcacctatgtaaggggagtttatcgccatggaatttcagatgaagcatgaaaaa 459
    ||||| || ||||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 692 CTGCTCTTTACATTTAAAGAAACTTTTTCGCGAGGGACGGTTCAACTGAAACTTCGAAA 749

RESULT 12
US-08-906-957-1
; Sequence 1, Application US/08906957
; Patent No. 5856142
; GENERAL INFORMATION:
; APPLICANT: LEGOUX, Richard
; APPLICANT: MALDONADO, Paul
; APPLICANT: SALOME, Marc
; TITLE OF INVENTION: Method for the extraction of
; TITLE OF INVENTION: periplasmic proteins of prokaryotic microorganisms in the
; TITLE OF INVENTION: presence of arginine
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bacon & Thomas
; STREET: 625 Slaters Lane - Fourth Floor
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/906,957
; FILING DATE: 06-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/594,469
; FILING DATE:
; APPLICATION NUMBER: FR 95 01083
; FILING DATE: 31-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FICHTER, Richard E
; REGISTRATION NUMBER: 26,382
; REFERENCE/DOCKET NUMBER: REF/LEGOUX
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 683-0500
; TELEFAX: (703) 683-1080
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4410 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-906-957-1

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; APPLICATION NUMBER: FR 91 03904
; FILING DATE: 29-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 16781/383
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 336 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-371-121-24

Query Match 14.8%; Score 187.4; DB 1; Length 336;
Best Local Similarity 76.9%; Pred. No. 1.4e-46;
Matches 256; Conservative 0; Mismatches 71; Indels 6; Gaps 2;

QY 118 gccctgtgactccctcccaacccctcaaggagctcattgaggagctgggtcaacatcaccc 177
Db 2 GCCCTGTGCTCCCTCTACAGCCCTCAGGGAGCTCATTTGAGGAGCTGGTCAACATCACCC 61

QY 178 agaatc---aggcatccctctgcaacggcagcatggtgtggagctgaacctgaccgccg 234
Db 62 AGAACCAGAGGCTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAACCTGACAGCTG 121

QY 235 gcatgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgccatccaaa 294
Db 122 GCATGTACTGTGCAGCCCTGGAATCCCTGATCAACGTGTGAGGCTGCAGTGCATCGAGA 181

QY 295 ggaccagaggtgctgaaagcactgtgctctcaaaagcccgccgagg---gatttcca 351
Db 182 AGACCCAGAGGATGCTGAGCGGATTTCTGCCCGCACAAAGGTTCTCAGCTGGGCGAGTTTCCA 241

QY 352 gtgaacgagcgccgagacacccaaattgaagtgtccagttgtgtaaaacacctgctcacct 411
Db 242 GCTTGCATGTCGAGACACCAAAATCGAGGTGGCCAGTTTGTAAAGGACGCTGCTCTTAC 301

QY 412 atgtaaggggagtttatcgccatggaatttca 444
Db 302 ATTTAAAGAAACTTTTTCGGGAGGACGGTTCA 334

RESULT 14
US-08-371-121-2
; Sequence 2, Application US/08371121
; Patent No. 5652123
; GENERAL INFORMATION:
; APPLICANT: CAPUT, Daniel
; APPLICANT: FERRARA, Pascual
; APPLICANT: GUILLEMOT, Jean-Claude
; APPLICANT: LEPLATOIS, Pascal
; APPLICANT: MINTY, Adrian
; APPLICANT: KAGHAD, Mourad
; APPLICANT: LABIT-LE BOUTEILLER, Christine
; APPLICANT: MAGAZIN, Marilyn
; TITLE OF INVENTION: Protein having a cytokine type
; TITLE OF INVENTION: activity, recombinant DNA coding for this protein,
; TITLE OF INVENTION: transformed cells and microorganisms.
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/371,121
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/938,161
; FILING DATE: 30-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR92/00280
; FILING DATE: 27-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91 00137
; FILING DATE: 08-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91 03904
; FILING DATE: 29-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 16781/383
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 336 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-371-121-2

Query Match 14.6%; Score 185.8; DB 1; Length 336;
Best Local Similarity 76.6%; Pred. No. 4.2e-46;
Matches 255; Conservative 0; Mismatches 72; Indels 6; Gaps 2;

QY 118 gccctgtgactccctcccaacccctcaaggagctcattgaggagctgggtcaacatcaccc 177
Db 2 GCCCTGTGCTCCCTCTACAGCCCTCAGGGAGCTCATTTGAGGAGCTGGTCAACATCACCC 61

QY 178 agaatc---aggcatccctctgcaacggcagcatggtgtggagctgaacctgaccgccg 234
Db 62 AGAACCAGAGGCTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAACCTGACAGCTG 121

QY 235 gcatgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgccatccaaa 294
Db 122 ACATGTACTGTGCAGCCCTGGAATCCCTGATCAACGTGTGAGGCTGCAGTGCATCGAGA 181

QY 295 ggaccagaggtgctgaaagcactgtgctctcaaaagcccgccgagg---gatttcca 351
Db 182 AGACCCAGAGGATGCTGAGCGGATTTCTGCCCGCACAAAGGTTCTCAGCTGGGCGAGTTTCCA 241

QY 352 gtgaacgagcgccgagacacccaaattgaagtgtccagttgtgtaaaacacctgctcacct 411
Db 242 GCTTGCATGTCGAGACACCAAAATCGAGGTGGCCAGTTTGTAAAGGACGCTGCTCTTAC 301

QY 412 atgtaaggggagtttatcgccatggaatttca 444
Db 302 ATTTAAAGAAACTTTTTCGGGAGGACGGTTCA 334

RESULT 15
US-08-371-121-26
; Sequence 26, Application US/08371121
; Patent No. 5652123
; GENERAL INFORMATION:
; APPLICANT: CAPUT, Daniel
```







GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: May 13, 2001, 14:30:23 ; Search time 472.02 Seconds  
(without alignments)  
482.341 Million cell updates/sec

Title: US-09-451-527-102  
Perfect score: 390  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 678276 seqs, 291890651 residues

Total number of hits satisfying chosen parameters: 1356552

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	390	100.0	390	21	255563 Canine interleukin
2	390	100.0	390	21	255564 Canine interleukin
3	390	100.0	1269	21	255561 Canine interleukin
4	390	100.0	1269	21	255562 Canine interleukin
5	377	96.7	393	21	255557 Canine interleukin
6	377	96.7	393	21	255558 Canine interleukin
7	377	96.7	1302	21	255555 Canine interleukin
8	377	96.7	1302	21	255556 Canine interleukin
9	330	84.6	330	21	255565 Canine mature inte
10	330	84.6	330	21	255566 Canine mature inte
11	317	81.3	333	21	255559 Canine mature inte

C	12	317	81.3	333	21	255560 Canine mature inte
	13	278	71.3	278	21	255554 Canine interleukin
	14	256	65.6	272	21	255553 Canine interleukin
	15	230.8	59.2	1270	21	F21334 Human low adenosin
	16	230.8	59.2	1270	21	A35212 Human adenosine re
	17	230.8	59.2	1282	21	F21332 Human low adenosin
	18	230.8	59.2	1290	15	A35210 Human adenosine re
	19	230.8	59.2	1290	15	Q56692 Sequence encoding
	20	230.8	59.2	6952	21	F21333 Human low adenosin
	21	230.8	59.2	6952	21	A35211 Human adenosine re
	22	230.8	59.2	14978	21	F21338 Human low adenosin
	23	230.8	59.2	14978	21	A35216 Human adenosine re
	24	229.2	58.8	1297	13	Q28947 Cytokine NC30. Q
	25	187.4	48.1	336	13	Q28944 Gly41-Cytokine cod
	26	185.8	47.6	336	13	Q28943 Asp41-Cytokine cod
	27	168.6	43.2	1212	15	Q56693 Sequence encoding
	28	101.8	26.1	5670	21	F21331 Human low adenosin
	29	101.8	26.1	5670	21	F21337 Human low adenosin
	30	101.8	26.1	5670	21	A35209 Human adenosine re
	31	101.8	26.1	5670	21	A35215 Human adenosine re
	32	99	25.4	166	21	255552 Canine interleukin
	33	44.6	11.4	60	13	Q28942 Cytokine signal se
	34	44.6	11.4	102	13	Q28941 Cytokine signal se
	35	40.8	10.5	2460	11	Q06086 Plasmid pZPC13 enc
	36	37.2	9.5	66	20	Z32227 Human interleukin
	37	35.8	9.2	2249	18	T74283 Cellulose binding
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	39	35.8	9.2	3187	17	T10922 Laccase gene. Myc
	40	35.8	9.2	3192	18	T72106 Myceliophthora the
	41	35.8	9.2	3192	18	T63318 M. thermophila lac
	42	35.8	9.2	3192	21	Z24236 Dominant-negative
	43	34.4	8.8	772	19	V48405 Human neuronal nic
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ALIGNMENTS

RESULT 1  
Z55563 ID Z55563 standard; cDNA; 390 BP.  
XX AC Z55563;  
XX AC  
DT 14-MAR-2000 (first entry)  
XX DE Canine interleukin-13 (IL-13) clone 78 cDNA coding region.  
XX DE Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;  
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.  
XX OS Canis familiaris.  
XX PN WO9961618-A2.  
XX PD 02-DEC-1999.  
XX PF 28-MAY-1999; 99WO-US11942.  
XX PR 29-MAY-1998; 98US-0087306.  
XX (HESK-) HESKA CORP.  
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;  
XX WPI; 2000-072623/06.  
DR P-PSDB; Y58223.  
XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
PT useful for treating or preventing e.g. tumors or autoimmune disease -  
PS Claim 11; Page 238-239; 264pp; English.

XX Sequences Z55552-Z55560 and Z55561-Z55566 represent cDNA  
CC sequences encoding canine interleukin-13 (IL-13) clones 80  
CC and 78 respectively. The invention relates to canine  
CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or  
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline  
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage  
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these  
CC immunoregulatory proteins. The proteins, their associated  
CC nucleic acids, specific antibodies and inhibitors may be used as  
CC vaccines for therapeutic or prophylactic regulation of an immune  
CC response in animals (particularly cats, dogs, horses and humans).  
CC They may be used to treat autoimmune or infectious diseases including  
CC allergies, tumours, inflammation and graft rejection, and to increase  
CC the response from a co-administered antigen. The nucleotide sequences  
CC can also be used for the recombinant production of a protein, while  
CC nucleotide fragments are useful as probes, as amplification primers and  
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
CC The proteins may be used to raise antibodies and to screen for  
CC modulators of activity, while the antibodies may be used in detection,  
CC and in drug targeting.  
XX Sequence 390 BP; 92 A; 117 C; 99 G; 82 T; 0 other;

Query Match 100.0%; Score 390; DB 21; Length 390;  
Best Local Similarity 100.0%; Pred. No. 1.9e-102;  
Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 atggcgctctggtgactgtggtcattgctctcacctgctcggtggtgccttgcctccccg 60  
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Db 121 cagaatcaggcatccctctgcaacggcgagcatggtgtgagcgtcaacctgaccgccggc 180  
Qy 181 atgtactgcgcagctctagaatctctgatcaatgtctcgcactgcagcgccatccaaagg 240  
Db 181 atgtactgcgcagctctagaatctctgatcaatgtctcgcactgcagcgccatccaaagg 240  
Qy 241 acccagaggatgctgaagcactgtgctctcaaaagcccgcgaggatttccagtga 300  
Db 241 acccagaggatgctgaagcactgtgctctcaaaagcccgcgaggatttccagtga 300  
Qy 301 cgcagccgagacacccaaattgaagtgtatccagttggtgaaaaacctgtcacctatgta 360  
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RESULT 2  
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ID Z55564 standard; cDNA: 390 BP.  
XX  
AC Z55564;  
XX  
DT 14-MAR-2000 (first entry)  
XX  
DE Canine interleukin-13 (IL-13) clone 78 cDNA coding region complement.  
XX  
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;  
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.  
OS Canis familiaris.

PN WO9961618-A2.  
XX  
PD 02-DEC-1999.  
XX  
PF 28-MAY-1999; 99WO-US11942.  
XX  
PR 29-MAY-1998; 98US-0087306.  
XX  
PA (HESK-) HESKA CORP.  
XX  
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;  
XX  
DR WPI; 2000-072623/06.  
DR P-PSDB; Y58223.  
XX  
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
PT useful for treating or preventing e.g. tumors or autoimmune disease  
XX  
PS Claim 1i; Page 239; 264pp; English.  
XX  
CC Sequences Z55552-Z55560 and Z55561-Z55566 represent cDNA  
CC sequences encoding canine interleukin-13 (IL-13) clones 80  
CC and 78 respectively. The invention relates to canine  
CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or  
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline  
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage  
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these  
CC immunoregulatory proteins. The proteins, their associated  
CC nucleic acids, specific antibodies and inhibitors may be used as  
CC vaccines for therapeutic or prophylactic regulation of an immune  
CC response in animals (particularly cats, dogs, horses and humans).  
CC They may be used to treat autoimmune or infectious diseases including  
CC allergies, tumours, inflammation and graft rejection, and to increase  
CC the response from a co-administered antigen. The nucleotide sequences  
CC can also be used for the recombinant production of a protein, while  
CC nucleotide fragments are useful as probes, as amplification primers and  
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
CC The proteins may be used to raise antibodies and to screen for  
CC modulators of activity, while the antibodies may be used in detection,  
CC and in drug targeting.  
XX  
SQ Sequence 390 BP; 82 A; 99 C; 117 G; 92 T; 0 other;

Query Match 100.0%; Score 390; DB 21; Length 390;  
Best Local Similarity 100.0%; Pred. No. 1.9e-102;  
Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 atggcgctctggtgactgtggtcattgctctcacctgctcggtggtgccttgcctccccg 60  
Db 390 ATGGCGCTCTGTTGACTGTGGTCATTGCTCTCACCTGCTCGGTGGCCTTGCTCCCG 331  
Qy 61 agccctgtgactccctcccaaccctcaaggagctcattgaggagctggtcaacatcacc 120  
Db 330 AGCCCTGTGACTCCCTCCCCAACCCCTCAAGGAGCTCATTGAGGAGCTGGTCAACATCACC 271  
Qy 121 cagaatcaggcatccctctgcaacggcgagcatggtgtgagcgtcaacctgaccgccggc 180  
Db 270 CAGAAATCAGGCATCCCTCTGCAACGGCAGCATGCTGTGGAGCGTCAACCTGACCGCCGGC 211  
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Qy 241 acccagaggatgctgaagcactgtgctctcaaaagcccgcgaggatttccagtga 300  
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Qy 301 cgcagccgagacacccaaattgaagtgtatccagttggtgaaaaacctgtcacctatgta 360  
Db 90 CGCAGCCCGAGACACCAAAATTGAAGTGATCCAGTTGGTGAAAAACCTGCTCACCTATGTA 31  
Qy 361 aggggagtttatcgccatggaaaatttcaga 390



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ID Z55561 standard; cDNA; 1269 BP.  
XX  
AC Z55561;  
XX  
DT 14-MAR-2000 (first entry)  
XX  
DE Canine interleukin-13 (IL-13) clone 78 cDNA.  
XX  
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;  
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.  
XX  
OS Canis familiaris.  
XX  
FH Key Location/Qualifiers  
FT CDS 57..449  
FT /\*tag= a  
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XX  
PN WO9961618-A2.  
XX  
PD 02-DEC-1999.  
XX  
PF 28-MAY-1999; 99WO-US11942.  
XX  
PR 29-MAY-1998; 98US-0087306.  
XX  
PA (HESK-) HESKA CORP.  
XX  
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;  
XX  
DR WPI; 2000-072623/06.  
P-PSDB; Y58223.  
XX  
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
PT useful for treating or preventing e.g. tumors or autoimmune disease  
XX  
PS Claim 11; Page 235-236; 264pp; English.  
XX  
CC Sequences Z55552-Z55560 and Z55561-Z55566 represent cDNA  
CC sequences encoding canine interleukin-13 (IL-13) clones 80  
CC and 78 respectively. The invention relates to canine  
CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or  
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline  
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage  
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these  
CC immunoregulatory proteins. The proteins, their associated  
CC nucleic acids, specific antibodies and inhibitors may be used as  
CC vaccines for therapeutic or prophylactic regulation of an immune  
CC response in animals (particularly cats, dogs, horses and humans).  
CC They may be used to treat autoimmune or infectious diseases including  
CC allergies, tumours, inflammation and graft rejection, and to increase  
CC the response from a co-administered antigen. The nucleotide sequences  
CC can also be used for the recombinant production of a protein, while  
CC nucleotide fragments are useful as probes, as amplification primers and  
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
CC The proteins may be used to raise antibodies and to screen for  
CC modulators of activity, while the antibodies may be used in detection,  
CC and in drug targeting.  
XX  
SQ Sequence 1269 BP; 302 A; 320 C; 340 G; 307 T; 0 other;

Query Match 100.0%; Score 390; DB 21; Length 1269;  
Best Local Similarity 100.0%; Pred. NO. 2.8e-102;  
Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 177 cagaatcaggcatccctctctgcaacggcagcatggtgtgagcgtcaacctgaccgccgc 236  
  
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Db 237 atgtactgcgagctctagaatctctgatcaatgtctccgactgcagcgccatccaaagg 296  
  
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Db 297 acccagagatgctgaaagcactgtgctctcaaaaagcccgaggatttccagtga 356  
  
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QY 361 aggggagtttatcgccatggaatttcaga 390  
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RESULT 4  
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ID Z55562 standard; cDNA; 1269 BP.  
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AC Z55562;  
XX  
DT 14-MAR-2000 (first entry)  
XX  
DE Canine interleukin-13 (IL-13) clone 78 cDNA complement.  
XX  
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;  
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.  
XX  
OS Canis familiaris.  
XX  
FH Key Location/Qualifiers  
FT CDS complement (821..1213)  
FT /\*tag= a  
FT /product= "Canine IL-13 clone 78"  
XX  
PN WO9961618-A2.  
XX  
PD 02-DEC-1999.  
XX  
PF 28-MAY-1999; 99WO-US11942.  
XX  
PR 29-MAY-1998; 98US-0087306.  
XX  
PA (HESK-) HESKA CORP.  
XX  
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;  
XX  
DR WPI; 2000-072623/06.  
P-PSDB; Y58223.  
XX  
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
PT useful for treating or preventing e.g. tumors or autoimmune disease  
XX  
PS Claim 11; Page 237-238; 264pp; English.  
XX  
CC Sequences Z55552-Z55560 and Z55561-Z55566 represent cDNA  
CC sequences encoding canine interleukin-13 (IL-13) clones 80  
CC and 78 respectively. The invention relates to canine  
CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or  
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline

CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage  
CC colony-stimulating factor (GMCSF), and nucleotides which encode these  
CC immunoregulatory proteins. The proteins, their associated  
CC nucleic acids, specific antibodies and inhibitors may be used as  
CC vaccines for therapeutic or prophylactic regulation of an immune  
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CC allergies, tumours, inflammation and graft rejection, and to increase  
CC the response from a co-administered antigen. The nucleotide sequences  
CC can also be used for the recombinant production of a protein, while  
CC nucleotide fragments are useful as probes, as amplification primers and  
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
CC The proteins may be used to raise antibodies and to screen for  
CC modulators of activity, while the antibodies may be used in detection,  
CC and in drug targetting.

XX Sequence 1269 BP; 307 A; 340 C; 320 G; 302 T; 0 other;

Query Match 100.0%; Score 390; DB 21; Length 1269;  
Best Local Similarity 100.0%; Pred. No. 2.8e-102;  
Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atggcgctctgtgactggtgactggtcattgctctcacctgcctcggtggccttgcctccccg 60  
Db 1213 ATGGCGCTCTGTTGACTGTGGTCAATGCTCTCACCTGCCTGGTGGCCTTGCTCCCG 1154  
QY 61 agccctgtgactccctcccaaccctcaaggagctcattgaggagctggtcaacatcacc 120  
Db 1153 AGCCCTGTGACTCCCTCCCAACCCTCAAGGAGCTCATTTGAGGAGCTGGTCAACATCACC 1094  
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Db 973 ACCCAGAGGATGCTGAAGCACTGTGCTCTCAAAAGCCCGGCGAGGGATTTCAGTGAA 914  
QY 301 cgcagccgagacaccaaattgaagtgtatccagttggtgaaaaaacctgtcacctatgta 360  
Db 913 CGCAGCCGAGACACCAAAATTGAAGTGATCCAGTTGGTGAAAAACCTGCTCACCTATGTA 854  
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RESULT 5  
Z55557  
ID Z55557 standard; cDNA; 393 BP.

XX AC Z55557;

XX 14-MAR-2000 (first entry)

DE Canine interleukin-13 (IL-13) clone 80 cDNA coding region.

KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;  
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.

OS Canis familiaris.

XX WO9961618-A2.

XX 02-DEC-1999.

XX 28-MAY-1999; 99WO-US11942.

XX

PR 29-MAY-1998; 98US-0087306.

XX (HESK-) HESKA CORP.

PI Sim G, Yang S, Dreitz MJ, Wonderling RS;

XX WPI; 2000-072623/06.

DR P-PSDB; Y58221.

XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
PT useful for treating or preventing e.g. tumors or autoimmune disease -

PS Claim 1i; Page 232-233; 264pp; English.

XX Sequences Z55552-Z55560 and Z55561-Z55566 represent cDNA

CC sequences encoding canine interleukin-13 (IL-13) clones 80

CC and 78 respectively. The invention relates to canine

CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or

CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline

CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage

CC colony-stimulating factor (GMCSF), and nucleotides which encode these

CC immunoregulatory proteins. The proteins, their associated

CC nucleic acids, specific antibodies and inhibitors may be used as

CC vaccines for therapeutic or prophylactic regulation of an immune

CC response in animals (particularly cats, dogs, horses and humans).

CC They may be used to treat autoimmune or infectious diseases including

CC allergies, tumours, inflammation and graft rejection, and to increase

CC the response from a co-administered antigen. The nucleotide sequences

CC can also be used for the recombinant production of a protein, while

CC nucleotide fragments are useful as probes, as amplification primers and

CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).

CC The proteins may be used to raise antibodies and to screen for

CC modulators of activity, while the antibodies may be used in detection,

CC and in drug targetting.

XX

SQ Sequence 393 BP; 93 A; 118 C; 100 G; 82 T; 0 other;

Query Match 96.7%; Score 377; DB 21; Length 393;  
Best Local Similarity 99.2%; Pred. No. 1e-98;  
Matches 390; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 1 atggcgctctgtgactggtgactggtcattgctctcacctgcctcggtggccttgcctccccg 60  
Db 1 atggcgctctgtgactggtgactggtgctcattgctctcacctgcctcggtggccttgcctccccg 60

QY 61 agccctgtgactccctcccaaccctcaaggagctcattgaggagctggtcaacatcacc 120  
Db 61 agccctgtgactccctcccaaccctcaaggagctcattgaggagctggtcaacatcacc 120

QY 121 cagaatcaggcatccctctgcaacggcagcatggtgtgagcgtcaacctgaccgcccgc 180  
Db 121 cagaatcaggcatccctctgcaacggcagcatggtgtgagcgtcaacctgaccgcccgc 180

QY 181 atgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgccatccaaagg 240  
Db 181 atgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgccatccaaagg 240

QY 241 acccagaggatgctgaaagcactgtgctctcctcaaaagcccgagg---gattccagt 297  
Db 241 acccagaggatgctgaaagcactgtgctctcctcaaaagcccgagggagattccagt 300

QY 298 gaacgcagcgagacaccaaattgaagtgatccagttggtgaaaaaacctgtcacctat 357  
Db 301 gaacgcagcgagacaccaaattgaagtgatccagttggtgaaaaaacctgtcacctat 360

QY 358 gtaagggagtttatcgccatggaaaatttcaga 390

Db 361 gtaagggagtttatcgccatggaaaatttcaga 393

RESULT 6  
Z55558/c

255558 standard; cDNA; 393 BP.  
255558;  
14-MAR-2000 (first entry)  
Canine interleukin-13 (IL-13) clone 80 cDNA coding region complement.  
Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;  
immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.  
Canis familiaris.  
WO9961618-A2.  
02-DEC-1999.  
28-MAY-1999; 99WO-US11942.  
29-MAY-1998; 98US-0087306.  
(HESK-) HESKA CORP.  
Sim G, Yang S, Dreitz MJ, Wonderling RS;  
WPI; 2000-072623/06.  
P-PSDB; Y58221.  
Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
useful for treating or preventing e.g. tumors or autoimmune disease  
Claim 1i; Page 233; 264pp; English.  
Sequences 255552-255560 and 255561-255566 represent cDNA  
sequences encoding canine interleukin-13 (IL-13) clones 80  
and 78 respectively. The invention relates to canine  
IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or  
feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline  
interferon-alpha (IFN-alpha) and feline granulocyte macrophage  
colony-stimulating factor (GM-CSF), and nucleotides which encode these  
immunoregulatory proteins. The proteins, their associated  
nucleic acids, specific antibodies and inhibitors may be used as  
vaccines for therapeutic or prophylactic regulation of an immune  
response in animals (particularly cats, dogs, horses and humans).  
They may be used to treat autoimmune or infectious diseases including  
allergies, tumours, inflammation and graft rejection, and to increase  
the response from a co-administered antigen. The nucleotide sequences  
can also be used for the recombinant production of a protein, while  
modulators of activity, while the antibodies may be used in detection,  
and in drug targeting.  
Sequence 393 BP; 82 A; 100 C; 118 G; 93 T; 0 other;

Query Match 96.7%; Score 377; DB 21; Length 393;  
Best Local Similarity 99.2%; Pred. No. 1e-98;  
Matches 390; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 1 atggcgctctggtgactgtggtcattgctctacctgcctcggtgacctgctcccg 60  
|||||  
DB 393 ATGGCGCTCTGGTTGACTGTGGTCAATTGCTCTCACCTGCCTCGGTGGCCTGCCCTCCCG 334  
61 agccctgtgactccctcccaaccctcaaggagctcattgaggagctggtcaacatcacc 120  
|||||  
DB 333 AGCCCTGTGACTCCCTCCCAACCCCTCAAGGAGCTCATTGAGGAGCTGGTCAACATCACC 274  
121 cagaatcaggatccctctgcaacggcagcatggtgtggagcgtcaacctgaccgcggc 180  
|||||  
DB 273 CAGAATCAGGCATCCCTCTGCAACGGCAGCATGCTGTGGAGCGTCAACCTGACCGCCGC 214

QY 181 atgtactgcgagctctagaatctctgatcaatgtctccgactgcagcgcatccaaagg 240  
|||||  
DB 213 ATGTACTGCGCAGCTCTAGAATCTCTGATCAATGTCTCCGACTGCAGCGCATCCAAAGG 154  
QY 241 acccagagatgctgaaagcactgtgctctcaaaagcccgcgagg---gatttccagt 297  
|||||  
DB 153 ACCCAGAGGATGCTGAAAGCACTGTGCTCTCAAAAGCCCGCGGCGGCGAGATTCCAGT 94  
QY 298 gaacgcagcgagacacacaaaattgaagtgtatccagttggtgaaaaaacctgtcacctat 357  
|||||  
DB 93 GAACGCAGCGGAGACACCAAAATTGAAGTGATCCAGTTGGTGAAAAACCTGCTCACCTAT 34  
QY 358 gtaaggaggagtttatcgccatggaaatttcaga 390  
|||||  
DB 33 GTAAGGGGAGTTTATCGCCATGGAAATTTTCAGA 1  
RESULT 7  
ID 255555 standard; cDNA; 1302 BP.  
XX 255555;  
AC 255555;  
DT 14-MAR-2000 (first entry)  
XX Canine interleukin-13 (IL-13) clone 80 cDNA.  
DE Canine interleukin-13 (IL-13) clone 80 cDNA.  
XX Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;  
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.  
KW Canis familiaris.  
OS  
XX  
XX Key Location/Qualifiers  
FH 52..447  
FT /\*tag= a  
FT /product= "Canine IL-13 clone 80"  
XX WO9961618-A2.  
PN 02-DEC-1999.  
PD 28-MAY-1999; 99WO-US11942.  
XX 29-MAY-1998; 98US-0087306.  
PR (HESK-) HESKA CORP.  
XX  
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;  
XX WPI; 2000-072623/06.  
DR P-PSDB; Y58221.  
XX  
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
useful for treating or preventing e.g. tumors or autoimmune disease  
XX Claim 1i; Page 229-230; 264pp; English.  
PS  
XX Sequences 255552-255560 and 255561-255566 represent cDNA  
sequences encoding canine interleukin-13 (IL-13) clones 80  
and 78 respectively. The invention relates to canine  
IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or  
feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline  
interferon-alpha (IFN-alpha) and feline granulocyte macrophage  
colony-stimulating factor (GM-CSF), and nucleotides which encode these  
immunoregulatory proteins. The proteins, their associated  
nucleic acids, specific antibodies and inhibitors may be used as  
vaccines for therapeutic or prophylactic regulation of an immune  
response in animals (particularly cats, dogs, horses and humans).  
They may be used to treat autoimmune or infectious diseases including  
allergies, tumours, inflammation and graft rejection, and to increase  
the response from a co-administered antigen. The nucleotide sequences  
can also be used for the recombinant production of a protein, while  
modulators of activity, while the antibodies may be used in detection,  
and in drug targeting.  
Sequence 393 BP; 82 A; 100 C; 118 G; 93 T; 0 other;



CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
CC The proteins may be used to raise antibodies and to screen for  
CC modulators of activity, while the antibodies may be used in detection,  
CC and in drug targeting.

XX Sequence 1302 BP; 337 A; 318 C; 340 G; 307 T; 0 other;

Query Match 96.7%; Score 377; DB 21; Length 1302;  
Best Local Similarity 99.2%; Pred. No. 1.5e-98;  
Matches 390; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 1 atggcgctctggtgactggtgattgctctcaccctgcctcgtggtgacctgctcccg 60  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 52 atggcgctctggtgactggtgattgctctcaccctgcctcgtggtgacctgctcccg 111  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 61 agccctgtgactccctcccaaccctcaaggagctcattgaggagctggtcaacatcacc 120  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 112 agccctgtgactccctcccaaccctcaaggagctcattgaggagctggtcaacatcacc 171  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 121 cagaatcaggcatccctctgcaacggcagcatggtgtggagctgcaacctgaccgccgc 180  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 172 cagaatcaggcatccctctgcaacggcagcatggtgtggagctgcaacctgaccgccgc 231  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 181 atgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgccatccaaagg 240  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 232 atgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgccatccaaagg 291  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 241 acccagaggatgctgaaagcactgtgctctcctcaaaagcccgccagg---gatttcaggt 297  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 292 acccagaggatgctgaaagcactgtgctctcctcaaaagcccgccaggcagatttcaggt 351  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 298 gaacgcagcgcagacacccaaattgaagtgtccagttggtgaaacacctgtcacctat 357  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 352 gaacgcagcgcagacacccaaattgaagtgtccagttggtgaaacacctgtcacctat 411  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 358 gtaaggggagtttatcgccatggaatttcaga 390  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 412 gtaaggggagtttatcgccatggaatttcaga 444  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

RESULT 8  
Z55556/C  
ID Z55556 standard; cDNA; 1302 BP.  
XX Z55556;  
AC Z55556;  
XX Z55556;  
DT 14-MAR-2000 (first entry)  
XX Canine interleukin-13 (IL-13) clone 80 cDNA complement.  
DE Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;  
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.  
XX Canis familiaris.  
OS Key Location/Qualifiers  
FH complement (856..1251)  
FT /\*tag= a  
FT /product= "Canine IL-13 clone 80"  
XX WO9961618-A2.  
PN 02-DEC-1999.  
XX 28-MAY-1999; 99WO-US11942.  
XX 29-MAY-1998; 98US-0087306.  
PR (HESK-) HESKA CORP.  
PA Sim G, Yang S, Dreitz MJ, Wonderling RS;  
PI  
XX

DR WPI; 2000-072623/06.  
DR P-PSDB; Y58221.  
XX  
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
PT useful for treating or preventing e.g. tumors or autoimmune disease  
XX  
PS Claim 1i; Page 231-232; 264pp; English.  
XX

CC Sequences Z55552-Z55560 and Z55561-Z55566 represent cDNA  
CC sequences encoding canine interleukin-13 (IL-13) clones 80  
CC and 78 respectively. The invention relates to canine  
CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or  
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline  
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage  
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these  
CC immunoregulatory proteins. The proteins, and inhibitors associated  
CC nucleic acids, specific antibodies and inhibitors may be used as  
CC vaccines for therapeutic or prophylactic regulation of an immune  
CC response in animals (particularly cats, dogs, horses and humans).  
CC They may be used to treat autoimmune or infectious diseases including  
CC allergies, tumours, inflammation and graft rejection, and to increase  
CC the response from a co-administered antigen. The nucleotide sequences  
CC can also be used for the recombinant production of a protein, while  
CC nucleotide fragments are useful as probes, as amplification primers and  
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
CC The proteins may be used to raise antibodies and to screen for  
CC modulators of activity, while the antibodies may be used in detection,  
CC and in drug targeting.  
XX  
SQ Sequence 1302 BP; 307 A; 340 C; 318 G; 337 T; 0 other;

Query Match 96.7%; Score 377; DB 21; Length 1302;  
Best Local Similarity 99.2%; Pred. No. 1.5e-98;  
Matches 390; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 1 atggcgctctggtgactggtgattgctctcaccctgcctcgtggtgacctgctcccg 60  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 1251 ATGGCGCTCTGGTTGACTGTGGTTCATTGCTCTCACCTCGCTCGGTGGCCTGCCCG 1192  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 61 agccctgtgactccctcccaaccctcaaggagctcattgaggagctggtcaacatcacc 120  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 1191 AGCCCTGTGACTCCCTCCCCAACCCCTCAAGGAGCTCATGTAGGAGCTGGTCAACATCACC 1132  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 121 cagaatcaggcatccctctgcaacggcagcatggtgtggagctgcaacctgaccgccgc 180  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 1131 CAGAATCAGGCATCCCTCTGCAACGGCAGCATGGTGTGAGCGTCAACCTGACCGCGGC 1072  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 181 atgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgccatccaaagg 240  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 1071 ATGTACTGCGCAGCTCTAGAATCTCTGATCAATGTCTCCGACTGCAGCGCCATCCCAAAG 1012  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 241 acccagaggatgctgaaagcactgtgctctcctcaaaagcccgccagg---gatttcaggt 297  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 1011 ACCCAGAGGATGCTGAAAGCAGCTGTGCTCTCAAAAGCCCGCGGCGAGATTTCCAGT 952  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 298 gaacgcagcgcagacacccaaattgaagtgtccagttggtgaaacacctgtcacctat 357  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 951 GAACGCAGCGGAGACACCAAATTTGAAGTGATCCAGTTGGTGAAAAAACCTGCTCACCTAT 892  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 358 gtaaggggagtttatcgccatggaatttcaga 390  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 891 GTAAGGGGAGTTTATCGCCCATGGAATTTTCAGA 859  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

RESULT 9  
Z55565  
ID Z55565 standard; cDNA; 330 BP.  
XX  
AC Z55565;  
XX  
DT 14-MAR-2000 (first entry)  
XX



DE Canine mature interleukin-13 (IL-13) clone 78 cDNA.  
XX Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;  
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.  
KW  
XX Canis familiaris.  
OS  
XX  
PN WO9961618-A2.  
XX  
PD 02-DEC-1999.  
XX  
XX 28-MAY-1999; 99WO-US11942.  
PF  
XX 29-MAY-1998; 98US-0087306.  
PR  
XX (HESK-) HESKA CORP.  
PA  
XX Sim G, Yang S, Dreitz MJ, Wonderling RS;  
PI WPI; 2000-072623/06.  
XX P-PSDB; Y58224.  
DR  
XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
PT useful for treating or preventing e.g. tumors or autoimmune disease  
PT  
XX Claim 1i; Page 239-240; 264pp; English.  
PS  
XX Sequences 255552-255560 and 255561-255566 represent cDNA  
CC sequences encoding canine interleukin-13 (IL-13) clones 80  
CC and 78 respectively. The invention relates to canine  
CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or  
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline  
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage  
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these  
CC immunoregulatory proteins. The proteins, their associated  
CC nucleic acids, specific antibodies and inhibitors may be used as  
CC vaccines for therapeutic or prophylactic regulation of an immune  
CC response in animals (particularly cats, dogs, horses and humans).  
CC They may be used to treat autoimmune or infectious diseases including  
CC allergies, tumours, inflammation and graft rejection, and to increase  
CC the response from a co-administered antigen. The nucleotide sequences  
CC can also be used for the recombinant production of a protein, while  
CC nucleotide fragments are useful as probes, as amplification primers and  
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
CC The proteins may be used to raise antibodies and to screen for  
CC modulators of activity, while the antibodies may be used in detection,  
CC and in drug targeting.  
XX  
SQ Sequence 330 BP; 88 A; 96 C; 82 G; 64 T; 0 other;

Query Match 84.6%; Score 330; DB 21; Length 330;  
Best Local Similarity 100.0%; Pred. No. 2.7e-85;  
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 agccctgtgactccctccccaaccctcaaggagctcattgaggagctggtcaacatcacc 120  
DB 1 agccctgtgactccctccccaaccctcaaggagctcattgaggagctggtcaacatcacc 60

QY 121 cagaatcaggcatccctctgcaacggcaggcatggtgtggagcgtcaacctgaccgcgggc 180  
DB 61 cagaatcaggcatccctctgcaacggcaggcatggtgtggagcgtcaacctgaccgcgggc 120

QY 181 atgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgcacatccaaagg 240  
DB 121 atgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgcacatccaaagg 180

QY 241 acccagaggatgctgaaagcactgtgtctctcaaaaagcccgccggcaggattccagtga 300  
DB 181 acccagaggatgctgaaagcactgtgtctctcaaaaagcccgccggcaggattccagtga 240

QY 301 cgcagccgagacaccaaattgaagtatccagttggtgaaaaaacctgctcacctatgta 360  
DB 121 cgcagccgagacaccaaattgaagtatccagttggtgaaaaaacctgctcacctatgta 360

Db 241 cgcagccgagacaccaaattgaagtatccagttggtgaaaaaacctgctcacctatgta 300  
QY 361 aggggagtttatcgcccatggaatttcaga 390  
DB 301 aggggagtttatcgcccatggaatttcaga 330

RESULT 10  
Z55566/c  
ID Z55566 standard; cDNA; 330 BP.  
XX  
AC Z55566;  
XX  
DT 14-MAR-2000 (first entry)  
XX  
DE Canine mature interleukin-13 (IL-13) clone 78 cDNA complement.  
XX  
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;  
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.  
XX  
OS Canis familiaris.  
XX  
PN WO9961618-A2.  
XX  
PD 02-DEC-1999.  
XX  
PF 28-MAY-1999; 99WO-US11942.  
XX  
PR 29-MAY-1998; 98US-0087306.  
XX  
PA (HESK-) HESKA CORP.  
XX  
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;  
XX WPI; 2000-072623/06.  
DR P-PSDB; Y58224.  
XX  
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
PT useful for treating or preventing e.g. tumors or autoimmune disease  
XX  
PS Claim 1i; Page 241; 264pp; English.  
XX  
CC Sequences 255552-255560 and 255561-255566 represent cDNA  
CC sequences encoding canine interleukin-13 (IL-13) clones 80  
CC and 78 respectively. The invention relates to canine  
CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or  
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline  
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage  
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these  
CC immunoregulatory proteins. The proteins, their associated  
CC nucleic acids, specific antibodies and inhibitors may be used as  
CC vaccines for therapeutic or prophylactic regulation of an immune  
CC response in animals (particularly cats, dogs, horses and humans).  
CC They may be used to treat autoimmune or infectious diseases including  
CC allergies, tumours, inflammation and graft rejection, and to increase  
CC the response from a co-administered antigen. The nucleotide sequences  
CC can also be used for the recombinant production of a protein, while  
CC nucleotide fragments are useful as probes, as amplification primers and  
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
CC The proteins may be used to raise antibodies and to screen for  
CC modulators of activity, while the antibodies may be used in detection,  
CC and in drug targeting.  
XX  
SQ Sequence 330 BP; 64 A; 82 C; 96 G; 88 T; 0 other;

Query Match 84.6%; Score 330; DB 21; Length 330;  
Best Local Similarity 100.0%; Pred. No. 2.7e-85;  
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 agccctgtgactccctccccaaccctcaaggagctcattgaggagctggtcaacatcacc 120  
DB 330 AGCCCTGTGACTCCCTCCCAACCCCTCAAGGAGCTCATTTGAGGAGCTGGTCAACATCACC 271

QY 121 cagaatcaggcatccctctgcaacggcagcatggtgtgagcgtcaacctgaccgcggc 180  
|||||  
Db 270 CAGAAATCAGGCATCCCTCTGCAACGGCAGCATGGTGTGGAGCGTCAACCTGACCGCGGC 211  
|||||  
QY 181 atgtactgcgcagctctagaaatctctgatcaatgtctccgactgcagcgccatccaaaagg 240  
|||||  
Db 210 ATGTACTGCGCAGCTCTAGAAATCTCTGATCAATGTCTCCGACTGCAGCGCCATCCAAAG 151  
|||||  
QY 241 acccagaggtgctgaaagcactgtgctctcaaaaagcccgaggcaggtttccagtgaa 300  
|||||  
Db 150 ACCCAGAGGATGCTGAAAGCACTGTGCTCTCAAAAGCCCGGCGGAGGATTCCAGTGAA 91  
|||||  
QY 301 cgcagccgagacacacaaattgaagtgtatccagttggtgaaaaaacctgtcacctatgta 360  
|||||  
Db 90 CGCAGCCGAGACACCAAAATTGAAGTGATCCAGTTGGTGAAAAACCTGCTCACCTATGTA 31  
|||||  
QY 361 aggggagtttatcgccatggaatttcaga 390  
|||||  
Db 30 AGGGGAGTTTATCGCCATGGAAATTTTCAGA 1  
|||||  
RESULT 11  
Z55559  
ID Z55559 standard; cDNA; 333 BP.  
XX  
AC Z55559;  
XX  
DT 14-MAR-2000 (first entry)  
XX  
DE Canine mature interleukin-13 (IL-13) clone 80 cDNA.  
XX  
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;  
immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.  
XX  
OS Canis familiaris.  
XX  
PN WO9961618-A2.  
XX  
PD 02-DEC-1999.  
XX  
PF 28-MAY-1999; 99WO-US11942.  
XX  
PR 29-MAY-1998; 98US-0087306.  
XX  
PA (HESK-) HESKA CORP.  
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;  
XX  
WPI; 2000-072623/06.  
DR P-PSDB; Y58222.  
XX  
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
useful for treating or preventing e.g. tumors or autoimmune disease  
XX  
PS Claim 11; Page 233-234; 264pp; English.  
XX  
CC Sequences Z55552-Z55560 and Z55561-255566 represent cDNA  
sequences encoding canine interleukin-13 (IL-13) clones 80  
and 78 respectively. The invention relates to canine  
IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or  
feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline  
interferon-alpha (IFN-alpha) and feline granulocyte macrophage  
colony-stimulating factor (GM-CSF), and nucleotides which encode these  
immunoregulatory proteins. The proteins, their associated  
nucleic acids, specific antibodies and inhibitors may be used as  
vaccines for therapeutic or prophylactic regulation of an immune  
response in animals (particularly cats, dogs, horses and humans).  
They may be used to treat autoimmune or infectious diseases including  
allergies, tumours, inflammation and graft rejection, and to increase  
the response from a co-administered antigen. The nucleotide sequences  
can also be used for the recombinant production of a protein, while  
nucleotide fragments are useful as probes, as amplification primers and

CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
CC The proteins may be used to raise antibodies and to screen for  
CC modulators of activity, while the antibodies may be used in detection,  
CC and in drug targeting.  
XX  
SQ Sequence 333 BP; 89 A; 97 C; 83 G; 64 T; 0 other;  
Query Match 81.3%; Score 317; DB 21; Length 333;  
Best Local Similarity 99.1%; Pred. No. 1.4e-81;  
Matches 330; Conservative 0; Mismatches 0; Indels 3; Gaps 1;  
QY 61 agccctgtgactccctcccccacccctcaaggagctcattgaggagctggtcaacatcacc 120  
|||||  
Db 1 agccctgtgactccctcccccacccctcaaggagctcattgaggagctggtcaacatcacc 60  
|||||  
QY 121 cagaatcaggcatccctctgcaacggcagcatggtgtggagcgtcaacctgaccgcggc 180  
|||||  
Db 61 cagaatcaggcatccctctgcaacggcagcatggtgtggagcgtcaacctgaccgcggc 120  
|||||  
QY 181 atgtactgcgcagctctagaaatctctgatcaatgtctccgactgcagcgccatccaaaagg 240  
|||||  
Db 121 atgtactgcgcagctctagaaatctctgatcaatgtctccgactgcagcgccatccaaaagg 180  
|||||  
QY 241 acccagaggtgctgaaagcactgtgtctctcaaaaagcccgagg---gatttcacgt 297  
|||||  
Db 181 acccagaggtgctgaaagcactgtgtctctcaaaaagcccgaggcagatttcacgt 240  
|||||  
QY 298 gaacgcagcgcagacacacaaaattgaagtgtccagttggtgaaaaaacctgtcacctat 357  
|||||  
Db 241 gaacgcagcgcagacacacaaaattgaagtgtccagttggtgaaaaaacctgtcacctat 300  
|||||  
QY 358 gtaaggggagtttatcgccatggaatttcaga 390  
|||||  
Db 301 gtaaggggagtttatcgccatggaatttcaga 333  
|||||  
RESULT 12  
Z55560/c  
ID Z55560 standard; cDNA; 333 BP.  
XX  
AC Z55560;  
XX  
DT 14-MAR-2000 (first entry)  
XX  
DE Canine mature interleukin-13 (IL-13) clone 80 cDNA complement.  
XX  
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;  
immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.  
XX  
OS Canis familiaris.  
XX  
PN WO9961618-A2.  
XX  
PD 02-DEC-1999.  
XX  
PF 28-MAY-1999; 99WO-US11942.  
XX  
PR 29-MAY-1998; 98US-0087306.  
XX  
PA (HESK-) HESKA CORP.  
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;  
XX  
WPI; 2000-072623/06.  
DR P-PSDB; Y58222.  
XX  
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
useful for treating or preventing e.g. tumors or autoimmune disease  
XX  
PS Claim 11; Page 235; 264pp; English.  
XX  
CC Sequences Z55552-Z55560 and Z55561-255566 represent cDNA

sequences encoding canine interleukin-13 (IL-13) clones 80 and 78 respectively. The invention relates to canine IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline interferon-alpha (IFN-alpha), and feline granulocyte macrophage colony-stimulating factor (GM-CSF), and nucleotides which encode these immunoregulatory proteins. The proteins, their associated nucleic acids, specific antibodies and inhibitors may be used as vaccines for therapeutic or prophylactic regulation of an immune response in animals (particularly cats, dogs, horses and humans). They may be used to treat autoimmune or infectious diseases including allergies, tumours, inflammation and graft rejection, and to increase the response from a co-administered antigen. The nucleotide sequences can also be used for the recombinant production of a protein, while nucleotide fragments are useful as probes, as amplification primers and as sources of inhibitory therapeutics (e.g., antisense oligonucleotides). The proteins may be used to raise antibodies and to screen for modulators of activity, while the antibodies may be used in detection, and in drug targeting.

Sequence 333 BP; 64 A; 83 C; 97 G; 89 T; 0 other;

Query Match 81.3%; Score 317; DB 21; Length 333;  
Best Local Similarity 99.1%; Pred. No. 1.4e-81;  
Matches 330; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 61 agccctgtgactccctcccaacccctcaaggagctcattgaggagctggtcaacatcacc 120  
|||||  
Db 333 AGCCCTGTGACTCCCTCCCAACCCCTCAAGGAGCTCATTGAGGAGCTGGTCAACATCACC 274  
|||||  
QY 121 cagaatcaggcatccctctgcaacggcagcatggtgtggagcgtcaacctgaccgcggc 180  
|||||  
Db 273 CAGAATCAGGATCCCTCTGCAACGGCAGCATGTTGTGGAGCGTCAACCTGACCCCGGC 214  
|||||  
QY 181 atgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgccatccaaaagg 240  
|||||  
Db 213 ATGTACTGGCAGCTCTAGAAATCTCTGATCAATGTCTCCGACTGCAGCGCCATCCAAAGG 154  
|||||  
QY 241 acccagagatgctgaaagcactgtgctctcaaaagcccgcgagg--gattccagt 297  
|||||  
Db 153 ACCCAGAGATGCTGAAAGCACTGTGCTCTCAAAAGCCCGCGGCGAGGCAGATTTCAGT 94  
|||||  
QY 298 gaacgcagcgcagacacacaaaattgaagtgatccagttggtgaaaaacctgctcacctat 357  
|||||  
Db 93 GAACGCAGCCGAGACACCAAAATTGAAGTGATCCAGTTGGTGAAAAACCTGCTCACCTAT 34  
|||||  
QY 358 gtaagggagtttatcgccatggaaaatttcaga 390  
|||||  
Db 33 GTAAGGGAGTTTATCGCCCATGGAAATTTTCAGA 1  
|||||

RESULT 13  
Z55554  
ID Z55554 standard; cDNA; 278 BP.  
XX  
AC Z55554;  
XX  
DT 14-MAR-2000 (first entry)  
XX  
DE Canine interleukin-13 (IL-13) cDNA probe.  
XX  
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;  
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.  
XX  
OS Canis familiaris.  
XX  
PN WO9961618-A2.  
XX  
XX 02-DEC-1999.  
PD  
XX 28-MAY-1999; 99WO-US11942.  
PF  
XX

29-MAY-1998; 98US-0087306.  
(HESK-) HESKA CORP.  
Sim G, Yang S, Dreitz MJ, Wonderling RS;  
WPI; 2000-072623/06.  
Nucleic acids encoding immunoregulatory proteins from cats or dogs, useful for treating or preventing e.g. tumors or autoimmune disease  
Claim 1i; Page 229; 264pp; English.  
Sequences Z55552-Z55560 and Z55561-Z55566 represent cDNA sequences encoding canine interleukin-13 (IL-13) clones 80 and 78 respectively. The invention relates to canine IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline interferon-alpha (IFN-alpha) and feline granulocyte macrophage colony-stimulating factor (GM-CSF), and nucleotides which encode these immunoregulatory proteins. The proteins, their associated nucleic acids, specific antibodies and inhibitors may be used as vaccines for therapeutic or prophylactic regulation of an immune response in animals (particularly cats, dogs, horses and humans). They may be used to treat autoimmune or infectious diseases including allergies, tumours, inflammation and graft rejection, and to increase the response from a co-administered antigen. The nucleotide sequences can also be used for the recombinant production of a protein, while nucleotide fragments are useful as probes, as amplification primers and as sources of inhibitory therapeutics (e.g., antisense oligonucleotides). The proteins may be used to raise antibodies and to screen for modulators of activity, while the antibodies may be used in detection, and in drug targeting.

Sequence 278 BP; 58 A; 93 C; 69 G; 58 T; 0 other;

Query Match 71.3%; Score 278; DB 21; Length 278;  
Best Local Similarity 100.0%; Pred. No. 1.9e-70;  
Matches 278; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atggcgctctggtgactggtggtcattgtctctcacctgcctcggtggcctgcctccccg 60  
|||||  
Db 1 atggcgctctggtgactggtggtcattgtctctcacctgcctcggtggcctgcctccccg 60  
|||||  
QY 61 agccctgtgactccctcccaacccctcaaggagctcattgaggagctggtcaacatcacc 120  
|||||  
Db 61 agccctgtgactccctcccaacccctcaaggagctcattgaggagctggtcaacatcacc 120  
|||||  
QY 121 cagaatcaggcatccctctgcaacggcagcatggtgtggagcgtcaacctgaccgcggc 180  
|||||  
Db 121 cagaatcaggcatccctctgcaacggcagcatggtgtggagcgtcaacctgaccgcggc 180  
|||||  
QY 181 atgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgccatccaaaagg 240  
|||||  
Db 181 atgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgccatccaaaagg 240  
|||||  
QY 241 acccagagatgctgaaagcactgtgtgtcttcaaaaagcc 278  
|||||  
Db 241 acccagagatgctgaaagcactgtgtgtcttcaaaaagcc 278  
|||||

RESULT 14  
Z55553  
ID Z55553 standard; cDNA; 272 BP.  
XX  
AC Z55553;  
XX  
DT 14-MAR-2000 (first entry)  
XX  
DE Canine interleukin-13 (IL-13) cDNA fragment nCaIL13-272.  
XX  
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;



KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.  
XX  
OS Canis familiaris.  
XX  
PN WO9961618-A2.  
XX  
PD 02-DEC-1999.  
XX  
XX 28-MAY-1999; 99WO-US11942.  
PF  
XX 29-MAY-1998; 98US-0087306.  
PR  
XX (HESK-) HESKA CORP.  
PA  
XX  
PI Slim G, Yang S, Dreitz MJ, Wonderling RS;  
XX  
XX WPI; 2000-072623/06.  
DR  
XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
PT useful for treating or preventing e.g. tumors or autoimmune disease  
PT  
XX  
PS Claim 11; Page 228; 264pp; English.  
XX  
CC Sequences Z55552-Z55560 and Z55561-Z55566 represent cDNA  
CC sequences encoding canine interleukin-13 (IL-13) clones 80  
CC and 78 respectively. The invention relates to canine  
CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or  
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline  
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage  
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these  
CC immunoregulatory proteins. The proteins, their associated  
CC nucleic acids, specific antibodies and inhibitors may be used as  
CC vaccines for therapeutic or prophylactic regulation of an immune  
CC response in animals (particularly cats, dogs, horses and humans).  
CC They may be used to treat autoimmune or infectious diseases including  
CC allergies, tumours, inflammation and graft rejection, and to increase  
CC the response from a co-administered antigen. The nucleotide sequences  
CC can also be used for the recombinant production of a protein, while  
CC nucleotide fragments are useful as probes, as amplification primers and  
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
CC The proteins may be used to raise antibodies and to screen for  
CC modulators of activity, while the antibodies may be used in detection,  
CC and in drug targeting.  
XX  
SQ Sequence 272 BP; 64 A; 91 C; 69 G; 48 T; 0 other;

Query Match 65.6%; Score 256; DB 21; Length 272;  
Best Local Similarity 98.9%; Pred. No. 3.8e-64;  
Matches 269; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 45 tggccttgccctcccgagccctgtgactccctcccccacccctcaaggagctcattgagga 104  
|||||  
Db 1 tggccttgccctcccgagccctgtgactccctcccccacccctcaaggagctcattgagga 60  
QY 105 gctggtcaacatcacccagaatcaggcatccctctgcaacggcgagcatggtgtggagcgt 164  
|||||  
Db 61 gctggtcaacatcacccagaatcaggcatccctctgcaacggcgagcatggtgtggagcgt 120  
QY 165 caacctgaccgcccgtactgtactgcgcagctctagaaatctctgatcaatgtctccgactg 224  
|||||  
Db 121 caacctgaccgcccgtactgtactgcgcagctctagaaatctctgatcaatgtctccgactg 180  
QY 225 cagcgccatccaaaggaccagaggatgctgaaagcactgtgctctcaaaagccccgcgc 284  
|||||  
Db 181 cagcgccatccaaaggaccagaggatgctgaaagcactgtgctctcaaaagccccgcgc 240  
QY 285 agg---gatttccagtaacgcagccgagaca 313  
|||  
Db 241 agggcagatttccagtaacgcagccgagaca 272

RESULT 15.

F21334  
ID F21334 standard; DNA; 1270 BP.  
XX  
AC F21334;  
XX  
DT 14-MAR-2001 (first entry)  
XX  
DE Human low adenosine antisense oligonucleotide related sequence #2901.  
XX  
KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;  
KW human; airway disorder; bronchoconstriction; lung inflammation;  
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;  
KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;  
KW respiratory obstruction; pulmonary obstruction; impeded respiration;  
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;  
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;  
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;  
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;  
KW cancer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200062736-A2.  
XX  
PD 26-OCT-2000.  
XX  
PF 24-MAR-2000; 2000WO-US08020.  
XX  
PR 06-APR-1999; 99US-0127958.  
XX  
PA (UYEC-) UNIV EAST CAROLINA.  
PA (NYCE/) NYCE J W.  
XX  
PI Nyce JW;  
XX  
DR WPI; 2000-679539/66.  
XX  
PT Low adenosine (A) content antisense oligonucleotides which do not  
PT trigger adenosine receptors during metabolism, useful e.g. for treating  
PT cancers and respiratory obstructions -  
XX  
PS Disclosure; Page 1336; 1592pp; English.  
XX  
CC The present invention describes low adenosine (A) content antisense  
CC oligonucleotides and compositions (I) comprising them. In the antisense  
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.  
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,  
CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.  
CC The antisense oligonucleotides and (I) can be used to down-regulate the  
CC expression and or activity of target polypeptides associated with  
CC lung/respiratory disorders and malignancies, such as stimulating and  
CC activating peptide factors and transmitters, transcription factors,  
CC immunoglobulins and antibodies, antibody receptors, cytokines and  
CC chemokines, endogenously produced specific and non-specific enzymes,  
CC binding proteins, adhesion molecules and their receptors, cytokine and  
CC chemokine receptors, adenosine receptors, bradykinin receptors, central  
CC nervous system (CNS) and peripheral nervous and non-nervous system  
CC transmitters, defensins, growth factors, vasoactive peptides and  
CC receptors, binding proteins and malignancy associated proteins. The  
CC antisense oligonucleotides may be used in this way to treat disorders  
CC including respiratory obstruction (especially pulmonary obstruction  
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)  
CC and/or surfactant hypoproduction which are associated with a disease or  
CC condition selected from pulmonary vasoconstriction, inflammation,  
CC allergies, asthma, impeded respiration, respiratory distress syndrome  
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary  
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),  
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,  
CC and/or cancer. F18434 to F21543 represent human polynucleotide fragments  
CC and antisense oligonucleotides used in the exemplification of the  
CC present invention.  
XX





GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: May 13, 2001, 14:21:41 ; Search time 226.02 Seconds  
(without alignments)  
301.279 Million cell updates/sec

Title: US-09-451-527-102  
Perfect score: 390  
Sequence: 1 atggcgctctgttgactgt.....atcgccatggaatttcaga 390

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 302621 seqs, 87301344 residues

Total number of hits satisfying chosen parameters: 605242

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_NA:\*  
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2: /cgnl\_7/ptodata/1/ina/5B\_COMB.seq:\*  
3: /cgnl\_7/ptodata/1/ina/6A\_COMB.seq:\*  
4: /cgnl\_7/ptodata/1/ina/6B\_COMB.seq:\*  
5: /cgnl\_7/ptodata/1/ina/PCTUS\_COMB.seq:\*  
6: /cgnl\_7/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	230.8	59.2	1290	1 US-08-012-543-1	Sequence 1, Appli
2	230.8	59.2	1290	5 PCT-US93-07645A-1	Sequence 1, Appli
3	230.8	59.2	1290	5 PCT-US93-07645-1	Sequence 1, Appli
4	229.2	58.8	1297	1 US-08-371-121-15	Sequence 15, Appli
5	188	48.2	384	1 US-08-371-121-17	Sequence 17, Appli
6	187.4	48.1	336	1 US-08-371-121-24	Sequence 24, Appli
7	186.2	47.7	425	1 US-08-594-469-4	Sequence 4, Appli
8	186.2	47.7	425	2 US-08-906-957-4	Sequence 4, Appli
9	186.2	47.7	4410	1 US-08-594-469-1	Sequence 1, Appli
10	186.2	47.7	4410	2 US-08-906-957-1	Sequence 1, Appli
11	185.8	47.6	336	1 US-08-371-121-2	Sequence 2, Appli
12	168.6	43.2	447	1 US-08-371-121-26	Sequence 26, Appli
13	168.6	43.2	1212	1 US-08-012-543-3	Sequence 3, Appli
14	168.6	43.2	1212	5 PCT-US93-07645A-3	Sequence 3, Appli
15	168.6	43.2	1212	5 PCT-US93-07645-3	Sequence 3, Appli
16	44.6	11.4	60	1 US-08-371-121-12	Sequence 12, Appli
17	44.6	11.4	102	1 US-08-371-121-10	Sequence 10, Appli
18	39.6	10.2	54	1 US-08-371-121-11	Sequence 11, Appli
19	39.6	10.2	96	1 US-08-371-121-9	Sequence 9, Appli
20	35.8	9.2	2249	3 US-08-814-052-19	Sequence 19, Appli
21	35.8	9.2	2300	3 US-08-814-052-18	Sequence 18, Appli
22	35.8	9.2	3183	2 US-08-939-218A-1	Sequence 1, Appli
23	35.8	9.2	3187	5 PCT-US95-05815-1	Sequence 1, Appli
24	35.8	9.2	3192	1 US-08-706-037-26	Sequence 26, Appli
25	35.8	9.2	3192	1 US-08-940-661A-1	Sequence 1, Appli
26	35.8	9.2	3192	2 US-09-083-485-1	Sequence 1, Appli
27	35.8	9.2	3192	2 US-09-005-397-26	Sequence 26, Appli

28	34.4	8.8	1322	4 US-09-128-450-27	Sequence 27, Appli
29	34.4	8.8	1521	1 US-08-496-855A-3	Sequence 3, Appli
30	34.4	8.8	1521	2 US-07-938-154-9	Sequence 9, Appli
31	34.4	8.8	1521	5 PCT-US91-02311-9	Sequence 9, Appli
32	34.4	8.8	2450	2 US-08-466-589-9	Sequence 9, Appli
33	34.4	8.8	2450	2 US-08-700-636-9	Sequence 9, Appli
34	34.4	8.8	2450	3 US-08-467-574-9	Sequence 9, Appli
35	33.2	8.5	2712	3 US-09-025-691-4	Sequence 4, Appli
36	32.4	8.3	720	4 US-09-094-359-3	Sequence 3, Appli
37	32.4	8.3	720	4 US-09-094-359-7	Sequence 7, Appli
38	32.4	8.3	720	4 US-09-172-063-11	Sequence 11, Appli
39	32.4	8.3	720	4 US-09-172-063-13	Sequence 13, Appli
40	32.4	8.3	762	1 US-08-532-390-40	Sequence 40, Appli
41	32.4	8.3	762	4 US-08-717-294-40	Sequence 40, Appli
42	32.4	8.3	768	4 US-09-094-359-11	Sequence 11, Appli
43	32.4	8.3	850	4 US-09-062-102-2	Sequence 2, Appli
44	32.4	8.3	972	4 US-09-172-063-27	Sequence 27, Appli
45	32.4	8.3	972	4 US-09-172-063-29	Sequence 29, Appli

ALIGNMENTS

RESULT 1  
US-08-012-543-1  
; Sequence 1, Application US/08012543  
; Patent No. 5596072  
; GENERAL INFORMATION:  
; APPLICANT: Culpepper, Janice  
; APPLICANT: McKenzie, Andrew  
; APPLICANT: Dang, Warren  
; APPLICANT: de Waal Malefyt, Rene  
; APPLICANT: Heath, Andrew  
; APPLICANT: Aversa, Gregorio  
; APPLICANT: Briere, Francine  
; APPLICANT: Banchereau, Jacques  
; APPLICANT: de Vries, Jan  
; APPLICANT: Zurawski, Gerard  
; TITLE OF INVENTION: Human Interleukin-13  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/012,543  
; FILING DATE: 01-FEB-1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/933,416  
; FILING DATE: 21-AUG-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0302K1  
; TELEPHONE: 415-852-9196  
; TELEFAX: 415-496-1200  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1290 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA

FEATURE:
NAME/KEY: CDS
LOCATION: 45..443
US-08-012-543-1

Query Match
Best Local Similarity 59.2%; Score 230.8; DB 1; Length 1290;
Matches 306; Conservative 0; Mismatches 82; Indels 6; Gaps 2;

QY 1 atggcgctctggttgactgtggtcattgctctcacctgctcgtggtggtgcttgcctccccg 60
Db 45 ATGGCGCTTTTGTGACCAACGGTCATTGCTCTCACTTGCCCTGGCGGCTTGGCCTCCCCA 104
QY 61 agccctgtgactccctcccaaccctcaaggagctcattgaggagctggtcaacatcacc 120
Db 105 GGCCCTGTGCCCTCCCTCTACAGCCCTCAGGAGCTCATTTGAGGAGCTGGTCAACATCACC 164
QY 121 cagaatc---aggcatccctctgcaacggcagcatggtgtggagcgtcaacctgaccgcc 177
Db 165 CAGAACCCAGAAAGGCTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAACCTGACAGCT 224
QY 178 ggcattgactgcgcagctctagaatctctgatcaatgtctccgactgcagcgccatccaa 237
Db 225 GGCATGTACTGTGCAGCCCTGGAATCCCTGATCAACGTGTGAGGCTGCAGTGCCATCGAG 284
QY 238 aggacccagaggatgctgaaagcactgtgctctcaaaaagcccgcggcagg---gatttcc 294
Db 285 AAGACCCAGAGGATGCTGAGCGGATTTCTGCCCGCACAAAGGTCTCAGCTGGGCGAGTTTTC 344
QY 295 agtgaacgcagccgagacacacaaattgaagtgtatccagttggtgaaaaacctgctcacc 354
Db 345 AGCTTGCAATGTCGAGACACCAAAATCGAGGTGGCCCGCAGTTTGTAAAGGACCTGCTCTTA 404
QY 355 tatgtaagggagtttatcgccatggaaatttca 388
Db 405 CATTTAAAGAAACTTTTTCGCGAGGGACGGTTCA 438

RESULT 2
PCT-US93-07645A-1
; Sequence 1, Application PC/TUS9307645A
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Human Interleukin-13
; NUMBER OF SEQUENCES: 6
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.5
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07645A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/012543
; FILING DATE: 01-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/010977
; FILING DATE: 29-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/933416
; FILING DATE: 21-AUG-1992
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1290 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
PCT-US93-07645A-1

Query Match
Best Local Similarity 59.2%; Score 230.8; DB 5; Length 1290;
Matches 306; Conservative 0; Mismatches 82; Indels 6; Gaps 2;

Best Local Similarity 77.7%; Pred. No. 6.8e-62;
Matches 306; Conservative 0; Mismatches 82; Indels 6; Gaps 2;
QY 1 atggcgctctggttgactgtggtcattgctctcacctgctcgtggtggtgcttgcctccccg 60
Db 45 ATGGCGCTTTTGTGACCAACGGTCATTGCTCTCACTTGCCCTGGCGGCTTGGCCTCCCCA 104
QY 61 agccctgtgactccctcccaaccctcaaggagctcattgaggagctggtcaacatcacc 120
Db 105 GGCCCTGTGCCCTCCCTCTACAGCCCTCAGGAGCTCATTTGAGGAGCTGGTCAACATCACC 164
QY 121 cagaatc---aggcatccctctgcaacggcagcatggtgtggagcgtcaacctgaccgcc 177
Db 165 CAGAACCCAGAAAGGCTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAACCTGACAGCT 224
QY 178 ggcattgactgcgcagctctagaatctctgatcaatgtctccgactgcagcgccatccaa 237
Db 225 GGCATGTACTGTGCAGCCCTGGAATCCCTGATCAACGTGTGAGGCTGCAGTGCCATCGAG 284
QY 238 aggacccagaggatgctgaaagcactgtgctctcaaaaagcccgcggcagg---gatttcc 294
Db 285 AAGACCCAGAGGATGCTGAGCGGATTTCTGCCCGCACAAAGGTCTCAGCTGGGCGAGTTTTC 344
QY 295 agtgaacgcagccgagacacacaaattgaagtgtatccagttggtgaaaaacctgctcacc 354
Db 345 AGCTTGCAATGTCGAGACACCAAAATCGAGGTGGCCCGCAGTTTGTAAAGGACCTGCTCTTA 404
QY 355 tatgtaagggagtttatcgccatggaaatttca 388
Db 405 CATTTAAAGAAACTTTTTCGCGAGGGACGGTTCA 438

RESULT 3
PCT-US93-07645-1
; Sequence 1, Application PC/TUS9307645
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Human Interleukin-13
; NUMBER OF SEQUENCES: 6
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.5
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07645
; FILING DATE: 19930818
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/012543
; FILING DATE: 01-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/010977
; FILING DATE: 29-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/933416
; FILING DATE: 21-AUG-1992
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1290 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
PCT-US93-07645-1

Query Match
Best Local Similarity 59.2%; Score 230.8; DB 5; Length 1290;
Matches 306; Conservative 0; Mismatches 82; Indels 6; Gaps 2;
QY 1 atggcgctctggttgactgtggtcattgctctcacctgctcgtggtggtgcttgcctccccg 60
Db 45 ATGGCGCTTTTGTGACCAACGGTCATTGCTCTCACTTGCCCTGGCGGCTTGGCCTCCCCA 104







Db 122 GCATGTACTGTGCAGCCCTGGAATCCCTGATCAACGTGTTCAGGCTGCAGTGCCTCGAGA 181  
QY 239 ggaccagagagctgtaaagcactgtgctctcaaaagcccgccgagcagg--gattccca 295  
Db 182 AGACCCAGAGGATGCTGAGCGGATTCTGCCCGCACAAAGTCTCAGCTGGGCAGTTTCCA 241  
QY 296 gtgaacgcagccgagacacacaaaattgaagtgtatccagttgggtgaaacacctgctcacct 355  
Db 242 GCTTGCATGTCCGAGACACCAAAATCGAGGTGGCCAGTTTGTAAAGGACCTGCTCTTAC 301  
QY 356 atgtaaggggagtttatcccatgggaaatttca 388  
Db 302 ATTTAAAGAAACTTTTTCGCGAGGGACGGTTCA 334  
RESULT 7  
US-08-594-469-4  
; Sequence 4, Application US/08594469  
; Patent No. 5700665  
; GENERAL INFORMATION:  
; APPLICANT: LEGOUX, Richard  
; APPLICANT: MALDONADO, Paul  
; APPLICANT: SALOME, Marc  
; TITLE OF INVENTION: Method for the extraction of  
; TITLE OF INVENTION: periplasmic proteins of prokaryotic microorganisms in the  
; TITLE OF INVENTION: presence of arginine  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Bacon & Thomas  
; STREET: 625 Slaters Lane - Fourth Floor  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: USA  
; ZIP: 22314  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/594,469  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 95 01083  
; FILING DATE: 31-JAN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: FICHTER, Richard E  
; REGISTRATION NUMBER: 26,382  
; REFERENCE/DOCKET NUMBER: REF/LEGOUX  
; TELEPHONE: (703) 683-0500  
; TELEFAX: (703) 683-1080  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 425 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-594-469-4

Query Match 47.7%; Score 186.2; DB 1; Length 425;  
Best Local Similarity 75.5%; Pred. No. 2.4e-48;  
Matches 259; Conservative 0; Mismatches 78; Indels 6; Gaps 2;

QY 52 gcctccccgagccctgtgactccctcccccacccctcaaggagctcattgaggagctgggtc 111  
Db 55 GCCTTCGCTGGCCTGTGCCTCCCACTAGTACCTCCCTCAGGGAGCTCATTTGAGGAGCTGGTC 114  
QY 112 aacatcaccacagaatc---aggcatccctctgtgaacggcagcatggtgtggagcgtcaac 168

Db 115 AACATCACCAGAACCAAGGCTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAAC 174  
QY 169 ctgaccgcggcactgtactgcgcagctctagaatctctgatcaatgtctccgactgcagc 228  
Db 175 CTGACAGCTGGCATGTACTGTGCAGCCCTCGAATCCCTGATCAACGTGTGAGGCTGCAGT 234  
QY 229 gccatccaaagaccagagagtgctgaaagcactgtgctctcaaaagcccgccgagcagg- 287  
Db 235 GCCATCGAAGAACCCAGAGGATGCTGAGCGGATTCTGCCCGCACAAAGTCTCAGCTGGG 294  
QY 288 --gattccagtgaaacgcagccgagacacacaaaattgaagtgtatccagttgggtgaaaaac 345  
Db 295 CAGTTTTCAGCTTGATGTCCGAGACACCAAAATCGAGGTGGCCCGAGTTTGTAAAGGAC 354  
QY 346 ctgctcacctatgtaaggggagtttatcccatgggaaatttca 388  
Db 355 CTGCTCTTACATTTAAAGAAACTTTTTCGCGAGGGACGGTTCA 397  
RESULT 8  
US-08-906-957-4  
; Sequence 4, Application US/08906957  
; Patent No. 5856142  
; GENERAL INFORMATION:  
; APPLICANT: LEGOUX, Richard  
; APPLICANT: MALDONADO, Paul  
; APPLICANT: SALOME, Marc  
; TITLE OF INVENTION: Method for the extraction of  
; TITLE OF INVENTION: periplasmic proteins of prokaryotic microorganisms in the  
; TITLE OF INVENTION: presence of arginine  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Bacon & Thomas  
; STREET: 625 Slaters Lane - Fourth Floor  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: USA  
; ZIP: 22314  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/906,957  
; FILING DATE: 06-AUG-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/594,469  
; FILING DATE:  
; APPLICATION NUMBER: FR 95 01083  
; FILING DATE: 31-JAN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: FICHTER, Richard E  
; REGISTRATION NUMBER: 26,382  
; REFERENCE/DOCKET NUMBER: REF/LEGOUX  
; TELEPHONE: (703) 683-0500  
; TELEFAX: (703) 683-1080  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 425 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-906-957-4

Query Match 47.7%; Score 186.2; DB 2; Length 425;  
Best Local Similarity 75.5%; Pred. No. 2.4e-48;  
Matches 259; Conservative 0; Mismatches 78; Indels 6; Gaps 2;



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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-906-957-1

Query Match      47.7%; Score 186.2; DB 2; Length 4410;
Best Local Similarity 75.5%; Pred. No. 5.6e-48;
Matches 259; Conservative 0; Mismatches 78; Indels 6; Gaps 2;

QY 52 gcctcccgagccctgtgactccctcccccacccctcaaggagctcattgaggagtggtc 111
   ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 392 GCCTTCGCTGGCCCTGTGCCTCCAGTACTGCCCTCAGGGAGCTCATTGAGGAGCTGGTC 451

QY 112 aacatcaccagaatc---aggcatccctctgcaacggcagcatggtgtggagcgtcaac 168
   ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 452 AACATCACCAGAACCAAGAGGCTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAAC 511

QY 169 ctgaccgcgggcatgtactgcgcagctctagaatctctgatcaatgtctccgactgcagc 228
   ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 512 CTGACAGCTGGCATGTACTGTGCAGCCCTGGAATCCCTGATCAACGTGTACAGCTGCAGT 571

QY 229 gccatccaaaggaccagaggtgctgaaagcactgtgctctcctcaaaagcccgcggcagg- 287
   ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 572 GCCATCGAGAAAGACCCAGAGGATGTGAGCGGATTTGCCCCGCACAAAGTCTCAGCTGGG 631

QY 288 --gatttcagtgaaacgcagccgagacacacaaattgaagtgtccagttggtgaaaaaac 345
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 632 CAGTTTTCAGCTTGATGTCCGAGACACCAAAATCGAGGTGGCCCCAGTTTGTAAAGGAC 691

QY 346 ctgctcacctatgtaaggggagttttatcgcccatggaatttca 388
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Db 692 CTGCTCTTACATTAAAGAAACITTTTTCGGGAGGGACGGTTCA 734

RESULT 11
US-08-371-121-2
; Sequence 2, Application US/08371121
; Patent No. 5652123
; GENERAL INFORMATION:
; APPLICANT: CAPUT, Daniel
; APPLICANT: FERRARA, Pascual
; APPLICANT: GUILLEMOT, Jean-Claude
; APPLICANT: LEPLATOIS, Pascal
; APPLICANT: MINTY, Adrian
; APPLICANT: KAGHAD, Mourad
; APPLICANT: LABIT-LE BOUTEILLER, Christine
; APPLICANT: MAGAZIN, Marilyn
; TITLE OF INVENTION: Protein having a cytokine type
; TITLE OF INVENTION: activity, recombinant DNA coding for this protein,
; TITLE OF INVENTION: transformed cells and microorganisms.
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/371,121
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/938,161
; FILING DATE: 30-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR92/00280
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; FILING DATE: 27-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91 00137
; FILING DATE: 08-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91 03904
; FILING DATE: 29-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 16781/383
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 336 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-371-121-2

Query Match      47.6%; Score 185.8; DB 1; Length 336;
Best Local Similarity 76.6%; Pred. No. 2.9e-48;
Matches 255; Conservative 0; Mismatches 72; Indels 6; Gaps 2;

QY 62 gccctgtgactccctcccccacccctcaaggagctcattgaggagctggtcaacatcaccc 121
   ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 2 GCCCTGTGCTCCCTCTACAGCCCTCAGGGAGCTCATTGAGGAGCTGGTCAACATCACCC 61

QY 122 agaatc---aggcatccctctgcaacggcagcatggtgtggagcgtcaacctgaccgccc 178
   ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 62 AGAACGAGAAAGGCTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAACCTGACAGCTG 121

QY 179 gcatgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgcacccaaa 238
   ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 122 ACATGTACTGTGCAGCCCTGGAATCCCTGATCAACGTGTGAGGCTGCCATCGAGA 181

QY 239 ggaccagagaggtgctgaaagcactgtgctctcctcaaaagcccgcggcagg---gatttcca 295
   ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 182 AGACCCAGAGGATGCTGAGCGGATTCTGCCCCGCACAAGGTCTCAGCTGGCAGTTTCCA 241

QY 296 gtgaacgcagccgagacacacacaaatgaagtgtccagttggtgaaaaacctgctcacct 355
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 242 GCTTGCATGTCGAGACACCAAAATCGAGGTGGCCAGTTTGTAAAGGAGCCTGCTCTTAC 301

QY 356 atgtaaggggagtttatcgcccatggaaatttca 388
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Db 302 ATTTAAAGAAACTTTTTCGGGAGGGACGGTTCA 334

RESULT 12
US-08-371-121-26
; Sequence 26, Application US/08371121
; Patent No. 5652123
; GENERAL INFORMATION:
; APPLICANT: CAPUT, Daniel
; APPLICANT: FERRARA, Pascual
; APPLICANT: GUILLEMOT, Jean-Claude
; APPLICANT: LEPLATOIS, Pascal
; APPLICANT: MINTY, Adrian
; APPLICANT: KAGHAD, Mourad
; APPLICANT: LABIT-LE BOUTEILLER, Christine
; APPLICANT: MAGAZIN, Marilyn
; TITLE OF INVENTION: Protein having a cytokine type
; TITLE OF INVENTION: activity, recombinant DNA coding for this protein,
; TITLE OF INVENTION: transformed cells and microorganisms.
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
```



STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington, D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/371,121  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/938,161  
FILING DATE: 30-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/FR92/00280  
FILING DATE: 27-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 91 00137  
FILING DATE: 08-JAN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 91 03904  
FILING DATE: 29-MAR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: SAXE, Bernhard D.  
REGISTRATION NUMBER: 28,665  
REFERENCE/DOCKET NUMBER: 16781/383  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 447 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cdna  
US-08-371-121-26

Db 403 CTCAGCTACACAAAGCAACTGTTTCGCCACGGCCCTTC 441  
RESULT 13  
US-08-012-543-3  
; Sequence 3, Application US/08012543  
; Patent No. 5596072  
; GENERAL INFORMATION:  
; APPLICANT: Culpepper, Janice  
; APPLICANT: McKenzie, Andrew  
; APPLICANT: Dang, Warren  
; APPLICANT: de Waal Malefyt, Rene  
; APPLICANT: Heath, Andrew  
; APPLICANT: Aversa, Gregorio  
; APPLICANT: Briere, Francine  
; APPLICANT: Banchereau, Jacques  
; APPLICANT: de Vries, Jan  
; APPLICANT: Zurawski, Gerard  
; TITLE OF INVENTION: Human Interleukin-13  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/012,543  
; FILING DATE: 01-FEB-1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/933,416  
; FILING DATE: 21-AUG-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0302K1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-852-9196  
; TELEFAX: 415-496-1200  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1212 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cdna  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 70..465  
; US-08-012-543-3

Query Match 43.2%; Score 168.6; DB 1; Length 447;  
Best Local Similarity 68.2%; Pred. No. 6.2e-43;  
Matches 272; Conservative 0; Mismatches 109; Indels 18; Gaps 2;

QY 1 atggcgctctggtgactgtggtcattgtctctcacctgcctcggtggccttgcctccccg 60  
|||||  
Db 49 ATGGCGCTCTGGTGACTGCAGTCTCTGGCTCTTGGTGGCTCGCCGCCCA 108  
QY 61 agcc-----ctgtgactccctcccccaaccctcaaggagctcattgaggagctg 108  
|||||  
Db 109 GGGCCGGTGCCCAAGATCTGTGTCTCTCCCTCTGACCCCTTAAGGAGCTTATTGAGGAGCTG 168  
QY 109 gtcaacatcacccaggaatcaggcatccctctgcaacggcagcatggtgtggagcgtcaac 168  
|||||  
Db 169 AGCAACATCACACAAGACCAAGACTCCCTGTGTGCAACGGCAGCATGGTATGGAGTGTGGAC 228  
QY 169 ctgaccgcccgcgatgtactgcgcagctctagaatctctgatcaatgtctccgactgcagc 228  
|||||  
Db 229 CTGGCCGCTGGCGGGTCTGTGTAGCCCTGGATTCCCTTGACCAACATCTCCAATTGCAAT 288  
QY 229 gccatccaaaggaccagaggatgctgaaagcactgtgctctctcaaaaagcccgcgagg 288  
|||||  
Db 289 GCCATCTACAGGACCCAGAGGATATTGCATGGCCCTCTGTAAACCGCAAGCCCCCACTACG 348  
QY 289 atttccagtgaaacgcagcagagacacacaaaattgaagtgtaccagttggtgaaaaacctg 348  
|||||  
Db 349 GTCTCCA-----GCCTCCCGGATACCAAAATCGAAGTAGCCCACTTTATAACAAACTG 402  
QY 349 ctcacctatgtaaggggagtttatcgccatggaaatttc 387  
|||||

Query Match 43.2%; Score 168.6; DB 1; Length 1212;  
Best Local Similarity 68.2%; Pred. No. 9.1e-43;  
Matches 272; Conservative 0; Mismatches 109; Indels 18; Gaps 2;  
QY 1 atggcgctctggtgactgtggtcattgtggtcattgtctctcacctgcctcggtggccttgcctccccg 60  
|||||  
Db 70 ATGGCGCTCTGGTGACTGCAGTCTCTGGCTCTTGGTGGCTCTCGCCGCCCA 129  
QY 61 agcc-----ctgtgactccctcccccaaccctcaaggagctcattgaggagctg 108  
|||||  
Db 130 GGGCCGGTGCCCAAGATCTGTGTCTCTCCCTCTGACCCCTTAAGGAGCTTATTGAGGAGCTG 189  
QY 109 gtcaacatcacccaggaatcaggcatccctctgcaacggcagcatggtgtggagcgtcaac 168  
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[illegible]

RESULT 14  
PCT-US93-07645A-3  
; Sequence 3, Application PC/TUS9307645A  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: Human Interleukin-13  
; NUMBER OF SEQUENCES: 6  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Macintosh 6.0.5  
; SOFTWARE: Microsoft Word 5.1a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US93/07645A  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/012543  
; FILING DATE: 01-FEB-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/010977  
; FILING DATE: 29-JAN-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/933416  
; FILING DATE: 21-AUG-1992  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1212 base pairs.  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
PCT-US93-07645A-3

	Query Match	43.2%;	Score 168.6;	DB 5;	Length 1212;
	Best Local Similarity	58.2%;	Pred. No. 9.	le-43;	
	Matches 272;	Conservative 0;	Mismatches 109;	Indels 18;	Gaps 2;
QY	1	atggcgctctgttgactgtggtcattgctctcacctgccttcogtggcccttgccctcccgcg	60		
Db	70	ATGGCGCTCTGGGTGACTGCAGTCCTGGCTCTTGGCTTGCCCTGGTGGTCTCGCGGCCCCA	129		
QY	61	agcc-----ctgtgaactcccccccccaacccataaggagctcataggagctg	108		
Db	130	GGCGCGGTGCCAAGATCTGTGTCTCTCCCTCTGACCCCTTAAGGAGCTTATTGAGGAGCTG	189		
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Db	190	AGCAACATCACACAAGACCAGACTCCCCTGTGCAACGGCAGCATGGTATGGAGTGTGGAC	249		
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Db	250	CTGGCCGCTGGCGGGTTCTGTGTAGCCCTGGATTCCCTTGACCAACATCTCCAATTGCAAT	309		
QY	229	gccatccaaaggaccagggagtctgaaaagcactgtgctctctcaaaagcccgcggcaggg	288		

Db 310 GCCATCTACAGGACCCAGAGGATATTGCATGGCCTCTGTAAACCGCAAGGCCCCCACTACG 369  
 QY 289 atttccagtgaaacgcagccgagacacacccaaaaattgaagtgatccagttggtgaaaaacctg 348  
 Db 370 GTCTCCA-----GCCTCCCCGATACCAAAATCGAAGTAGCCCCACTTTATATAACAAAACTG 423  
 QY 349 ctcacctatgtaagggagtttatcgcccatggaaatttc 387  
 Db 424 CTCAGCTACACAAAGCAACTGTTTCGCCACGGCCCCCTTC 462  
  
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 PCT-US93-07645-3  
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 ; APPLICANT:  
 ; TITLE OF INVENTION: Human Interleukin-13  
 ; NUMBER OF SEQUENCES: 6  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: Apple Macintosh  
 ; OPERATING SYSTEM: Macintosh 6.0.5  
 ; SOFTWARE: Microsoft Word 5.1a  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/US93/07645  
 ; FILING DATE: 19930818  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/012543  
 ; FILING DATE: 01-FEB-1993  
 ; PRIOR APPLICATION DATA:  
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 ; FILING DATE: 29-JAN-1993  
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 ; FILING DATE: 21-AUG-1992  
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 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1212 base pairs  
 ; TYPE: nucleic acid  
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 ; TOPOLOGY: linear  
 PCT-US93-07645-3

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Query Match      43.2%; Score 168.6; DB 5; Length 1212;
Best Local Similarity 68.2%; Pred. No. 9.le-43;
Matches 272; Conservative 0; Mismatches 109; Indels 18; Gaps 2;

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QY 61 agcc-----ctgtgactccctccccaaacctcaaggagctcattgaggagctg 108
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Db 130 GGGCCGGTGCCAAAGATCTGTGTCTCTCCCTCTGACCCCTTAAGGAGCTTATTGAGGAGCTG 189
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QY 109 gtcaacatcacccagaatacaggcatccctctgcaacggcagcatggtgtggagcgtaac 168
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Db 310 GCCATCTACAGGACCCAGAGGATATTGCATGGCCCTCTGTAAACCGCAAGCCCCCACTACG 369
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QY 289 atttccagtgaaacgcagccgagacacacaaaaattgaaagtatccagtttggtgaaaaacctg 348
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Qy	349	ctcacatgtaagggggagtttatgcccatggaatttc	387
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Search completed: May 13, 2001, 14:21:44  
Job time: 17855 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 13, 2001, 11:40:38 ; Search time 5997.24 Seconds  
(without alignments)  
568.108 Million cell updates/sec

Title: US-09-451-527-102  
Perfect score: 390  
Sequence: 1 atggcgctctggttgactgt.....atgccatggaaatttcaga 390

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 9623517 seqs, 4368049070 residues

Total number of hits satisfying chosen parameters: 19247034

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query				Description	
	No.	Score	Match	Length	ID	
1	43.4	11.1	581	219	AZ305110	IM0005P05
2	40	10.3	463	24	AI712497	UI-R-AF1-
3	39	10.0	477	218	AZ261971	RPCI-23-1
4	39	10.0	521	215	AZ027551	RPCI-23-3
c	5	37.8	994	231	CNS040ZX	Tetraodon
	6	36.8	9.4	141	BE907816	601501924
	7	36.6	9.4	329	BF292210	WHE2208_A
	8	36.4	9.3	277	BE593226	WS1_99_B0
c	9	36.4	9.3	411	AQ001086	CIT-HSP-2
	10	36.4	9.3	537	BE357229	DG1_147_B
	11	35.6	9.1	230	BE498968	WHE0969_G
c	12	35.6	9.1	537	AV387571	AV387571
c	13	35.6	9.1	1070	BE536034	601062471
c	14	35.2	9.0	177	AI909438	IL-BT208-
	15	35.2	9.0	570	AI746678	ul06b05.Y
c	16	35.2	9.0	757	BG260311	602371427
	17	35	9.0	359	AI209519	b0e07al.f
18	34.8	8.9	507	138	BE705147	SC02_08f0

C	19	34.6	8.9	965	217	AZ201624	SP_0053_A
	20	34.4	8.8	462	143	BF039993	BP250023B
	21	34.4	8.8	544	13	AA880435	vw89f07.r
	22	34.4	8.8	553	106	AU075583	AU075583
	23	34.4	8.8	700	113	AW318852	un08d12.y
	24	34.4	8.8	712	115	AW475303	un64b04.y
	25	34.4	8.8	1056	144	BF143984	601791238
	26	34.2	8.8	477	151	BF625277	HVSMEa000
	27	34.2	8.8	535	161	BE032541	131940_MA
	28	34.2	8.8	546	161	BE032543	131942_MA
	29	34.2	8.8	616	106	AU066538	AU066538
	30	34.2	8.8	691	150	BF620464	HVSMEC001
	31	34.2	8.8	2275	14	AF034173	AF034173
	32	34	8.7	341	163	BE127683	DEPA1432
	33	34	8.7	370	166	BE363650	WS1_64_G1
	34	34	8.7	562	166	BE361027	DG1_69_A0
C	35	34	8.7	704	230	CNS02PBO	AL207789 Tetraodon
	36	34	8.7	1122	141	BE889888	601512140
	37	33.8	8.7	498	150	BF606532	273595_MA
C	38	33.6	8.6	487	138	BE704828	SC02_03b0
	39	33.6	8.6	577	166	BE402120	CSB004F06
	40	33.6	8.6	714	166	BE414190	SCU007.CO
	41	33.6	8.6	727	164	BE216356	HV_CEB001
	42	33.6	8.6	891	151	BF685554	602140603
	43	33.6	8.6	902	106	AL522415	AL522415
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C	45	33.4	8.6	569	211	AQ780112	HS_3169_A

ALIGNMENTS

RESULT	1						
AZ305110							
LOCUS	AZ305110	581 bp	DNA	GSS	29-SEP-2000		
DEFINITION	IM0005P05R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0005P05 R, DNA sequence.						
ACCESSION	AZ305110						
VERSION	AZ305110.1	GI:10341800					
KEYWORDS	GSS.						
SOURCE	house mouse.						
ORGANISM	Mus musculus						
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.						
AUTHORS	1 (bases 1 to 581)						
	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.						
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts						
JOURNAL	Unpublished (2000)						
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0005 row: P column: 05 Seq primer: CACACAGGAACAGCTATGACC Class: plasmid ends High quality sequence stop: 581.						
FEATURES	Location/Qualifiers						
source	1..581						
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	/strain="C57BL/6J"						
	/db_xref="taxon:10090"						
	/clone="UUGC1M0005P05"						
	/clone_lib="Mouse 10kb plasmid UUGC1M library"						
	/sex="Male"						

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 169 a 139 c 153 g 120 t  
ORIGIN

Query Match 11.1%; Score 43.4; DB 219; Length 581;  
Best Local Similarity 76.8%; Pred. No. 0.098;  
Matches 53; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

Qy	1	atggcgctctgtgactgtggtcattgctctcacctgcctcggtgccttgcctccccg	60
Db	513	ATGGCGCTCTGGTGACTGCAGTCCTGGCTCTGCTTGGTGTCTCGCGCCCCA	572
Qy	61	agccctgtg	69
Db	573	GGGCCGGTG	581

RESULT	2						
AI712497							
LOCUS	AI712497	463 bp	mRNA	EST	08-JUN-1999		
DEFINITION	UI-R-AF1-aap-b-12-0-UI.s1 UI-R-AF1 Rattus norvegicus cDNA clone UI-R-AF1-aap-b-12-0-UI 3', mRNA sequence.						
ACCESSION	AI712497						
VERSION	AI712497.1	GI:5016297					
KEYWORDS	EST.						
SOURCE	Norway rat.						
ORGANISM	Rattus norvegicus						
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.						
REFERENCE	1 (bases 1 to 463)						
AUTHORS	Bonaldo,M.F., Lennon,G. and Soares,M.B.						
TITLE	Normalization and subtraction: two approaches to facilitate gene discovery						
JOURNAL	Genome Res. 6 (9), 791-806 (1996)						
MEDLINE	97044477						
COMMENT	Contact: Soares, MB Program for Rat Gene Discovery and Mapping University of Iowa 451 Eckstein Medical Research Building Iowa City, IA 52242, USA Tel: 319 335 8250 Fax: 319 335 9565 Email: msoares@blue.weeg.uiowa.edu Oligo-dt track not found, Not I site shown in beginning of sequence is likely internal to the message. cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com) Seq primer: M13 Forward POLYA-No.						
FEATURES	Location/Qualifiers						
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	/organism="Rattus norvegicus"						
	/strain="Sprague-Dawley"						







Db	224	GACTTGATGTCCATGAGCCGGTGGTACTCCTGATTCCTGCCGCTCACTATCAGCTCGCAC	283
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Db	284	TCGCCCCAGCTGGGCTTCAATACCCCTGATCAGCGCCTGGTATTATTGCGCCAGTTGGGCT	343
QY	158	ggagcgltcaacctgaccgcgcgcgcatgtactgcgcagctctagaatctctgatcaatgtct	217
Db	344	CCAAAGCGCGCCTCCGTTTCTGCCAGTGTGTTCTTCCAAGGCAGCTTTCATGCTCAGCT	403
QY	218	ccgactgcagcgccatccaaaggaccagaggatgc	253
Db	404	GTGACTGCAGCTCAATCTCAAGACCCCTGAAGGGGTGC	439

RESULT	7		
BF292210			
LOCUS	329 bp	mrna	EST
DEFINITION	WHE2208_A08_B16ZS Aegilops speltoides anther cDNA library Aegilops speltoides cDNA clone WHE2208_A08_B16, mRNA sequence.		
ACCESSION	BF292210		
VERSION	BF292210.1	GI:11223274	
KEYWORDS	EST.		
SOURCE	Aegilops speltoides.		
ORGANISM	Aegilops speltoides		
	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Triticeae; Aegilops.		
REFERENCE	1 (bases 1 to 329)		
AUTHORS	Akhunov,E., Anderson,O.D., Chao,S., Chin,A., Choi,D.W., Close,T.J., Fenton,R.D, Han,P.S., Hsia,C.C., Kang,Y., Kianian,P., Lazo,G.R., Miller,R., Otto,C., Rausch,C.J., Seaton,C.L., Simons,K., Tong,J.C. and Zhang,D.		
TITLE	The structure and function of the expressed portion of the wheat genomes - Another cDNA library from Aegilops speltoides		
JOURNAL	Unpublished (2000)		
COMMENT	Contact: Olin Anderson US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center 800 Buchanan Street, Albany, CA 94710, USA Tel: 5105595773 Fax: 5105595818 Email: oandersn@pw.usda.gov Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20 Seq primer: Stratagene SK primer.		

	Query Match	9.4%;	Score 36.6;	DB 146;	Length 329;			
	Best Local Similarity	50.9%;	Pred. No. 6.9;					
Matches	87; Conservative	0;	Mismatches	84;	Indels	0;	Gaps	0;
QY	20	tgggtcattgctctcacctgcctcggtgccccttgccctccccagccctgtgactccctccc	79					
DG	158	TGCCCATCTCTCCTCCCTTCGTCCAGAAATCATCGCCGCAGATTTCGGGACCTACTTCC	217					
QY	80	caaccctcaaggagctcatgtaggagctggtcaacatcacccagaatacaggcatccctct	139					
DG	218	TCATCTTCGCGGGGTGCGCGCGGTGACCATCAACAAGACGAAGGGCAGATCACGTTCC	277					
QY	140	gaacaggcagcatggtgtggagcggtcaacctgacgcggcatgtactgcg	190					
DG	278	CCGGCGTGCGCCATCGTGTGGGGCCCTCGCCCGTGATGGTGATGGTGTACTCCG	328					

RESULT	8				
BE593226					
LOCUS		277 bp	mrna	EST	18-AUG-2000
DEFINITION		WS1_99_B03.gl_A002 Water-stressed 1 (WS1) Sorghum bicolor cDNA, mRNA sequence.			
ACCESSION		BE593226			
VERSION		BE593226.1	GI:9848299		
KEYWORDS		EST.			
SOURCE		sorghum.			
ORGANISM		Sorghum bicolor Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae ; Andropogoneae; Sorghum. 1 (bases 1 to 277) Cordonnier-Pratt,M.-M., Gingle,A., Marsala,C., Sudman,M. and Pratt ,L.H.			
REFERENCE		An EST database from Sorghum: water-stressed plants			
AUTHORS		Unpublished (2000)			
TITLE		Contact: Cordonnier-Pratt MM			
JOURNAL		Department of Botany			
COMMENT		The University of Georgia Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA Tel: 706 542 1860 Fax: 706 542 1805 Email: mmpratt@uga.edu Sequences have been trimmed to exclude PolyA, vector and regions below Phred quality 16. The threshold for highest quality sequence is 20. Seq primer: PolyTMix High quality sequence start: 5 High quality sequence stop: 246 POLYA=NO.			

	Query Match	9.3%;	Score 36.4;	DB 137;	Length 277;
	Best Local Similarity	53.5%;	Pred. NO. 7.5;		
	Matches 76;	Conservative	0;	Mismatches 66;	Indels 0; Gaps 0;
Qy	84	cctcaaggagcgtcattgaggagctgggtcaacatcacccagaatcaggcatccctcttgc aa	143		
Db	22	CCCCATGGAGAGGCTCGGGGAGCCCGGCACATCGCGCGGTGGTTCCTCTGCAC	81		
Qy	144	cggcagcatggtgtggagcggtcaacctgaccgccggcatgtactgcgcagtctagaatc	203		









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/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: kidney; Vector: pME18S-FL3; Site_1: DraIII
(CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA
was primed with an oligo(dT) primer
(ATGTGGCCCTTTTCTTTTCTTTT); double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested
and cloned into distinct DraIII sites of the pME18S-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCTGCTCTAAAGCTGCG and 3' end
primer CGACCTGCAGCTCGAGCACACA."
```

```
BASE COUNT      140 a      153 c      190 g      79 t      8 others
ORIGIN
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Query Match      9.0%; Score 35.2; DB 24; Length 570;
Best Local Similarity 50.3%; Pred. NO. 19;
Matches 85; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY      28 gctctcacctgcctcggtggccttgccctcccgagccctgtgactccctcccaaccctc 87
      || || || || || || || || || || || || || || || || || || || ||
Db      323 GCCATGAGCAGGCCCATGATCCAAAGTGTACTACAGGCCAGTGGATCAGTACAGCAACCAG 382

QY      88 aaggagctcattgaggagctgtgtcaacatcacccagaaatcaggcatccctctgcaacggc 147
      || || || || || || || || || || || || || || || || || || || ||
Db      383 AACAACTTCGTGCACGACTGGTGCAATATCACCATCAAGCAGCACACGGTCACCCACCACC 442

QY      148 agcatggtgtggagcgtcaacctgaccgcccggcatgtactgcgcagctc 196
      || || || || || || || || || || || || || || || || || || || ||
Db      443 ACCAAAGGGGAGAACTTCACCGAGACCGGATGTGAAGAAATGATGNAGCGC 491
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Search completed: May 13, 2001, 11:40:52  
Job time: 16527 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 13, 2001, 14:25:11 ; Search time 9342.78 Seconds  
(without alignments)  
615.627 Million cell updates/sec

Title: US-09-451-527-102  
Perfect score: 390  
Sequence: 1 atggcgctctgttgactgt.....atcgccatggaaatttcaga 390

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1283235 seqs, 7373929652 residues

Total number of hits satisfying chosen parameters: 2566470

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:\*

1: gb\_bal:\*

2: gb\_ba2:\*

3: gb\_ba3:\*

4: gb\_in1:\*

5: gb\_in2:\*

6: gb\_in3:\*

7: gb\_om:\*

8: gb\_ov:\*

9: gb\_pat1:\*

10: gb\_pat2:\*

11: gb\_ph:\*

12: gb\_pl1:\*

13: gb\_pl2:\*

14: gb\_pl3:\*

15: gb\_pl4:\*

16: em\_bal:\*

17: em\_ba2:\*

18: em\_fun:\*

19: em\_htgo\_hum:\*

20: em\_htgo\_inv:\*

21: em\_htgo\_rod:\*

22: em\_htg\_hum1:\*

23: em\_htg\_hum2:\*

24: em\_htg\_hum3:\*

25: em\_htg\_hum4:\*

26: em\_htg\_hum5:\*

27: em\_htg\_hum6:\*

28: em\_htg\_hum7:\*

29: em\_htg\_hum8:\*

30: em\_htg\_inv1:\*

31: em\_htg\_inv2:\*

32: em\_htg\_other:\*

33: em\_htg\_rod:\*

34: em\_hum1:\*

35: em\_hum2:\*

36: em\_hum3:\*

37: em\_hum4:\*

38: em\_hum5:\*

39: em\_hum6:\*

40: em\_hum7:\*

41: em\_in:\*

42: em\_om:\*

43: em\_or:\*

44: em\_ov:\*

45: em\_pat:\*

46: em\_ph:\*

47: em\_pl:\*

48: em\_ro:\*

49: em\_sts:\*

50: em\_sy:\*

51: em\_un:\*

52: em\_vi:\*

53: gb\_sts1:\*

54: gb\_sts2:\*

55: gb\_sts3:\*

56: gb\_sy:\*

57: gb\_un:\*

58: gb\_vil:\*

59: gb\_vi2:\*

60: gb\_htg1:\*

61: gb\_htg2:\*

62: gb\_htg3:\*

63: gb\_htg4:\*

64: gb\_htg5:\*

65: gb\_htg6:\*

66: gb\_htg7:\*

67: gb\_htg8:\*

68: gb\_htg9:\*

69: gb\_htg10:\*

70: gb\_htg11:\*

71: gb\_htg12:\*

72: gb\_htg13:\*

73: gb\_htg14:\*

74: gb\_htg15:\*

75: gb\_htg16:\*

76: gb\_htg17:\*

77: gb\_htg18:\*

78: gb\_htg19:\*

79: gb\_htg20:\*

80: gb\_htg21:\*

81: gb\_htg22:\*

82: gb\_htg23:\*

83: gb\_htg24:\*

84: gb\_htg25:\*

85: gb\_pr1:\*

86: gb\_pr2:\*

87: gb\_pr3:\*

88: gb\_pr4:\*

89: gb\_pr5:\*

90: gb\_pr6:\*

91: gb\_pr7:\*

92: gb\_pr8:\*

93: gb\_pr9:\*

94: gb\_rol:\*

95: gb\_ro2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	377	96.7	1302	7	AF244915	AF244915 Canis fam
2	230.8	59.2	1270	93	HUMILI3A	L06801 Homo sapien
3	230.8	59.2	1282	92	HSNC30	X69079 H.sapiens i
4	230.8	59.2	1290	10	I34548	I34548 Sequence 1
5	229.2	58.8	417	88	AF043334	AF043334 Homo sapi
6	229.2	58.8	1297	9	A29948	A29948 Coding sequ
7	229.2	58.8	1297	10	I58488	I58488 Sequence 15
8	203.8	52.3	343	7	AF072807	AF072807 Bos tauru
9	188	48.2	384	9	A29950	A29950 Nucleic aci
10	188	48.2	384	10	I58489	I58489 Sequence 17
11	187.4	48.1	336	9	A29931	A29931 Sequence co

12	187.4	48.1	336	10	I58494	I58494 Sequence 24
13	186.2	47.7	425	9	AR027065	AR027065 Sequence
14	186.2	47.7	425	10	I86198	I86198 Sequence 4
15	186.2	47.7	4410	9	A52326	A52326 Sequence 1
16	186.2	47.7	4410	9	AR027062	AR027062 Sequence
17	186.2	47.7	4410	10	I86195	I86195 Sequence 1
18	185.8	47.6	336	9	A29930	A29930 Sequence co
19	185.8	47.6	336	10	I58481	I58481 Sequence 2
20	168.6	43.2	447	10	I58495	I58495 Sequence 26
21	168.6	43.2	1207	94	MUSSTCPE	M23504 Mus musculu
22	168.6	43.2	1212	10	I34549	I34549 Sequence 3
23	163.2	41.8	443	94	RATIL13A	L26913 Rattus Norv
24	130.8	33.5	213343	78	AF276990	AF276990 Canis fam
25	101.8	26.1	3714	93	HUM11DC99Z	L42080 Homo sapien
26	101.8	26.1	4600	93	HUMIL13B	L13029 Human inter
27	101.8	26.1	4740	93	HSU10307	U10307 Human inter
28	101.8	26.1	5670	93	HSU31120	U31120 Human inter
29	101.8	26.1	50282	85	AC004039	AC004039 Homo sapi
30	101.8	26.1	78469	75	AC074127	AC074127 Homo sapi
31	101.8	26.1	78469	75	AC074127	AC074127 Homo sapi
32	92.2	23.6	3520	7	BTA132441	AJ132441 Bos tauru
33	71	18.2	3395	93	HUM11DC98Z	L42079 Homo sapien
34	61.6	15.8	4376	94	MUSIL13A	L13028 Mouse inter
35	61.6	15.8	142732	88	AC084392	AC084392 Homo sapi
36	61.6	15.8	159500	94	AC005742	AC005742 Mus muscu
37	61.6	15.8	237823	66	AC020886	AC020886 Mus muscu
38	44.6	11.4	60	9	A29941	A29941 Oligonucleo
39	44.6	11.4	60	10	I58485	I58485 Sequence 12
40	44.6	11.4	102	9	A29939	A29939 Sequence co
41	44.6	11.4	102	10	I58483	I58483 Sequence 10
42	40.8	10.5	1008	94	RATNACHRR5	M33952 Rat neurona
43	40.8	10.5	2461	95	RNU42976	U42976 Rattus norv
44	40.8	10.5	38390	3	SC2H12	AL359215 Streptomy
45	39.6	10.2	54	9	A29940	A29940 Sequence co

ALIGNMENTS

RESULT	1					
AF244915	AF244915	1302 bp	mRNA	MAM	16-OCT-2000	
LOCUS	Canis familiaris interleukin-13 mRNA, complete cds.					
DEFINITION	Canis familiaris interleukin-13 mRNA, complete cds.					
ACCESSION	AF244915					
VERSION	AF244915.1	GI:7528273				
KEYWORDS						
SOURCE	dog.					
ORGANISM	Canis familiaris					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.					
AUTHORS	Yang, S., Boroughs, K.L. and McDermott, M.J.					
TITLE	Canine interleukin-13: molecular cloning of full-length cDNA and expression of biologically active recombinant protein					
JOURNAL	J. Interferon Cytokine Res. 20 (9), 779-785 (2000)					
MEDLINE	20485146					
PUBMED	11032397					
REFERENCE	2 (bases 1 to 1302)					
AUTHORS	Yang, S.					
TITLE	Direct Submission					
JOURNAL	Submitted (13-MAR-2000) Allergy and Immunology, Heska Corporation, 1613 Prospect Parkway, Fort Collins, CO 80525, USA					
FEATURES	Location/Qualifiers					
Source	1. .1302					
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	/db_xref="taxon:9615"					
5'UTR	1. .51					
CDS	52. .447					
	/codon_start=1					
	/product="interleukin-13"					
	/protein_id="AAF63204.1"					
	/db_xref="GI:7528274"					
	/translation="MALWLTVVIALTCLGLASPSVTPSPTLKELIEELVNITQNA					

3'UTR	SLCNGSMVSVNLTAGMYCAALESLINVSDCSAIQRTQRMKALCSQKPAAGQISSER					
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ORIGIN	SRDTKIEVIQLVKNLLTYVRGVYRHGFR"					
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Query Match	96.7%; Score 377; DB 7; Length 1302;					
Best Local Similarity	99.2%; Pred. No. 3.4e-86;					
Matches 390; Conservative	0; Mismatches 0; Indels 3; Gaps 1;					
QY	1 atggcgctctggttgactggtgattgctctcacctgcctcggtggccttgccctcccg 60					
Db						
52	ATGGCGCTCTGGTTGACTGTGGTCATTGCTCTCACCTGCCTGGTGGCCTTGCCTCCCG 111					
QY	61 agccctgtgactccctcccaaccctcaaggagctcatgtaggagctggtcaacatcacc 120					
Db						
112	AGCCCTGTGACTCCCTCCCAACCCTCAAGGAGCTCATTTGAGGAGCTGGTCAACATCACC 171					
QY	121 cagaatcaggcatccctctgcaacggcagcatggtgtgagcgtcaacctgaccgcggc 180					
Db						
172	CAGAAATCAGGCATCCCTCTGCAACGGCAGCATGGTGTGAGCGCTCAACCTGACCGCGGC 231					
QY	181 atgtactgcgagctctagaatctctgatcaatgtctcgactgcagcgccatccaaagg 240					
Db						
232	ATGTACTGCGCAGCTCTAGAAATCTCTGATCAATGTCTCCGACTGCAGCGCCATCCAAAGG 291					
QY	241 acccagaggatgctgaaagcactgtgctctcaaaagcccgcggcagg---gatttcagt 297					
Db						
292	ACCCAGAGGATGCTGAACCACTGTGCTCTCAAAAGCCCGCGGCGAGATTTCCAGT 351					
QY	298 gaacgcagccgagacaccaaattgaagtgtatccagttggtgaaaaaacctgtcacctat 357					
Db						
352	GAACGCAGCCGAGACACCAAAATGAAGTGATCCAGTTGTTGTAACCAACCTGCTCACCTAT 411					
QY	358 gtaaggggagtttatcgccatggaaatttcaga 390					
Db						
412	GTAAGGGGAGTTTATCGCCATGGAAATTTTCAGA 444					
RESULT	2					
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LOCUS	Homo sapiens interleukin 13 mRNA, complete cds.					
DEFINITION	Homo sapiens interleukin 13 mRNA, complete cds.					
ACCESSION	L06801					
VERSION	L06801.1	GI:186275				
KEYWORDS	cytokine; growth factor; interleukin 13; regulatory protein.					
SOURCE	Homo sapiens cDNA to mRNA.					
ORGANISM	Homo sapiens					
REFERENCE	1 (bases 1 to 1270)					
AUTHORS	McKenzie, A.N.J., Culpepper, J.A., de Waal Malefyt, R., Briere, F., Punnonen, J., Aversa, G., Sato, A., Dang, W., Cocks, B.G., Menon, S., de Vries, J.E., Banchereau, J. and Zurawski, G.R.					
TITLE	Interleukin-13, a T cell-derived cytokine that regulates human monocyte and B cell function					
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 90, 3735-3739 (1993)					
MEDLINE	93234572					
FEATURES	Location/Qualifiers					
source	1. .1270					
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	/db_xref="taxon:9606"					
CDS	45. .443					
	/codon_start=1					
	/product="interleukin 13"					
	/protein_id="AAA36107.1"					
	/db_xref="GI:186276"					
	/translation="MALLTTVIALTCLGGFASPGVPVPPSTALRELIEELVNITONQK					
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	HVRDTKIEVAQFVKDLLLHLKLFREGFRN"					
	polyA_site. 1270					
BASE COUNT	288 a 335 c 336 g 311 t					











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QY 232 atccaaaggaccagaggtgctgaaagcactgtgtctctcaaaagcccgcggcagg---g 288
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Db 196 ATCGAAGACCCAGAGGATGCTGAGCGGATTCTGCCCGCACAAAGGTCTCAGCTGGGCAG 255

QY 289 attccagtgaaacgcagcgagacacacaaattgaagtgatccagttggtgaaaaacctg 348
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Db 256 TTTTCCAGCTTGCAATGTCGAGACACCAAAATCGAGGTGGCCAGTTTGTAAGGACCTG 315

QY 349 ctcacctatgtaaggaggtttatcgccatggaaaatttca 388
   ||| | | ||| | | ||| | | ||| | | ||| | | ||| | | ||| | |
Db 316 CTCTTACATTTAAAGAAACTTTTTCGGGAGGACGGTTCA 355

RESULT 11
LOCUS A29931 336 bp DNA PAT 23-JUN-1995
DEFINITION Sequence coding for the mature cytokine like protein.
ACCESSION A29931
VERSION A29931.1 GI:1249019
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM artificial sequence.
REFERENCE 1 (bases 1 to 336)
AUTHORS Caput,D., Ferrara,P., Guillemot,J.C., Kaghad,M., Labit-le
TITLE Bouteiller,C., Leplatols,P., Magazin,M. and Minty,A.
JOURNAL Protein having cytokin type activity, recombinant DNA coding for
this protein, transformed cells and microorganisms
PATENT: EP 0506574-A 3 30-SEP-1992;
ELF SANOFI
FEATURES
source Location/Qualifiers
1. .336
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BASE COUNT 80 a 95 c 90 g 71 t
ORIGIN
Query Match 48.1%; Score 187.4; DB 9; Length 336;
Best Local Similarity 76.9%; Pred. NO. 1.1e-37;
Matches 256; Conservative 0; Mismatches 71; Indels 6; Gaps 2;

QY 62 gccctgtgactccctcccaaccctcaaggagctcattgaggagctggtcaacatcaccc 121
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Db 2 GCCCTGTGCCCTCCCTCTACAGCCCTCAGGGAGCTCATTGAGGAGCTGGTCAACATCACCC 61

QY 122 agaatc---aggcatccctctgcaacggcgagcatggtgtggagcggtcaacctgaccgcg 178
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Db 62 AGAACCAGAGGCTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAACCTGCCATCGAGA 121

QY 179 gcatgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgcacccaa 238
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Db 122 GCATGTACTGTGCAGCCCTGGAATCCCTGATCAACGTGTGAGGTGCAGTGCCATCGAGA 181

QY 239 ggaccagaggtgtaaaagcactgtgtctctcaaaagcccgcggcagg---gatttcca 295
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QY 296 gtgaacgcagccgagacacacaaattgaagtgatccagttggtgaaaaacctgctcacct 355
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Db 242 GCTTGCATGTCCGAGACACCAAAATCGAGGTGGCCCGAGTTGTAAAGGACCTGCTCTTAC 301

QY 356 atgtaaggggagtttatcgccatggaaaatttca 388
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Db 302 ATTTAAGAAACTTTTTCGGGAGGACGGTTCA 334

RESULT 13
LOCUS AR027065 425 bp DNA PAT 29-SEP-1999
DEFINITION Sequence 4 from patent US 5856142.
ACCESSION AR027065
VERSION AR027065.1 GI:5937905
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 425)
AUTHORS Legoux,R., Maldonado,P. and Salome,M.
TITLE Method for the extraction of periplasmic proteins from prokaryotic
microorganisms in the presence of arginine
JOURNAL Patent: US 5856142-A 4 05-JAN-1999;
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source Location/Qualifiers
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BASE COUNT 100 a 116 c 110 g 99 t
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Best Local Similarity 75.5%; Pred. NO. 2.1e-37;
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QY 52 gcctccccgagccctgtgactccctcccccaaccctcaaggagctcattgaggagctggtc 111
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KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 336)
AUTHORS Caput,D., Ferrara,P., Guillemot,J., Kaghad,M., Labit-le
Bouteiller,C., Leplatols,P., Magazin,M. and Minty,A.
TITLE Protein having interleukin 13 activity, recombinant DNA coding for
this protein, transformed cells and microorganisms
JOURNAL Patent: US 5652123-A 24 29-JUL-1997;
FEATURES
source Location/Qualifiers
1. .336
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BASE COUNT 80 a 95 c 90 g 71 t
ORIGIN
Query Match 48.1%; Score 187.4; DB 10; Length 336;
Best Local Similarity 76.9%; Pred. NO. 1.1e-37;
Matches 256; Conservative 0; Mismatches 71; Indels 6; Gaps 2;

QY 62 gccctgtgactccctcccaaccctcaaggagctcattgaggagctggtcaacatcaccc 121
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QY 239 ggaccagaggtgtaaaagcactgtgtctctcaaaagcccgcggcagg---gatttcca 295
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Db 302 ATTTAAGAAACTTTTTCGGGAGGACGGTTCA 334

RESULT 13
LOCUS AR027065 425 bp DNA PAT 29-SEP-1999
DEFINITION Sequence 4 from patent US 5856142.
ACCESSION AR027065
VERSION AR027065.1 GI:5937905
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 425)
AUTHORS Legoux,R., Maldonado,P. and Salome,M.
TITLE Method for the extraction of periplasmic proteins from prokaryotic
microorganisms in the presence of arginine
JOURNAL Patent: US 5856142-A 4 05-JAN-1999;
FEATURES
source Location/Qualifiers
1. .425
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ORIGIN
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Best Local Similarity 75.5%; Pred. NO. 2.1e-37;
Matches 259; Conservative 0; Mismatches 78; Indels 6; Gaps 2;

QY 52 gcctccccgagccctgtgactccctcccccaaccctcaaggagctcattgaggagctggtc 111
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Db 55 GCCTTCGCTGGCCCTGTGCCTCCAGTACTGCCCTCAGGGAGCTCATTCAGGAGCTGGTC 114
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RESULT 14
LOCUS I86198 425 bp DNA PAT 10-JUN-1998
DEFINITION Sequence 4 from patent US 5700665.
ACCESSION I86198
VERSION I86198.1 GI:3205916
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 425)
AUTHORS Legoux,R., Maldonado,P. and Salome,M.
TITLE Method for the extraction of periplasmic proteins from prokaryotic
microorganisms in the presence of arginine
JOURNAL Patent: US 5700665-A 4 23-DEC-1997;
FEATURES
source Location/Qualifiers
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BASE COUNT 100 a 116 c 110 g 99 t
ORIGIN

Query Match 47.7%; Score 186.2; DB 10; Length 425;
Best Local Similarity 75.5%; Pred. No. 2.1e-37;
Matches 259; Conservative 0; Mismatches 78; Indels 6; Gaps 2;

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RESULT 15
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LOCUS A52326 4410 bp DNA PAT 12-DEC-1997
DEFINITION Sequence 1 from Patent EP0725140.
ACCESSION A52326
VERSION A52326.1 GI:2851987
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 4410)
AUTHORS Legoux,R., Maldonado,P. and Salome,M.
TITLE Process of extraction of periplasmic proteins from prokaryotic
microorganisms in the presence of arginine
JOURNAL Patent: EP 0725140-A 1 07-AUG-1996;
COMMENT SANOFI SA (FR)
Other publication SK 10696 960904
Other publication CZ 9600290 960814
Other publication JP 8242879 960924
Other publication FI 960427 960801
Other publication PL 312543 960805
Other publication NO 960396 960801
Other publication FR 2729972 960802
Other publication CA 2168382 960801
Other publication AU 4224496 960808.
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1013..1253
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2506..4410
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BASE COUNT 1078 a 1142 c 1096 g 1094 t
ORIGIN
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Best Local Similarity 75.5%; Pred. No. 1.8e-37;
Matches 259; Conservative 0; Mismatches 78; Indels 6; Gaps 2;

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QY 112 aacatcacccagaatc---aggcatccctctgcaacggcagcatggtgtggagcgtcaac 168
Db 452 AACATCACCCAGAACAGAGGCTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAAC 511
QY 169 ctgaccgcggcatgtactgcgcagctctagaatctctgatcaatgtctccgactgcagc 228
Db 512 CTGACAGCTGGCATGTACTGTGCAGCCCTGGATCCCTGATCAACGTCAGGCTGCAGT 571
QY 229 gccatccaaaggaccagaggatgctgaaagcactgtgctctcaaaagccgcggcagg- 287
Db 572 GCCATCGAGAAGACCCAGAGGATGCTGAGCGGATTCTGCCCGCACAAAGTCTCAGCTGGG 631
QY 288 --gatttcagtgaaacgcagccgagacacacaaaattgaaagtatccagttggtgaaaaa 345
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Qy 346 ctgctcacctatgtaaggaggagtttatcgccatggaaaatttca 388  
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Search completed: May 13, 2001, 14:25:18  
Job time: 19398 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.  
OM nucleic - nucleic search, using sw model  
Run on: May 13, 2001, 14:25:18 ; Search time 9342.78 Seconds  
(without alignments)  
520.915 Million cell updates/sec

Title: US-09-451-527-104  
Perfect score: 330  
Sequence: 1 agccctgtgactccctcccc.....atgcccatggaaatttcaga 330

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1283235 seqs, 7373929652 residues  
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Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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11: gb\_ph:\*  
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23: em\_htg\_hum2:\*  
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90: gb\_pr6:\*  
91: gb\_pr7:\*  
92: gb\_pr8:\*  
93: gb\_pr9:\*  
94: gb\_rol:\*  
95: gb\_ro2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	317	96.1	1302	7	AF244915	AF244915 Canis fam
2	187.4	56.8	336	9	A29931	A29931 Sequence co
3	187.4	56.8	336	10	I58494	I58494 Sequence 24
4	187.4	56.8	1270	93	HUMIL13A	L06801 Homo sapien
5	187.4	56.8	1282	92	HSNC30	X69079 H.sapiens i
6	187.4	56.8	1290	10	I34548	I34548 Sequence 1
7	185.8	56.3	336	9	A29930	A29930 Sequence co
8	185.8	56.3	336	10	I58481	I58481 Sequence 2
9	185.8	56.3	417	88	AF043334	AF043334 Homo sapi
10	185.8	56.3	1297	9	A29948	A29948 Coding sequ
11	185.8	56.3	1297	10	I58488	I58488 Sequence 15

12	184.2	55.8	384	9	A29950	A29950 Nucleic aci
13	184.2	55.8	384	10	I58489	I58489 Sequence 17
14	182.6	55.3	425	9	AR027065	AR027065 Sequence
15	182.6	55.3	425	10	I86198	I86198 Sequence 4
16	182.6	55.3	4410	9	A52326	A52326 Sequence 1
17	182.6	55.3	4410	9	AR027062	AR027062 Sequence
18	182.6	55.3	4410	10	I86195	I86195 Sequence 1
19	163	49.4	343	7	AF072807	AF072807 Bos tauru
20	151.4	45.9	447	10	I58495	I58495 Sequence 26
21	151.4	45.9	1207	94	MUSSTCPE	M23504 Mus musculu
22	151.4	45.9	1212	10	I34549	I34549 Sequence 3
23	140.8	42.7	443	94	RATIL13A	L26913 Rattus Norv
24	106.4	32.2	213343	78	AF276990	AF276990 Canis fam
25	71.4	21.6	3714	93	HUM11DC992	L42080 Homo sapien
26	71.4	21.6	4600	93	HUMIL13B	L13029 Human inter
27	71.4	21.6	4740	93	HSU10307	U10307 Human inter
28	71.4	21.6	5670	93	HSU31120	U31120 Human inter
29	71.4	21.6	50282	85	AC004039	AC004039 Homo sapi
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35	49.4	15.0	142732	88	AC084392	AC084392 Homo sapi
36	49.4	15.0	159500	94	AC005742	AC005742 Mus muscu
37	49.4	15.0	237823	66	AC020886	AC020886 Mus muscu
38	40.8	12.4	38390	3	SC2H12	AL359215 Streptomy
39	39	11.8	13684	94	MUSGABAT	M92377 Mus musculu
40	37	11.2	39739	3	SCD16A	AL078618 Streptomy
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42	36.6	11.1	51440	12	AB025632	AB025632 Arabidops
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ALIGNMENTS

RESULT	1					
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LOCUS	AF244915	1302 bp	mrna	MAM	16-OCT-2000	
DEFINITION	Canis familiaris interleukin-13 mRNA, complete cds.					
ACCESSION	AF244915					
VERSION	AF244915.1	GI:7528273				
KEYWORDS						
SOURCE	dog.					
ORGANISM	Canis familiaris					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.					
AUTHORS	Yang,S., Boroughs,K.L. and McDermott,M.J.					
TITLE	Canine interleukin-13: molecular cloning of full-length cDNA and expression of biologically active recombinant protein					
JOURNAL	J. Interferon Cytokine Res. 20 (9), 779-785 (2000)					
MEDLINE	20485146					
PUBMED	11032397					
REFERENCE	2 (bases 1 to 1302)					
AUTHORS	Yang,S.					
TITLE	Direct Submission					
JOURNAL	Submitted (13-MAR-2000) Allergy and Immunology, Heska Corporation, 1613 Prospect Parkway, Fort Collins, CO 80525, USA					
FEATURES	Location/Qualifiers					
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5'UTR	1..51					
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ORIGIN						
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Best Local Similarity	99.1%;	Pred. No. 1.1e-72;				
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QY	61	cagaatcaggcatccctcttgcaacggcagcatggtgtggagcgtcaacctgaccgcccgc	120			
Db	172	CAGAATCAGGCATCCCTCTGCAACGGCAGCATGTTGTGGAGCGTCAACCTGACCGCCGGC	231			
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Db	232	ATGTACTGGCAGCTCTAGAAATCTCTGTATCAATGTCTCCGACTGCAGCGCCATCCAAAGG	291			
QY	181	accagaggatgctgaagcactgtgctctcaaaagcccgaggcagg---gattccagt	237			
Db	292	ACCCAGAGGATGCTGAAAGCACTGTGCTCTCAAAAGCCCGGCGGAGGAGTTCAGT	351			
QY	238	gaacgagccgagacacacaaattgaagtgtatccagttggtgaaaaacctgctcacctat	297			
Db	352	GAACGCAGCCGAGACACCAAAATTGAAGTGATCCAGTTGGTGAAAAACCTGCTACCTAT	411			
QY	298	gtaaggggagtttatcgccatggaaatttcaga	330			
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RESULT 2

A29931						
LOCUS	A29931	336 bp	DNA	PAT	23-JUN-1995	
DEFINITION	Sequence coding for the mature cytokine like protein.					
ACCESSION	A29931					
VERSION	A29931.1	GI:1249019				
KEYWORDS	synthetic construct.					
SOURCE	synthetic construct					
ORGANISM	artificial sequence.					
REFERENCE	1 (bases 1 to 336)					
AUTHORS	Caput,D., Ferrara,P., Guillemot,J.C., Kaghad,M., Labit-le Bouteiller,C., Leplatot,P., Magazin,M. and Minty,A.					
TITLE	Protein having cytokin type activity, recombinant DNA coding for this protein, transformed cells and microorganisms					
JOURNAL	Patent: EP 0506574-A 3 30-SEP-1992;					
FEATURES	ELF SANOFI					
source	Location/Qualifiers					
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	/db_xref="taxon:32630"					
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Matches 256;	Conservative	0;	Mismatches	71;	Indels	6;
Gaps	2;					
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Db	2	GCCTGTGCTCCCTCTACAGCCCTCAGGGAGCTCATTTGAGGAGCTGGTCAACATCACC	61			
QY	62	agaatc---agcatccctctgcaacggcagcatggtgtggagcgtcaacctgaccgccc	118			
Db	62	AGAACCAAGAGGCTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAACCTGACAGCTG	121			



QY	119	gcatgtactgcgcagctctagaaatctctgatcaatgtctccgactgcagcgccatccaaa	178
Db	122	GCATGTACTGTGCAGCCCTGGAATCCCTGATCAACGTGTGAGGCTGCAGTGCATCGAGA	181
QY	179	ggaccagagatgctgaaagcactgtgctctcaaaagcccgcgagg--gattcca	235
Db	182	AGACCCAGAGGATGCTGAGCGGATTCTGCCCGCACAAAGTCTCAGCTGGGCAGTTTCCA	241
QY	236	gtgaacgcagccgagacacacaaaattgaagtgcattccagttggtgaaaaaacctgtcacct	295
Db	242	GCTTGCATGTCGAGACACCAAAATCGAGGTGSCCCAGTTTGTAAAGGACCTGCTTAC	301
QY	296	atgtaaggggagtttatcgccatggaaatttca	328
Db	302	ATTTAAGAAACTTTTTCGCGAGGGACGGTTCA	334
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LOCUS	I58494	336 bp	DNA
DEFINITION	Sequence 24 from patent US 5652123.	PAT	07-OCT-1997
ACCESSION	I58494		
VERSION	I58494.1	GI:2477732	
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 336)		
AUTHORS	Caput,D., Ferrara,P., Guillemot,J., Kaghad,M., Labit-Le Bouteiller,C., Leplatois,P., Magazin,M. and Minty,A.		
TITLE	Protein having interleukin 13 activity, recombinant DNA coding for this protein, transformed cells and microorganisms		
JOURNAL	Patent: US 5652123-A 24 29-JUL-1997;		
FEATURES	Location/Qualifiers		
source	1. .336		
BASE COUNT	80 a 95 c 90 g 71 t		
ORIGIN	/organism="unknown"		
Query Match	56.8%;	Score 187.4;	DB 10;
Best Local Similarity	76.9%;	Pred. No. 9.3e-39;	
Matches	256;	Conservative 0;	Mismatches 71; Indels 6; Gaps 2;
QY	2	gccctgtgactccctcccaaccctcaaggagctcattgaggagctggtcaacatcaccc	61
Db	2	GCCCTGTGCCTCCCTCTACAGCCCTCAGGAGCTCATTGAGGAGCTGGTCAACATCACCC	61
QY	62	agaatc--aggcatccctctgcaacggcagcatggtgtggagcgtcaacctgaccg	118
Db	62	AGAACGAGAAGGCTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAACCTGACAGCTG	121
QY	119	gcatgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgccatccaaa	178
Db	122	GCATGTACTGTGCAGCCCTGGAATCCCTGATCAACGTGTCAGGCTGCAGTGCATCGAGA	181
QY	179	ggaccagagatgctgaaagcactgtgctctcaaaagcccgcgagg--gatttcca	235
Db	182	AGACCCAGAGGATGCTGAGCGGATTCTGCCCGCACAAAGTCTCAGCTGGGCAGTTTCCA	241
QY	236	gtgaacgcagccgagacacacaaaattgaagtgcattccagttggtgaaaaaacctgtcacct	295
Db	242	GCTTGCATGTCGAGACACCAAAATCGAGGTGGCCAGTTTGTAAAGGACCTGCTTAC	301
QY	296	atgtaaggggagtttatcgccatggaaatttca	328
Db	302	ATTTAAGAAACTTTTTCGCGAGGGACGGTTCA	334
RESULT	4		
HUMIL13A			
LOCUS	HUMIL13A	1270 bp	mrna
DEFINITION	Homo sapiens interleukin 13 mRNA, complete cds.	PRI	22-JUL-1993

ACCESSION	L06801		
VERSION	L06801.1	GI:186275	
KEYWORDS	cytokine; growth factor; interleukin 13; regulatory protein.		
SOURCE	Homo sapiens cDNA to mRNA.		
ORGANISM	Homo sapiens		
REFERENCE	1 (bases 1 to 1270)		
AUTHORS	McKenzie,A.N.J., Culpepper,J.A., de Waal Malefyt,R., Briere,F., Punnonen,J., Aversa,G., Sato,A., Dang,W., Cocks,B.G., Menon,S., de Vries,J.E., Banchereau,J. and Zurawski,G.R.		
TITLE	Interleukin-13, a T cell-derived cytokine that regulates human monocyte and B cell function		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 90, 3735-3739 (1993)		
MEDLINE	93234572		
FEATURES	Location/Qualifiers		
source	1. .1270		
CDS	/organism="Homo sapiens" /db_xref="taxon:9606" 45. .443 /codon_start=1 /product="interleukin 13" /protein_id="AAA36107.1" /db_xref="GI:186276" /translation="MALLLTIVIALTCLGGFASPGVPSTALRELIIELVNITQNQK APLCNGSMVWSINLTAGMYCAALESLINVSGCSAIEKTQRLMSLGGFCPHKVSAGQFSSL HVRDTKIEVAQFVKDLLLHLKLFREGFN"		
polyA_site	1270		
BASE COUNT	288 a 335 c 336 g 311 t		
ORIGIN			
Query Match	56.8%;	Score 187.4;	DB 93;
Best Local Similarity	76.9%;	Pred. No. 8.5e-39;	
Matches	256;	Conservative 0;	Mismatches 71; Indels 6; Gaps 2;
QY	2	gccctgtgactccctcccaaccctcaaggagctcattgaggagctggtcaacatcaccc	61
Db	106	GCCCTGTGCCTCCCTCTACAGCCCTCAGGGAGCTCATTGAGGAGCTGGTCAACATCACCC	165
QY	62	agaatc--aggcatccctctgcaacggcagcatggtgtggagcgtcaacctgaccg	118
Db	166	AGAACGAGAAGGCTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAACCTGACAGCTG	225
QY	119	gcatgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgccatccaaa	178
Db	226	GCATGTACTGTGCAGCCCTGGAATCCCTGATCAACGTGTGAGGCTGCAGTGCATCGAGA	285
QY	179	ggaccagagatgctgaaagcactgtgctctcaaaagcccgcgagg--gatttcca	235
Db	286	AGACCCAGAGGATGCTGAGCGGATTCTGCCCGCACAAAGTCTCAGCTGGGCAGTTTCCA	345
QY	236	gtgaacgcagccgagacacacaaaattgaagtgcattccagttggtgaaaaaacctgtcacct	295
Db	346	GCTTGCATGTCGAGACACCAAAATCGAGGTGGCCAGTTTGTAAAGGACCTGCTTAC	405
QY	296	atgtaaggggagtttatcgccatggaaatttca	328
Db	406	ATTTAAGAAACTTTTTCGCGAGGGACGGTTCA	438
RESULT	5		
HSNC30			
LOCUS	HSNC30	1282 bp	mrna
DEFINITION	H.sapiens interleukin-13 mRNA.		
ACCESSION	X69079		
VERSION	X69079.1	GI:297787	
KEYWORDS	lymphokine.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	1 (bases 1 to 1282)		

AUTHORS Minty,A.J.  
TITLE Direct Submission  
JOURNAL Submitted (02-NOV-1992) A.J. Minty, Sanofi-Elf Bio Recherches, Labège Innopole, Voie 1, BP 137, 31676 Labège Cedex, FRANCE  
REFERENCE 2 (bases 1 to 1282)  
AUTHORS Minty,A.J., Chalon,P., Derocq,J.M., Dumont,X., Guillemot,J.C., Kaghad,M., Labit,C., Leplatois,P., Liauzun,P., Miloux,B., Minty,C., Casellas,P., Loison,G., Lupker,J., Shire,D., Ferrara,P. and Caput,D.  
TITLE Interleukin-13 is a new human lymphokine regulating inflammatory and immune responses  
JOURNAL Nature 362 (6417), 248-250 (1993)  
MEDLINE 93211479  
FEATURES Location/Qualifiers  
source 1..1282  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/chromosome="5q 23-31"  
/cell\_type="peripheral blood lymphocytes"  
15..455  
/gene="NC30"  
15..116  
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/evidence=experimental  
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/db\_xref="SWISS-PROT:P35225"  
/translation="MHPLLNPLLALGLMALLTTVIALTCLGGFASGPPVPSTALR ELIEELVNITQNKAPLCNGSMVWSINLTAGMYCAALESLINVSGCSAIEKTQRM LSG FCPHKVSAGQFSSLHVRDTKIEVAQFVKDLLHLKLFREGFN"  
57..455  
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/note="alternative; ATG at 15 is an alternative start codon"  
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/evidence=experimental  
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/db\_xref="GI:673420"  
/db\_xref="SWISS-PROT:P35225"  
/translation="MALLTTVIALTCLGGFASGPPVPSTALRELIEELVNITQNK APLCNGSMVWSINLTAGMYCAALESLINVSGCSAIEKTQRM LSGFCPHKVSAGQFSSL HVRDTKIEVAQFVKDLLHLKLFREGFN"  
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/gene="NC30"  
/product="NC30; alternative"  
117..452  
/gene="NC30"  
/evidence=experimental  
238  
/gene="NC30"  
/replace="a"  
856..860  
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873..877  
/note="ATTTA motif"  
1134..1138  
/note="ATTTA motif"  
1153..1157  
/note="ATTTA motif"  
1264..1269  
polyA\_signal 293 a 341 c 337 g 311 t  
BASE COUNT 293 a 341 c 337 g 311 t  
ORIGIN  
Query Match 56.8%; Score 187.4; DB 92; Length 1282;  
Best Local Similarity 76.9%; Pred. No. 8.5e-39;  
Matches 256; Conservative 0; Mismatches 71; Indels 6; Gaps 2;

QY 2 gccctgtgactccctcccccaaccctcaaggagctcattgaggagctggtcaacatcaccc 61  
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Db 118 GCCCTGTGCCTCCCTCTACAGCCCTCAGGGAGCTCATTTGAGGAGCTGGTCAACATCACCC 177  
QY 62 agaatc---aggcatccctctgtcaaacggcagcatggtgtggagcgtcaaacctgaccgccg 118  
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QY 179 ggaccagaggatgctgaaagcactgtgctctcaaaagcccgcggcagg---gatttcca 235  
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QY 236 gtgaacgcagccgagacacacaaaattgaagtgtccagtgttgtaaaaaacctgtcacct 295  
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Db 358 GCTTGCAATGTCGAGACACCAAAATCGAGGTGGCCAGTTTGTAAAGGACCTGCTCTTAC 417  
QY 296 atgtaaggggagtttatcgccatggaaaatttca 328  
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Db 418 ATTTAAAGAAACTTTTTCGCGAGGGACGGTTCA 450  
RESULT 6  
LOCUS I34548 1290 bp DNA PAT 06-FEB-1997  
DEFINITION Sequence 1 from patent US 5596072.  
ACCESSION I34548  
VERSION I34548.1 GI:1825339  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1290)  
AUTHORS Culpepper,J., McKenzie,A., Dang,W. and Zurawski,G.  
TITLE Method of refolding human IL-13  
JOURNAL Patent: US 5596072-A 1 21-JAN-1997;  
FEATURES Location/Qualifiers  
source 1..1290  
/organism="unknown"  
BASE COUNT 308 a 335 c 336 g 311 t  
ORIGIN

Query Match 56.8%; Score 187.4; DB 10; Length 1290;  
Best Local Similarity 76.9%; Pred. No. 8.5e-39;  
Matches 256; Conservative 0; Mismatches 71; Indels 6; Gaps 2;  
QY 2 gccctgtgactccctcccccaaccctcaaggagctcattgaggagctggtcaacatcaccc 61  
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Db 106 GCCCTGTGCCTCCCTCTACAGCCCTCAGGGAGCTCATTTGAGGAGCTGGTCAACATCACCC 165  
QY 62 agaatc---aggcatccctctgtcaaacggcagcatggtgtggagcgtcaaacctgaccgccg 118  
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Db 166 AGAACCCAGAGGCTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAACCTGACAGCTG 225  
QY 119 gcatgtactgcgactcttagaatctctgatcaatgtctccgactgcagcgccatccaaa 178  
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Db 226 GCATGTACTGTGCAGCCCTGGAATCCCTGATCAACGTGTCAAGGTGCAGTGCCATCGAGA 285  
QY 179 ggaccagaggatgctgaaagcactgtgctctcaaaagcccgcggcagg---gatttcca 235  
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QY 236 gtgaacgcagccgagacacacaaaattgaagtgtatccagtgttgtaaaaaacctgtcacct 295  
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QY 296 atgtaaggggagtttatcgccatggaaaatttca 328  
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Db 406 ATTTAAAGAAACTTTTTCGCGAGGGACGGTTCA 438

RESULT 7

LOCUS A29930 336 bp DNA PAT 23-JUN-1995

DEFINITION Sequence coding for the mature cytokine like protein.

ACCESSION A29930

VERSION A29930.1 GI:1249018

KEYWORDS

SOURCE synthetic construct.

ORGANISM synthetic construct.

REFERENCE 1 (bases 1 to 336)

AUTHORS Caput,D., Ferrara,P., Guillemot,J.C.; Kaghad,M., Labit-le

TITLE Bouteiller,C., Leplatois,P., Magazin,M. and Minty,A.

JOURNAL Protein having cytokin type activity, recombinant DNA coding for this protein, transformed cells and microorganisms

Patent: EP 0506574-A 2 30-SEP-1992;

ELF SANOFI

FEATURES

source

Location/Qualifiers

1. .336

/organism="synthetic construct"

/db\_xref="taxon:32630"

BASE COUNT 81 a 95 c 89 g 71 t

ORIGIN

Query Match 56.3%; Score 185.8; DB 9; Length 336;

Best Local Similarity 76.6%; Pred. No. 2.4e-38;

Matches 255; Conservative 0; Mismatches 72; Indels 6; Gaps 2;

QY 2 gccctgtgactccctccccaaccctcaaggagctcattgaggagctgggtcaacatcaccc 61

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Db 2 GCCCTGTGCCTCCCTCTACAGCCCTCAGGGAGCTCATTGAGGAGCTGGTCAACATCACCC 61

QY 62 agaatc---aggcatccctctgcaacggcagctggtgagcgtcaaacctgacgcgcg 118

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TITLE Bouteiller,C., Leplatois,P., Magazin,M. and Minty,A.

JOURNAL Protein having cytokin type activity, recombinant DNA coding for this protein, transformed cells and microorganisms

Patent: EP 0506574-A 2 30-SEP-1992;

ELF SANOFI

FEATURES

source

Location/Qualifiers

1. .336

/organism="synthetic construct"

/db\_xref="taxon:32630"

BASE COUNT 81 a 95 c 89 g 71 t

ORIGIN

Query Match 56.3%; Score 185.8; DB 9; Length 336;

Best Local Similarity 76.6%; Pred. No. 2.4e-38;

Matches 255; Conservative 0; Mismatches 72; Indels 6; Gaps 2;

QY 2 gccctgtgactccctccccaaccctcaaggagctcattgaggagctgggtcaacatcaccc 61

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QY 62 agaatc---aggcatccctctgcaacggcagctggtgagcgtcaaacctgacgcgcg 118

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Db 62 AGAACCAGAGGCTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAACCTGACAGCTG 121

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QY 119 gcatgtactgcgagctctagaatctctgatcaatgtccgactgcccactgctcacct 295

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Db 62 AGAACCAGAGGCTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAACCTGACAGCTG 121

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QY 179 ggaccagagagctgctgaaagcactgtgctctcaaaagcccgcgagg---gatttcca 235

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Db 242 GCTTGCATGTCCGAGACACCAAAATCGAGGTGGCCAGTTTGTAAAGGACCTGCTCTTAC 301

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QY 296 atgtaaggaggagtttatcgccatggaaatttca 328

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Db 302 ATTTAAAGAAACTTTTTCGCGAGGGACGGTTCA 334

RESULT 8

LOCUS I58481 336 bp DNA PAT 07-OCT-1997

DEFINITION Sequence 2 from patent US 5652123.

ACCESSION I58481

VERSION I58481.1 GI:2477719

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 336)

AUTHORS Caput,D., Ferrara,P., Guillemot,J., Kaghad,M., Labit-Le

TITLE Bouteiller,C., Leplatois,P., Magazin,M. and Minty,A.

JOURNAL Protein having interleukin 13 activity, recombinant DNA coding for this protein, transformed cells and microorganisms

Patent: US 5652123-A 2 29-JUL-1997;

FEATURES

source

Location/Qualifiers

1. .336

/organism="unknown"

BASE COUNT 81 a 95 c 89 g 71 t

ORIGIN

Query Match 56.3%; Score 185.8; DB 10; Length 336;

Best Local Similarity 76.6%; Pred. No. 2.4e-38;

Matches 255; Conservative 0; Mismatches 72; Indels 6; Gaps 2;

QY 2 gccctgtgactccctccccaaccctcaaggagctcattgaggagctgggtcaacatcaccc 61

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Db 2 GCCCTGTGCCTCCCTCTACAGCCCTCAGGGAGCTCATTGAGGAGCTGGTCAACATCACCC 61

QY 62 agaatc---aggcatccctctgcaacggcagctggtgagcgtcaaacctgacgcgcg 118

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Db 242 GCTTGCATGTCCGAGACACCAAAATCGAGGTGGCCAGTTTGTAAAGGACCTGCTCTTAC 301

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QY 296 atgtaaggaggagtttatcgccatggaaatttca 328

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Db 302 ATTTAAAGAAACTTTTTCGCGAGGGACGGTTCA 334

RESULT 9

LOCUS AF043334 417 bp mRNA PRI 21-FEB-1998

DEFINITION Homo sapiens interleukin 13 precursor (IL13) mRNA, complete cds.

ACCESSION AF043334

VERSION AF043334.1 GI:2905619

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 417)

AUTHORS Jang,J.S. and Kim,B.E.

TITLE Direct Submission

JOURNAL Submitted (15-JAN-1998) Protein Engineering, General Institute of Technology, Hyundai Pharm. Ind. Co., Ltd., 213 Sosa Bon 1-dong, Sosa-gu, Bucheon 422-231, Korea

COMMENT

Nested PCR:

1) first PCR :

forward primer (5'-ctcaatcctctcctgttgga-3')

reverse primer (5'-tagtcaggctcctgtctctgc-3')

2) second PCR :

forward primer (5'-ctcatggcgctttttgttgaccacg-3')

reverse primer (5'-gatgctttcgaagtttcagttgaa-3').

FEATURES

source

Location/Qualifiers

1. .417

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/cell\_type="PHA-treated peripheral blood leukocyte"

1. .417

/gene="IL13"

1. .24

/gene="IL13"

/note="second PCR"

/PCR\_conditions="94C-1min, 50C-1min, 72C-3min, 30 cycles; DeltaCycler II from Ericomp"

4. .402

CDS

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/gene="IL13"
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/product="interleukin 13 precursor"
/protein_id="AAC03535.1"
/db_xref="GI:2905620"
/translation="MALLLTVTIALTCLGGFASPGVPVPPSTALRELIELVNITQNK
APLCNGSMVWSINLTAGMYCAALESINVSGCSAIEKTQRMGLGFCPHKVSAGQFSSL
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64..399
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/product="interleukin 13"
complement(394..417)
/note="second PCR"
BASE COUNT 91 a 121 c 108 g 97 t
ORIGIN

Query Match 56.3%; Score 185.8; DB 88; Length 417;
Best Local Similarity 76.6%; Pred. No. 2.4e-38;
Matches 255; Conservative 0; Mismatches 72; Indels 6; Gaps 2;

QY 2 gccctgtgactccctcccaaccctcaaggagctcattgaggagctggtcaacatcaccc 61
Db 65 GCCCTGTGCTCCCTCTACAGCCCTCAGGGAGCTCATTGAGGAGTGGTCAACATCACCC 124
QY 62 agaatc---aggcatccctctgcaacggcagcatggtgtgagcgctcaacctgaccgccg 118
Db 125 AGAACCCAGAGGCTCCGCTCTGCAATGGCAGCATGGTTTGGAGCATCAACCTGACAGCTG 184
QY 119 gcatgtactgcgcagctctagaatctctgatcaatgtctcgcagctgcagcgccatccaaa 178
Db 185 GCATGTACTGTGCAGCCCTGGAATCCCTGTATCAACGTGTCAAGCTGCAGTGCCATCGAGA 244
QY 179 ggaccagaggatgctgaaagcactgtgtctctcaaaaagcccgcgaggcagg---gatttcca 235
Db 245 AGACCCAGAGGATGCTGGCGGATTCTGCCCGCACAAAGGTCTCAGCTGGGCAGTTTTCCTCA 304
QY 236 gtgaacgcagccgagacaccaaattgaagtgtatccagttggtgaaaaacctgctcacct 295
Db 305 GCTTGATGTCCGAGACACCAAAATCGAGTGGCCAGTTGTGTAAGGACCTGCTCTTTAC 364
QY 296 atgtaaggggagtttatcgccatggaaaatttca 328
Db 365 ATTTAAAGAAACTTTTTCGCGAGGGACGGTTCA 397

RESULT 10
A29948 1297 bp DNA PAT 23-JUN-1995
LOCUS Coding sequence for protein with cytokine like activity.
DEFINITION A29948
ACCESSION A29948
VERSION A29948.1 GI:1249028
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM artificial construct.
REFERENCE 1 (bases 1 to 1297)
AUTHORS Caput,D., Ferrara,P., Guillemot,J.C., Kaghad,M., Labit-le
Bouteiller,C., Leplatois,P., Magazin,M. and Minty,A.
TITLE Protein having cytokin type activity, recombinant DNA coding for
this protein, transformed cells and microorganisms
JOURNAL Patent: EP 0506574-A 21 30-SEP-1992;
FEATURES
source Location/Qualifiers
1..1297
/organism="synthetic construct"
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15..455
/codon_start=1
/trans_table=11
/product="protein with cytokine like activity"
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/db_xref="GI:1249029"
/translation="MHPLLNPLLLALGLMALLTTVIALTCLGGFASPGVPVPPSTALR
ELJIELVNITQNKAPLCNGSMVWSINLTADMYCAALESINVSGCSAIEKTQRMLSG
FCPHKVSAGQFSSLHVROTKIEVAQFVKDLLHLKLFREGFN"
BASE COUNT 309 a 341 c 336 g 311 t
ORIGIN

Query Match 56.3%; Score 185.8; DB 9; Length 1297;
Best Local Similarity 76.6%; Pred. No. 2.2e-38;
Matches 255; Conservative 0; Mismatches 72; Indels 6; Gaps 2;

QY 2 gccctgtgactccctcccaaccctcaaggagctcattgaggagctggtcaacatcaccc 61
Db 118 GCCCTGTGCTCCCTCTACAGCCCTCAGGGAGCTCATTGAGGAGTGGTCAACATCACCC 177
QY 62 agaatc---aggcatccctctgcaacggcagcatggtgtgagcgctcaacctgaccgccg 118
Db 178 AGAACCCAGAGGCTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAACCTGACAGCTG 237
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QY 179 ggaccagaggatgctgaaagcactgtgtctctcaaaaagcccgcgaggcagg---gatttcca 235
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QY 236 gtgaacgcagccgagacaccaaattgaagtgtatccagttggtgaaaaacctgctcacct 295
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QY 296 atgtaaggggagtttatcgccatggaaaatttca 328
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RESULT 11
I58488 1297 bp DNA PAT 07-OCT-1997
LOCUS Sequence 15 from patent US 5652123.
DEFINITION I58488
ACCESSION I58488
VERSION I58488.1 GI:2477726
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1297)
AUTHORS Caput,D., Ferrara,P., Guillemot,J., Kaghad,M., Labit-Le
Bouteiller,C., Leplatois,P., Magazin,M. and Minty,A.
TITLE Protein having interleukin 13 activity, recombinant DNA coding for
this protein, transformed cells and microorganisms
JOURNAL Patent: US 5652123-A 15 29-JUL-1997;
FEATURES
source Location/Qualifiers
1..1297
/organism="unknown"
BASE COUNT 309 a 341 c 336 g 311 t
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Query Match 56.3%; Score 185.8; DB 10; Length 1297;
Best Local Similarity 76.6%; Pred. No. 2.2e-38;
Matches 255; Conservative 0; Mismatches 72; Indels 6; Gaps 2;

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Qy	179	ggaccacagagatgctgaaagcactgtgctctcaaaagcccgcggcagg---gattttcca	235
Db	298	AGACCCAGAGGATGCTGAGCGGATTCTGCCCGCACAAAGTCTCAGCTGGGCAGTTTTTCCA	357
Qy	236	gtgaacgcagccgcagagacacacaaaattgaagtgatccagttggtgaaaaaacctgctcacct	295
Db	358	GCTTGCATGTCGGAGACACCAAAATCGAGGTGGCCAGTTTGTAAAGGACCTGCTCTTAC	417
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LOCUS	A29950	384 bp	DNA
DEFINITION	Nucleic acid fragment B.		
ACCESSION	A29950		
VERSION	A29950.1	GI:1249030	
KEYWORDS	synthetic construct.		
SOURCE	synthetic construct		
ORGANISM	artificial sequence.		
REFERENCE	1 (bases 1 to 384)		
AUTHORS	Caput,D., Ferrara,P., Guillemot,J.C., Kaghad,M., Labit-le		
TITLE	Bouteiller,C., Leplatois,P., Magazin,M. and Minty,A.		
JOURNAL	Protein having cytokin type activity, recombinant DNA coding for		
	this protein, transformed cells and microorganisms		
PATENT	Patent: EP 0506574-A 23 30-SEP-1992;		
ELF SANOFI			
FEATURES			
source	Location/Qualifiers		
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BASE COUNT	97 a	104 c	99 g 84 t
ORIGIN			
Query Match 55.8%; Score 184.2; DB 9; Length 384;			
Best Local Similarity 76.3%; Pred. NO. 6.3e-38;			
Matches 254; Conservative 0; Mismatches 73; Indels 6; Gaps 2;			
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Db	23	GCCCTGTGCTCCCTCTACGGCCCTCAGGGAGCTCATTTGAGGAGCTGGTCAACATCACCC	82
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Db	83	AGAACGAGAAGGCTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAACCTGACAGCTG	142
QY	119	gcatgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgccatccaaa	178
Db	143	ACATGTACTGTGCAGCCCTGGAAATCCCTGATCAACGTTGTCAGGCTGCAGTGCCATCGAGA	202
QY	179	ggaccacagagatgctgaaagcactgtgctctcaaaagcccgcggcagg---gattttcca	235
Db	203	AGACCCAGAGGATGCTGAGCGGATTCTGCCCGCACAAAGTCTCAGCTGGGCAGTTTTTCCA	262
QY	236	gtgaacgcagccgcagagacacacaaaattgaagtgatccagttggtgaaaaaacctgctcacct	295
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QY	296	atgtaaggggagtttatcgccatggaaaatttca	328
Db	323	ATTTAAGAAACTTTTTCGCGAGGGACGGTTCA	355
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LOCUS	I58489	384 bp	DNA	PAT	07-OCT-1997
DEFINITION	Sequence 17 from patent US 5652123.				
ACCESSION	I58489				
VERSION	I58489.1	GI:2477727			
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 384)				
AUTHORS	Caput,D., Ferrara,P., Guillemot,J., Kaghad,M., Labit-Le Boutellier,C., Leplatois,P., Magazin,M. and Minty,A.				
TITLE	Protein having interleukin 13 activity, recombinant DNA coding for this protein, transformed cells and microorganisms				
JOURNAL	Patent: US 5652123-A 17 29-JUL-1997;				
FEATURES	Location/Qualifiers				
source	1..384				
	/organism="unknown"				
BASE COUNT	97 a	104 c	99 g	84 t	
ORIGIN					
Query Match	55.8%; Score 184.2; DB 10; Length 384;				
Best Local Similarity	76.3%; Pred. No. 6.3e-38;				
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QY	179	ggaccacagagatgctgaaagcactgtgctctcaaaagcccgcgcagg---gattttcca	235		
Db	203	AGACCCAGAGGATGCTGAGCGGATTCTGCCCGCACAAAGGTCTCAGCTGGGCAGTTTCCA	262		
QY	236	gtgaacgcagccgcagacacacaaaattgaagtgcattccagttggtgaaaaaacctgctcacct	295		
Db	263	GCTTGCATGTCGGAGACACCAAAATCGAGTGGCCCCAGTTTGTAAAGGACCTGCTCTTAC	322		
QY	296	atgtaaggggagtttatcgcccatggaaatttca	328		
Db	323	ATTTAAGAAACTTTTTCGCGAGGGACGGTTCA	355		
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DEFINITION	Sequence 4 from patent US 5856142.				
ACCESSION	AR027065				
VERSION	AR027065.1	GI:5937905			
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 425)				
AUTHORS	Legoux,R., Maldonado,P. and Salome,M.				
TITLE	Method for the extraction of periplasmic proteins from prokaryotic microorganisms in the presence of arginine				
JOURNAL	Patent: US 5856142-A 4 05-JAN-1999;				
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source	1..425				
	/organism="unknown"				
BASE COUNT	100 a	116 c	110 g	99 t	
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Query Match	55.3%; Score 182.6; DB 9; Length 425;				

Best Local Similarity 76.0%; Pred. No. 1.6e-37;		
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QY	62 agaatc--agggcatccctctgcaacaggcagcatgggtgtggagcgtcaacctgaccgcg 118	
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QY	119 gcatgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgccatccaaa 178	
Db	185 GCATGTACTGTGCAGCCCTGGAAATCCCTGTATCAACGTGTACGGCTGCAGTGCCATCGAGA 244	
QY	179 ggacccagaggatgctgaaagcaactgtgctctctcaaaagcccgggcagg--gattcca 235	
Db	245 AGACCCAGAGGATGCTAGCGGATCTGCCCGCACAGGTCTCAGCTGGGCAGTTTCCA 304	
QY	236 gtgaacgcagccgcagacacacaaaattgaaagtgatccagttggtgaaaaaacctgctcacct 295	
Db	305 GCTTGCATGTCAGGAGACACCAAAATCGAGGTGGCCCCAGTTTGTAAAGGACCTGCTCTTAC 364	
QY	296 atgtaaggggagtttatcgccatggaatttca 328	
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RESULT	15				
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DEFINITION	Sequence 4	from patent	US 5700665.		
ACCESSION	I86198				
VERSION	I86198.1	GI:3205916			
KEYWORDS	.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
	Unclassified.				
REFERENCE	1 (bases 1 to 425)				
AUTHORS	Legoux, R., Maldonado, P. and Salome, M.				
TITLE	Method for the extraction of periplasmic proteins from prokaryotic microorganisms in the presence of arginine				
JOURNAL	Patent: US 5700665-A 4 23-DEC-1997;				
FEATURES	Location/Qualifiers				
source	1. .425				
	/organism="unknown"				
BASE COUNT	100 a	116 c	110 g	99 t	
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Query Match	55.3%	Score 182.6;	DB 10;	Length 425;
Best Local Similarity	76.0%;	Pred. No. 1.6e-37;		
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QY	62	agaatc---aggcatccctctgcaacggcgagcatgggtgtggagcgtcaacctgacgcgcg	118	
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Db	185	GCATGTACTGTGCAGCCCTTGGAA'TCCCTGATCAACGCTGTACGCTGCAGTGCCTCGAGA	244	
QY	179	ggaccagagaggatgctgaagcacctgtgctctcctcaaaagcccggggcagg---gatttcca	235	
Db	245	AGACCCAGAGGATGCTGAGCGGAT'TCTGCCCGCACAAAGGCTCAGCTGGGCAGT'TTTC	304	
QY	236	gtgaacgcagccgagacaccaaattgaagtgatccagttggtgaaaaaacctgctcacct	295	
Db	305	GCTTGCATGTCCGAGACACCAAATCGAGGTGGCCAGTTTGTAAAGGACCTGCTCTTAC	364	

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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

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Searched: 678276 seqs, 291890651 residues

Total number of hits satisfying chosen parameters: 1356552

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	330	100.0	330	21	Canine mature inte
2	330	100.0	330	21	Canine mature inte
3	330	100.0	390	21	Canine interleukin
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5	330	100.0	1269	21	Canine interleukin
6	330	100.0	1269	21	Canine interleukin
7	317	96.1	333	21	Canine mature inte
8	317	96.1	333	21	Canine mature inte
9	317	96.1	393	21	Canine interleukin
10	317	96.1	393	21	Canine interleukin
11	317	96.1	1302	21	Canine interleukin

C	12	317	96.1	1302	21	Z55556	Canine interleukin
	13	240	72.7	272	21	Z55553	Canine interleukin
	14	218	66.1	278	21	Z55554	Canine interleukin
	15	187.4	56.8	336	13	Q28944	Gly41-Cytokine cod
	16	187.4	56.8	1270	21	F21334	Human low adenodin
	17	187.4	56.8	1270	21	A35212	Human adenosine re
	18	187.4	56.8	1282	21	F21332	Human low adenodin
	19	187.4	56.8	1282	21	A35210	Human adenosine re
	20	187.4	56.8	1290	15	Q56692	Sequence encoding
	21	187.4	56.8	6952	21	F21333	Human low adenodin
	22	187.4	56.8	6952	21	A35211	Human adenosine re
	23	187.4	56.8	14978	21	F21338	Human low adenodin
	24	187.4	56.8	14978	21	A35216	Human adenosine re
	25	185.8	56.3	336	13	Q28943	Asp41-Cytokine cod
	26	185.8	56.3	1297	13	Q28947	Cytokine NC30. Q
	27	151.4	45.9	1212	15	Q56693	Sequence encoding
	28	71.4	21.6	5670	21	F21331	Human low adenodin
	29	71.4	21.6	5670	21	F21337	Human low adenodin
	30	71.4	21.6	5670	21	A35209	Human adenosine re
	31	71.4	21.6	5670	21	A35215	Human adenosine re
	32	39	11.8	166	21	Z55552	Canine interleukin
	33	34	10.3	479	21	C38383	Zea mays DNA fragm
	34	34	10.3	1896	21	Z48297	S. coelicolor yesw
C	35	33.8	10.2	2792	20	X78074	Rat DTDST cDNA. R
	36	33.4	10.1	66	20	Z32227	Human interleukin
	37	33.4	10.1	772	19	V48405	Dominant-negative
	38	32.4	9.8	717	21	A93373	Enhanced green fluo
	39	32.4	9.8	717	21	A93374	Enhanced blue fluo
	40	32.4	9.8	717	21	A93375	Enhanced cyan fluo
	41	32.4	9.8	717	21	A27573	DNA encoding EGFP
	42	32.4	9.8	717	21	A27574	DNA encoding EBFP
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	44	32.4	9.8	720	21	C62377	CDNA encoding a gr
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ALIGNMENTS

RESULT 1  
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ID Z55565 standard; cDNA; 330 BP.  
XX  
AC Z55565;  
XX  
DT 14-MAR-2000 (first entry)  
XX  
DE Canine mature interleukin-13 (IL-13) clone 78 cDNA.  
XX  
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;  
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.  
XX  
OS Canis familiaris.  
XX  
PN WO9961618-A2.  
XX  
PD 02-DEC-1999.  
XX  
PF 28-MAY-1999; 99WO-US11942.  
XX  
PR 29-MAY-1998; 98US-0087306.  
XX  
PA (HESK-) HESKA CORP.  
XX  
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;  
XX  
DR WPI; 2000-072623/06.  
XX  
PT P-PSDB; Y58224.  
XX  
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
XX useful for treating or preventing e.g. tumors or autoimmune disease  
PS Claim 11.; Page 239-240; 264pp; English.



XX Sequences Z55552-Z55560 and Z55561-Z55566 represent cDNA  
CC sequences encoding canine interleukin-13 (IL-13) clones 80  
CC and 78 respectively. The invention relates to canine  
CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or  
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline  
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage  
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these  
CC immunoregulatory proteins. The proteins, their associated  
CC nucleic acids, specific antibodies and inhibitors may be used as  
CC vaccines for therapeutic or prophylactic regulation of an immune  
CC response in animals (particularly cats, dogs, horses and humans).  
CC They may be used to treat autoimmune or infectious diseases including  
CC allergies, tumours, inflammation and graft rejection, and to increase  
CC the response from a co-administered antigen. The nucleotide sequences  
CC can also be used for the recombinant production of a protein, while  
CC nucleotide fragments are useful as probes, as amplification primers and  
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
CC The proteins may be used to raise antibodies and to screen for  
CC modulators of activity, while the antibodies may be used in detection,  
CC and in drug targeting.  
XX  
SQ Sequence 330 BP; 88 A; 96 C; 82 G; 64 T; 0 other;

Query Match 100.0%; Score 330; DB 21; Length 330;  
Best Local Similarity 100.0%; Pred. No. 1.3e-88;  
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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QY 181 acccagaggtgctgaaagcactgtgctctcaaaagcccgaggcaggttccagttaa 240  
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ID Z55566 standard; cDNA; 330 BP.  
XX  
AC Z55566;  
XX  
DT 14-MAR-2000 (first entry)  
XX  
DE Canine mature interleukin-13 (IL-13) clone 78 cDNA complement.  
XX  
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;  
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.  
XX  
OS Canis familiaris.

XX WO9961618-A2.  
XX  
PD 02-DEC-1999.  
XX

PF 28-MAY-1999; 99WO-US11942.  
XX  
PR 29-MAY-1998; 98US-0087306.  
XX  
PA (HESK-) HESKA CORP.  
XX  
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;  
XX  
DR WPI; 2000-072623/06.  
DR P-PSDB; Y58224.  
XX  
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
PT useful for treating or preventing e.g. tumors or autoimmune disease  
XX  
PS Claim 1i; Page 241; 264pp; English.  
XX  
CC Sequences Z55552-Z55560 and Z55561-Z55566 represent cDNA  
CC sequences encoding canine interleukin-13 (IL-13) clones 80  
CC and 78 respectively. The invention relates to canine  
CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or  
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline  
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage  
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these  
CC immunoregulatory proteins. The proteins, their associated  
CC nucleic acids, specific antibodies and inhibitors may be used as  
CC vaccines for therapeutic or prophylactic regulation of an immune  
CC response in animals (particularly cats, dogs, horses and humans).  
CC They may be used to treat autoimmune or infectious diseases including  
CC allergies, tumours, inflammation and graft rejection, and to increase  
CC the response from a co-administered antigen. The nucleotide sequences  
CC can also be used for the recombinant production of a protein, while  
CC nucleotide fragments are useful as probes, as amplification primers and  
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
CC The proteins may be used to raise antibodies and to screen for  
CC modulators of activity, while the antibodies may be used in detection,  
CC and in drug targeting.  
XX  
SQ Sequence 330 BP; 64 A; 82 C; 96 G; 88 T; 0 other;

Query Match 100.0%; Score 330; DB 21; Length 330;  
Best Local Similarity 100.0%; Pred. No. 1.3e-88;  
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 270 CAGAATCAGGCATCCCTCTGCAACGGCAGCATGTTGTGGAGCGTCAACCTGACCGCGGC 211  
QY 121 atgtactgcgagctctagaaatctctgatcaatgtctccgactgcagcgccatccaaagg 180  
Db 210 ATGTACTGCGCAGCTCTAGAAATCTCTGATCAATGTCTCCGACTGCAGCGCCATCCAAAGG 151  
QY 181 acccagaggtgctgaaagcactgtgctctcaaaagcccgaggcaggttccagttaa 240  
Db 150 ACCCAGAGGATGCTGAAAGCACTGTGCTCTCAAAAGCCCGGACGGGATTTCCAGTGAA 91  
QY 241 cgcagccgagacacacaaattgaagtgtatccagttggtgaaaaacctgtcacctatgta 300  
Db 90 CGCAGCCGAGACACACAAATTTGAAGTGATCCAGTTGGTGAAAAACCTGCTCACCTATGTA 31  
QY 301 aggggagtttatcgccatggaaatttcaga 330  
Db 30 AGGGGAGTTTATCGCCCATGGAAATTTTCAGA 1

RESULT 3  
255563  
ID Z55563 standard; cDNA; 390 BP.  
XX

AC 255563;  
XX  
DT 14-MAR-2000 (first entry)  
XX  
DE Canine interleukin-13 (IL-13) clone 78 cDNA coding region.  
XX  
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;  
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.  
XX  
OS Canis familiaris.  
XX  
PN WO9961618-A2.  
XX  
PD 02-DEC-1999.  
XX  
PF 28-MAY-1999; 99WO-US11942.  
XX  
PR 29-MAY-1998; 98US-0087306.  
XX  
PA (HESK-) HESKA CORP.  
XX  
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;  
XX  
KW WPI; 2000-072623/06.  
DR P-PSDB; Y58223.  
XX  
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
PT useful for treating or preventing e.g. tumors or autoimmune disease  
XX  
PS Claim 1i; Page 238-239; 264pp; English.  
XX  
CC Sequences 255552-255560 and 255561-255566 represent cDNA  
CC sequences encoding canine interleukin-13 (IL-13) clones 80  
CC and 78 respectively. The invention relates to canine  
CC IL-4, canine or feline Flt-3 ligand, canine or feline IL-13, canine or  
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline  
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage  
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these  
CC immunoregulatory proteins. The proteins, their associated  
CC nucleic acids, specific antibodies and inhibitors may be used as  
CC vaccines for therapeutic or prophylactic regulation of an immune  
CC response in animals (particularly cats, dogs, horses and humans).  
CC They may be used to treat autoimmune or infectious diseases including  
CC allergies, tumours, inflammation and graft rejection, and to increase  
CC the response from a co-administered antigen. The nucleotide sequences  
CC can also be used for the recombinant production of a protein, while  
CC nucleotide fragments are useful as probes, as amplification primers and  
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
CC The proteins may be used to raise antibodies and to screen for  
CC modulators of activity, while the antibodies may be used in detection,  
CC and in drug targeting.  
XX  
SQ Sequence 390 BP; 92 A; 117 C; 99 G; 82 T; 0 other;

Query Match 100.0%; Score 330; DB 21; Length 390;  
Best Local Similarity 100.0%; Pred. No. 1.4e-88;  
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agccctgtgactccctcccaaccctcaaggagctcattgaggagctggtcaacatcacc 60  
|||||  
Db 61 agccctgtgactccctcccaaccctcaaggagctcattgaggagctggtcaacatcacc 120  
|||||  
QY 61 cagaatcaggcatccctctgcaacggcagcatggtgtggagcgtcaacctgaccgcggc 120  
|||||  
Db 121 cagaatcaggcatccctctgcaacggcagcatggtgtggagcgtcaacctgaccgcggc 180  
|||||  
QY 121 atgtactgcgagctctagaaatctctgatcaatgtctccgactgcagcgccatcaagg 180  
|||||  
Db 181 atgtactgcgagctctagaaatctctgatcaatgtctccgactgcagcgccatcaagg 240  
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QY 181 acccagaggatgctgaaagcactgtgctctcaaaagcccgccgagggatttcagtga 240  
|||||

Db 241 acccagaggatgctgaaagcactgtgctctcaaaagcccgccgagggatttcagtga 300  
QY 241 cgcagccgagacacacaaattgaagtgcagttggtgaaaaacctgctcacctatgta 300  
|||||  
Db 301 cgcagccgagacacacaaattgaagtgcagttggtgaaaaacctgctcacctatgta 360  
QY 301 aggggagtttatcgccatggaatttcaga 330  
|||||  
Db 361 aggggagtttatcgccatggaatttcaga 390  
RESULT 4  
255564/c  
ID Z55564 standard; cDNA; 390 BP.  
XX  
AC Z55564;  
XX  
DT 14-MAR-2000 (first entry)  
XX  
DE Canine interleukin-13 (IL-13) clone 78 cDNA coding region complement.  
XX  
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;  
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.  
XX  
OS Canis familiaris.  
XX  
PN WO9961618-A2.  
XX  
PD 02-DEC-1999.  
XX  
PF 28-MAY-1999; 99WO-US11942.  
XX  
PR 29-MAY-1998; 98US-0087306.  
XX  
PA (HESK-) HESKA CORP.  
XX  
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;  
XX  
DR WPI; 2000-072623/06.  
DR P-PSDB; Y58223.  
XX  
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
PT useful for treating or preventing e.g. tumors or autoimmune disease  
XX  
PS Claim 1i; Page 239; 264pp; English.  
XX  
CC Sequences 255552-255560 and 255561-255566 represent cDNA  
CC sequences encoding canine interleukin-13 (IL-13) clones 80  
CC and 78 respectively. The invention relates to canine  
CC IL-4, canine or feline Flt-3 ligand, canine or feline IL-13, canine or  
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline  
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage  
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these  
CC immunoregulatory proteins. The proteins, their associated  
CC nucleic acids, specific antibodies and inhibitors may be used as  
CC vaccines for therapeutic or prophylactic regulation of an immune  
CC response in animals (particularly cats, dogs, horses and humans).  
CC They may be used to treat autoimmune or infectious diseases including  
CC allergies, tumours, inflammation and graft rejection, and to increase  
CC the response from a co-administered antigen. The nucleotide sequences  
CC can also be used for the recombinant production of a protein, while  
CC nucleotide fragments are useful as probes, as amplification primers and  
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
CC The proteins may be used to raise antibodies and to screen for  
CC modulators of activity, while the antibodies may be used in detection,  
CC and in drug targeting.  
XX  
SQ Sequence 390 BP; 82 A; 99 C; 117 G; 92 T; 0 other;

Query Match 100.0%; Score 330; DB 21; Length 390;  
Best Local Similarity 100.0%; Pred. No. 1.4e-88;  
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agccctgtgactccctcccaaccctcaaggagctcattgagagctggtcaacatcacc 60  
Db 330 AGCCCTGTGACTCCCTCCCAACCCCTCAAGGAGCTCATTTGAGAGCTGGTCAACATCACC 271  
QY 61 cagaatcaggcatccctctgcaacggcagcatgggtgtggagcgtcaacacctgaccgcccgc 120  
Db 270 CAGAATCAGGCATCCCTCTGCAACGGCAGCATGGTGTGGAGCGTCAACCTGACCGCCGGC 211  
QY 121 atgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgccatccaaagg 180  
Db 210 ATGTACTGCGCAGCTCTAGAAATCTCTGATCAATGTCTCCGACTGCAGCGCCATCCAAAGG 151  
QY 181 acccagaggatgctgaaagcactgtgctctcaaaagcccgcgaggatttccagtga 240  
Db 150 ACCCAGAGGATGCTGAAAGCACCTGTCTCTCAAAAGCCCGCGCAGGGATTTCAGTGAA 91  
QY 241 cgcagccgagacaccaaattgaagtgatccagttggtgaaacacctgctcacctatgta 300  
Db 90 CCGAGCCGAGACACCAAAATTTGAAGTGATCCAGTTGGTGAAACCACTGCTCACCTATGTA 31  
QY 301 aggggagtttatcgccatggaaatttcaga 330  
Db 30 AGGGAGTTTATCGCCATGGAAATTTTCAGA 1  
RESULT 5  
Z55561  
ID Z55561 standard; cDNA; 1269 BP.  
XX  
AC Z55561;  
XX  
DT 14-MAR-2000 (first entry)  
XX  
DE Canine interleukin-13 (IL-13) clone 78 cDNA.  
XX  
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;  
KW Immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.  
XX  
OS Canis familiaris.  
XX  
FH Key Location/Qualifiers  
FT CDS 57..449  
FT /\*tag= a  
FT /product= "Canine IL-13 clone 78"  
XX  
PN WO9961618-A2.  
XX  
PD 02-DEC-1999.  
XX  
PF 28-MAY-1999; 99WO-US11942.  
XX  
PR 29-MAY-1998; 98US-0087306.  
XX  
PA (HESK-) HESKA CORP.  
XX  
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;  
XX  
DR WPI; 2000-072623/06.  
DR P-PSDB; Y58223.  
XX  
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
PT useful for treating or preventing e.g. tumors or autoimmune disease  
XX  
PS Claim 11; Page 235-236; 264pp; English.  
XX  
CC Sequences Z55552-Z55560 and Z55561-Z55566 represent cDNA  
CC sequences encoding canine interleukin-13 (IL-13) clones 80  
CC and 78 respectively. The invention relates to canine  
CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or  
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline  
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage  
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these

CC immunoregulatory proteins. The proteins, their associated  
CC nucleic acids, specific antibodies and inhibitors may be used as  
CC vaccines for therapeutic or prophylactic regulation of an immune  
CC response in animals (particularly cats, dogs, horses and humans).  
CC They may be used to treat autoimmune or infectious diseases including  
CC allergies, tumours, inflammation and graft rejection, and to increase  
CC the response from a co-administered antigen. The nucleotide sequences  
CC can also be used for the recombinant production of a protein, while  
CC nucleotide fragments are useful as probes, as amplification primers and  
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
CC The proteins may be used to raise antibodies and to screen for  
CC modulators of activity, while the antibodies may be used in detection,  
CC and in drug targeting.  
XX  
SQ Sequence 1269 BP; 302 A; 320 C; 340 G; 307 T; 0 other;  
Query Match 100.0%; Score 330; DB 21; Length 1269;  
Best Local Similarity 100.0%; Pred. No. 2.1e-88;  
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 agccctgtgactccctcccaaccctcaaggagctcattgagagctggtcaacatcacc 60  
Db 117 agccctgtgactccctcccaaccctcaaggagctcattgagagctggtcaacatcacc 176  
QY 61 cagaatcaggcatccctctgcaacggcagcatggtgtggagcgtcaacacctgaccgcccgc 120  
Db 177 cagaatcaggcatccctctgcaacggcagcatggtgtggagcgtcaacacctgaccgcccgc 236  
QY 121 atgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgccatccaaagg 180  
Db 237 atgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgccatccaaagg 296  
QY 181 acccagaggatgctgaaagcactgtgctctcaaaagcccgcgaggatttccagtga 240  
Db 297 acccagaggatgctgaaagcactgtgctctcaaaagcccgcgaggatttccagtga 356  
QY 241 cgcagccgagacaccaaattgaagtgatccagttggtgaaacacctgctcacctatgta 300  
Db 357 cgcagccgagacaccaaattgaagtgatccagttggtgaaacacctgctcacctatgta 416  
QY 301 aggggagtttatcgccatggaaatttcaga 330  
Db 417 aggggagtttatcgccatggaaatttcaga 446  
RESULT 6  
Z55562/C  
ID Z55562 standard; cDNA; 1269 BP.  
XX  
AC Z55562;  
XX  
DT 14-MAR-2000 (first entry)  
XX  
DE Canine interleukin-13 (IL-13) clone 78 cDNA complement.  
XX  
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;  
KW Immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.  
XX  
OS Canis familiaris.  
XX  
FH Key Location/Qualifiers  
FT CDS complement (821..1213)  
FT /\*tag= a  
FT /product= "Canine IL-13 clone 78"  
XX  
PN WO9961618-A2.  
XX  
PD 02-DEC-1999.  
XX  
PF 28-MAY-1999; 99WO-US11942.  
XX  
PR 29-MAY-1998; 98US-0087306.



```
XX (HESK-) HESKA CORP.
PA
XX
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;
XX
DR WPI; 2000-072623/06.
DR P-PSDB; Y58223.
XX
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,
PT useful for treating or preventing e.g. tumors or autoimmune disease
XX
PS Claim 11; Page 237-238; 264pp; English.
XX
CC Sequences 255552-255560 and 255561-255566 represent cDNA
CC sequences encoding canine interleukin-13 (IL-13) clones 80
CC and 78 respectively. The invention relates to canine
CC IL-4, canine or feline Flt-3 ligand, canine or feline IL-13, feline
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these
CC immunoregulatory proteins. The proteins, their associated
CC nucleic acids, specific antibodies and inhibitors may be used as
CC vaccines for therapeutic or prophylactic regulation of an immune
CC response in animals (particularly cats, dogs, horses and humans).
CC They may be used to treat autoimmune or infectious diseases including
CC allergies, tumours, inflammation and graft rejection, and to increase
CC the response from a co-administered antigen. The nucleotide sequences
CC can also be used for the recombinant production of a protein, while
CC nucleotide fragments are useful as probes, as amplification primers and
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
CC The proteins may be used to raise antibodies and to screen for
CC modulators of activity, while the antibodies may be used in detection,
CC and in drug targeting.
XX
SQ Sequence 1269 BP; 307 A; 340 C; 320 G; 302 T; 0 other;

Query Match 100.0%; Score 330; DB 21; Length 1269;
Best Local Similarity 100.0%; Pred. No. 2.1e-88;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agccctgtgactccctcccaaccctcaaggagctcattgaggagctggtcaacatcacc 60
Db 1153 AGCCCTGTGACTCCCTCCCAACCCCTCAAGGAGCTCATTGAGGAGCTGGTCAACATCACC 1094
QY 61 cagaatcaggcatccctctgcaacggcagcatggtgtgagcgtcaacctgaccgcggc 120
Db 1093 CAGAATCAGGCATCCCTCTGTGCAACGGCAGCATGGTGTGGAGCGTCAACCTGACCGCGGC 1034
QY 121 atgtactgcgagctctagaatctctgatcaatgtctccgactgcagcgccatccaaagg 180
Db 1033 ATGTACTGCGAGCTCTAGAATCTCTGATCAATGTCTCCGACTGCAGCGCCATCCAAAGG 974
QY 181 acccagaggatgctgaaagcactgtgctctcaaaagcccgaggcaggatttccagtga 240
Db 973 ACCCAGAGGATGCTGAAAGCACTGTGCTCTCAAAAGCCCGCGCAGGGATTTCACGTGAA 914
QY 241 cgcagccgagacacccaaaattgaagtgatccagttggtgaaacacctgctcacctatgta 300
Db 913 CGCAGCCGAGACACCAAAATTGAAGTGATCCAGTTGGTGAAAAACCTGCTCACCTATGTA 854
QY 301 aggggagtttatcgccatggaaatttcaga 330
Db 853 AGGGGAGTTTATCGCCATGGAAATTTTCAGA 824

RESULT 7
Z55559
ID Z55559 standard; cDNA; 333 BP.
XX
AC Z55559;
XX
DT 14-MAR-2000 (first entry)
```

```
XX Canine mature interleukin-13 (IL-13) clone 80 cDNA.
DE
XX
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
XX
OS Canis familiaris.
XX
PN WO9961618-A2.
XX
PD 02-DEC-1999.
XX
XX 28-MAY-1999; 99WO-US11942.
PF
XX 29-MAY-1998; 98US-0087306.
PR
XX (HESK-) HESKA CORP.
PA
XX Sim G, Yang S, Dreitz MJ, Wonderling RS;
PI
XX WPI; 2000-072623/06.
DR P-PSDB; Y58222.
XX
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,
PT useful for treating or preventing e.g. tumors or autoimmune disease
XX
PS Claim 11; Page 233-234; 264pp; English.
XX
CC Sequences 255552-255560 and 255561-255566 represent cDNA
CC sequences encoding canine interleukin-13 (IL-13) clones 80
CC and 78 respectively. The invention relates to canine
CC IL-4, canine or feline Flt-3 ligand, canine or feline IL-13, canine or
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these
CC immunoregulatory proteins. The proteins, their associated
CC nucleic acids, specific antibodies and inhibitors may be used as
CC vaccines for therapeutic or prophylactic regulation of an immune
CC response in animals (particularly cats, dogs, horses and humans).
CC They may be used to treat autoimmune or infectious diseases including
CC allergies, tumours, inflammation and graft rejection, and to increase
CC the response from a co-administered antigen. The nucleotide sequences
CC can also be used for the recombinant production of a protein, while
CC nucleotide fragments are useful as probes, as amplification primers and
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
CC The proteins may be used to raise antibodies and to screen for
CC modulators of activity, while the antibodies may be used in detection,
CC and in drug targeting.
XX
SQ Sequence 333 BP; 89 A; 97 C; 83 G; 64 T; 0 other;

Query Match 96.1%; Score 317; DB 21; Length 333;
Best Local Similarity 99.1%; Pred. No. 9.2e-85;
Matches 330; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 1 agccctgtgactccctcccaaccctcaaggagctcattgaggagctggtcaacatcacc 60
Db 1 agccctgtgactccctcccaaccctcaaggagctcattgaggagctggtcaacatcacc 60
QY 61 cagaatcaggcatccctctgcaacggcagcatggtgtgagcgtcaacctgaccgcggc 120
Db 61 cagaatcaggcatccctctgcaacggcagcatggtgtgagcgtcaacctgaccgcggc 120
QY 121 atgtactgcgagctctagaatctctgatcaatgtctccgactgcagcgccatccaaagg 180
Db 121 atgtactgcgagctctagaatctctgatcaatgtctccgactgcagcgccatccaaagg 180
QY 181 acccagaggatgctgaaagcactgtgctctcaaaagcccgaggcagg--gatttcagt 237
Db 181 acccagaggatgctgaaagcactgtgctctcaaaagcccgaggcaggatttcagt 240
QY 238 gaacycagcgagacacccaaaattgaagtgatccagttggtgaaaaaacctgctcacctat 297
```



|||||  
Db 241 gaacgcagccgagacacacaaattgaagtgtccagttgtgaaacacgtgtcacctat 300  
QY 298 gtaaggggagtttatcccatggaatttcaga 330  
Db 301 gtaaggggagtttatcccatggaatttcaga 333  
RESULT 8  
Z55560/c  
ID 255560 standard; cDNA; 333 BP.  
XX  
AC  
XX  
XX  
DT 14-MAR-2000 (first entry)  
XX  
XX  
DE Canine mature interleukin-13 (IL-13) clone 80 cDNA complement.  
XX  
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;  
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.  
XX  
OS Canis familiaris.  
XX  
XX  
PN WO9961618-A2.  
XX  
PD 02-DEC-1999.  
XX  
XX  
PF 28-MAY-1999; 99WO-US11942.  
XX  
PR 29-MAY-1998; 98US-0087306.  
XX  
PA (HESK-) HESKA CORP.  
XX  
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;  
XX  
XX  
DR WPI; 2000-072623/06.  
DR P-PSDB; Y58222.  
XX  
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
PT useful for treating or preventing e.g. tumors or autoimmune disease  
XX  
PS Claim 1i; Page 235; 264pp; English.  
XX  
CC Sequences 255552-255560 and 255561-255566 represent cDNA  
CC sequences encoding canine interleukin-13 (IL-13) clones 80  
CC and 78 respectively. The invention relates to canine  
CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or  
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline  
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage  
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these  
CC immunoregulatory proteins. The proteins, their associated  
CC nucleic acids, specific antibodies and inhibitors may be used as  
CC vaccines for therapeutic or prophylactic regulation of an immune  
CC response in animals (particularly cats, dogs, horses and humans).  
CC They may be used to treat autoimmune or infectious diseases including  
CC allergies, tumours, inflammation and graft rejection, and to increase  
CC the response from a co-administered antigen. The nucleotide sequences  
CC can also be used for the recombinant production of a protein, while  
CC nucleotide fragments are useful as probes, as amplification primers and  
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
CC The proteins may be used to raise antibodies and to screen for  
CC modulators of activity, while the antibodies may be used in detection,  
CC and in drug targetting.  
XX  
SQ Sequence 333 BP; 64 A; 83 C; 97 G; 89 T; 0 other;

Query Match 96.1%; Score 317; DB 21; Length 333;  
Best Local Similarity 99.1%; Pred. No. 9.2e-85;  
Matches 330; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 1 agccctgtgactccctcccaaccctcaaggagctcatgaggagctgtgtaacatcacc 60  
|||||

Db 333 AGCCCTGTGACTCCCTCCCAACCCTCAAGGAGCTCATTGAGGAGCTGGTCAACATCACC 274  
QY 61 cagaatcaggcatccctctgcaacggcagcatgtgtgagcgtcaacctgaccgcccgc 120  
|||||  
Db 273 CAGAATCAGGCATCCCTCTGCAACGGCAGCATGCTGTGGAGCGTCAACCTGACCGCCGC 214  
QY 121 atgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgccatccaaagg 180  
|||||  
Db 213 ATGTACTGGCAGCTCTAGAAATCTCTGTATCAATGTCTCCGACTGCAGCGCCATCCAAAG 154  
QY 181 acccagaggatgtgaaagcactgtgtctctcaaaagcccgcgagg---gattccagt 237  
|||||  
Db 153 ACCCAGAGGATGCTGAAAGCACTGTGTCTCTCAAAAGCCCGCGGAGGAGATTTCCAGT 94  
QY 238 gaacgcagccgagacacacaaattgaagtgtccagttgtgaaaaacctgtcacctat 297  
|||||  
Db 93 GAACGCAGCCGAGACACACCAAAATTGAAGTGATCCAGTTGGTGAAAAACCTGCTCACCTAT 34  
QY 298 gtaaggggagtttatcccatggaatttcaga 330  
Db 33 GTAAGGGGAGTTTATCGCCATGGAAATTTTCAGA 1  
RESULT 9  
Z55557  
ID 255557 standard; cDNA; 393 BP.  
XX  
AC  
XX  
XX  
DT 14-MAR-2000 (first entry)  
XX  
DE Canine interleukin-13 (IL-13) clone 80 cDNA coding region.  
XX  
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;  
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.  
XX  
OS Canis familiaris.  
XX  
PN WO9961618-A2.  
XX  
PD 02-DEC-1999.  
XX  
PF 28-MAY-1999; 99WO-US11942.  
XX  
PR 29-MAY-1998; 98US-0087306.  
XX  
PA (HESK-) HESKA CORP.  
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;  
XX  
XX  
DR WPI; 2000-072623/06.  
DR P-PSDB; Y58221..  
XX  
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
PT useful for treating or preventing e.g. tumors or autoimmune disease  
XX  
PS Claim 1i; Page 232-233; 264pp; English.  
XX  
CC Sequences 255552-255560 and 255561-255566 represent cDNA  
CC sequences encoding canine interleukin-13 (IL-13) clones 80  
CC and 78 respectively. The invention relates to canine  
CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or  
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline  
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage  
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these  
CC immunoregulatory proteins. The proteins, their associated  
CC nucleic acids, specific antibodies and inhibitors may be used as  
CC vaccines for therapeutic or prophylactic regulation of an immune  
CC response in animals (particularly cats, dogs, horses and humans).  
CC They may be used to treat autoimmune or infectious diseases including  
CC allergies, tumours, inflammation and graft rejection, and to increase  
CC the response from a co-administered antigen. The nucleotide sequences  
CC can also be used for the recombinant production of a protein, while

nucleotide fragments are useful as probes, as amplification primers and as sources of inhibitory therapeutics (e.g., antisense oligonucleotides). The proteins may be used to raise antibodies and to screen for modulators of activity, while the antibodies may be used in detection, and in drug targeting.

Query Match 96.1%; Score 317; DB 21; Length 393;  
Best Local Similarity 99.1%; Pred. NO. 9.8e-85;  
Matches 330; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY	1	agccctgtgactccctcccaacccctcaaggagctcattgaggagctggtcaacatcacc	60
Db	61	agccctgtgactccctcccaacccctcaaggagctcattgaggagctggtcaacatcacc	120
QY	61	cagaatcaggcatccctctgcaacggcagcatggtgtggagcgtcaacccctgacgcgcgc	120
Db	121	cagaatcaggcatccctctgcaacggcagcatggtgtggagcgtcaacccctgacgcgcgc	180
QY	121	atgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgccatccaaagg	180
Db	181	atgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgccatccaaagg	240
QY	181	accagaggatgctgaaagcactgtgctctcaaaaagcccgcgagg--gatttcacgt	237
Db	241	accagaggatgctgaaagcactgtgctctcaaaaagcccgcgagggtttccagt	300
QY	238	gaacgcagccgagacacaaaaattgaagtgtccagttggtgaaaaacccctgctcacctat	297
Db	301	gaacgcagccgagacacaaaaattgaagtgtccagttggtgaaaaacccctgctcacctat	360
QY	298	gtaaggggagtttatcgccatggaaatttcaga	330
Db	361	gtaaggggagtttatcgccatggaaatttcaga	393

RESULT	10	
Z55558/c		
ID	Z55558	standard; cDNA; 393 BP.
XX	AC	Z55558;
XX	AC	
DT	14-MAR-2000	(first entry)
XX		
DE	Canine interleukin-13 (IL-13)	clone 80 cDNA coding region complement
XX		
KW	Interleukin-13; IL-13;	antibody; canine; inhibitor; immune response;
KW	immunoregulation;	tumour; cancer; autoimmune disease; vaccine; ss.
XX		
OS	Canis familiaris.	
XX		
PN	WO9961618-A2.	
XX		
PD	02-DEC-1999.	
XX		
PF	28-MAY-1999;	99WO-US11942.
XX		
PR	29-MAY-1998;	98US-0087306.
XX		
PA	(HESK-)	HESKA CORP.
XX		
PI	Sim G, Yang S, Dreitz MJ,	Wonderling RS;
XX		
DR	WPI; 2000-072623/06.	
DR	P-PSDB; Y58221.	
XX		
PT	Nucleic acids encoding	immunoregulatory proteins from cats or dogs,
PT	useful for treating or	preventing e.g. tumors or autoimmune disease
XX		
PS	Claim 11; page 233;	264pp; English.
XX		

PN WO9961618-A2.  
XX  
PD 02-DEC-1999.  
XX  
PF 28-MAY-1999; 99WO-US11942.  
XX  
PR 29-MAY-1998; 98US-0087306.  
XX  
PA (HESK-) HESKA CORP.  
XX  
PI Sim G, Yang S, Drelitz MJ, Wonderling RS;  
XX  
DR WPI; 2000-072623/06.  
DR P-PSDB; Y58221.  
XX  
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
PT useful for treating or preventing e.g. tumors or autoimmune disease  
XX  
PS Claim 11; Page 229-230; 264pp; English.  
XX  
CC Sequences 255552-255560 and 255561-255566 represent cDNA  
CC sequences encoding canine interleukin-13 (IL-13) clones 80  
CC and 78 respectively. The invention relates to canine  
CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or  
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline  
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage  
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these  
CC immunoregulatory proteins. The proteins, their associated  
CC nucleic acids, specific antibodies and inhibitors may be used as  
CC vaccines for therapeutic or prophylactic regulation of an immune  
CC response in animals (particularly cats, dogs, horses and humans).  
CC They may be used to treat autoimmune or infectious diseases including  
CC allergies, tumours, inflammation and graft rejection, and to increase  
CC the response from a co-administered antigen. The nucleotide sequences  
CC can also be used for the recombinant production of a protein, while  
CC nucleotide fragments are useful as probes, as amplification primers and  
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
CC The proteins may be used to raise antibodies and to screen for  
CC modulators of activity, while the antibodies may be used in detection,  
CC and in drug targeting.  
XX  
SQ Sequence 1302 BP; 337 A; 318 C; 340 G; 307 T; 0 other;

Query Match 96.1%; Score 317; DB 21; Length 1302;  
Best Local Similarity 99.1%; Pred. No. 1.5e-84;  
Matches 330; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

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|||||  
Db 112 agccctgtgactccctcccccaacctcaaggagctcattgaggagctggtcaacatcacc 171  
|||||

QY 61 cagaatcaggcatccctctgcaacggcagcatggtgtggagcgtcaacctgaccgccggc 120  
|||||  
Db 172 cagaatcaggcatccctctgcaacggcagcatggtgtggagcgtcaacctgaccgccggc 231  
|||||

QY 121 atgtactgcgagctctagaatctctgatcaatgtctccgactgcagcgccatccaaagg 180  
|||||  
Db 232 atgtactgcgagctctagaatctctgatcaatgtctccgactgcagcgccatccaaagg 291  
|||||

QY 181 acccagaggatgctgaaagcactgtgctctcaaaagcccgccagg---gatttcaggt 237  
|||||  
Db 292 acccagaggatgctgaaagcactgtgctctcaaaagcccgccaggcagatttcaggt 351  
|||||

QY 238 gaacgcagccgagacaccaaattgaagtgtccagttggtgaaacacccgtgctcacctat 297  
|||||  
Db 352 gaacgcagccgagacaccaaattgaagtgtccagttggtgaaacacccgtgctcacctat 411  
|||||

QY 298 gtaaggggagtttatcgccatggaaatttcaga 330  
|||||  
Db 412 gtaaggggagtttatcgccatggaaatttcaga 444  
|||||

RESULT 12  
Z55556/c  
ID Z55556 standard; cDNA; 1302 BP.  
XX  
AC Z55556;  
XX  
DT 14-MAR-2000 (first entry)  
XX  
DE Canine interleukin-13 (IL-13) clone 80 cDNA complement.  
XX  
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;  
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.  
XX  
OS Canis familiaris.  
XX  
FH Key Location/Qualifiers  
FT CDS complement (856..1251)  
FT /\*tag= a  
FT /product= "Canine IL-13 clone 80"  
XX  
PN WO9961618-A2.  
XX  
PD 02-DEC-1999.  
XX  
PF 28-MAY-1999; 99WO-US11942.  
XX  
PR 29-MAY-1998; 98US-0087306.  
XX  
PA (HESK-) HESKA CORP.  
XX  
PI Sim G, Yang S, Drelitz MJ, Wonderling RS;  
XX  
DR WPI; 2000-072623/06.  
DR P-PSDB; Y58221.  
XX  
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
PT useful for treating or preventing e.g. tumors or autoimmune disease  
XX  
PS Claim 11; Page 231-232; 264pp; English.  
XX  
CC Sequences 255552-255560 and 255561-255566 represent cDNA  
CC sequences encoding canine interleukin-13 (IL-13) clones 80  
CC and 78 respectively. The invention relates to canine  
CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or  
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline  
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage  
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these  
CC immunoregulatory proteins. The proteins, their associated  
CC nucleic acids, specific antibodies and inhibitors may be used as  
CC vaccines for therapeutic or prophylactic regulation of an immune  
CC response in animals (particularly cats, dogs, horses and humans).  
CC They may be used to treat autoimmune or infectious diseases including  
CC allergies, tumours, inflammation and graft rejection, and to increase  
CC the response from a co-administered antigen. The nucleotide sequences  
CC can also be used for the recombinant production of a protein, while  
CC nucleotide fragments are useful as probes, as amplification primers and  
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
CC The proteins may be used to raise antibodies and to screen for  
CC modulators of activity, while the antibodies may be used in detection,  
CC and in drug targeting.  
XX  
SQ Sequence 1302 BP; 307 A; 340 C; 318 G; 337 T; 0 other;

Query Match 96.1%; Score 317; DB 21; Length 1302;  
Best Local Similarity 99.1%; Pred. No. 1.5e-84;  
Matches 330; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 1 agccctgtgactccctcccccaacctcaaggagctcattgaggagctggtcaacatcacc 60  
|||||  
Db 1191 AGCCCTGTGACTCCCTCCCCAACCCCTCAAGGAGCTCATTTGAGGAGCTGGTCAACATCACC 1132  
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QY 61 cagaatcaggcatccctctgcaacggcagcatggtgtggagcgtcaacctgaccgccggc 120  
|||||

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Db 1131 CAGAAATCAGGCATCCCTCTGTGCAACGGCAGCATGCTGTGGAGCGTCAACCTGACCGCCGGC 1072
QY 121 atgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgccatccaaagg 180
Db 1071 ATGTACTGCGAGCTCTAGAAATCTTGATCAATGTCTCCGACTGCAGCGCCATCCAAAGG 1012
QY 181 acccagagatgctgaaagcactgtgctctcaaaagcccgcgagcagg---gatttcaggt 237
Db 1011 ACCCAGAGGATGCTGAAAGCACTGTGCTCTCAAAAGCCCGCGGAGGCGCAGATTCCAGT 952
QY 238 gaacgcagcgagacacacaaattgaagtgatccagttggtgaaaaaacctgctcacctat 297
Db 951 GAACGCAGCGGAGACACCAAAATTGAAGTGATCCAGTTGGTGAAAAACCTGCTCACCTAT 892
QY 298 gtaagggagtttatcgccatggaaatttcaga 330
Db 891 GTAAGGGGAGTTTATCGCCCATGGAAATTTTCAGA 859

RESULT 13
Z55553
ID Z55553 standard; cDNA; 272 BP.
XX
AC Z55553;
XX
DT 14-MAR-2000 (first entry)
DE
XX Canine interleukin-13 (IL-13) cDNA fragment nCaIL13-272.
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
XX
OS Canis familiaris.
XX
PN WO9961618-A2.
XX
PD 02-DEC-1999.
XX
PF 28-MAY-1999; 99WO-US11942.
XX
PR 29-MAY-1998; 98US-0087306.
XX
PA (HESK-) HESKA CORP.
XX
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;
XX
DR WPI; 2000-072623/06.
XX
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,
PT useful for treating or preventing e.g. tumors or autoimmune disease
XX
PS Claim 1i; Page 228; 264pp; English.
XX
CC Sequences Z55552-Z55560 and Z55561-Z55566 represent cDNA
CC sequences encoding canine interleukin-13 (IL-13) clones 80
CC and 78 respectively. The invention relates to canine
CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these
CC immunoregulatory proteins. The proteins, their associated
CC nucleic acids, specific antibodies and inhibitors may be used as
CC vaccines for therapeutic or prophylactic regulation of an immune
CC response in animals (particularly cats, dogs, horses and humans).
CC They may be used to treat autoimmune or infectious diseases including
CC allergies, tumours, inflammation and graft rejection, and to increase
CC the response from a co-administered antigen. The nucleotide sequences
CC can also be used for the recombinant production of a protein, while
CC nucleotide fragments are useful as probes, as amplification primers and
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
CC The proteins may be used to raise antibodies and to screen for
CC modulators of activity, while the antibodies may be used in detection,
```

```

CC and in drug targeting.
XX
SQ Sequence 272 BP; 64 A; 91 C; 69 G; 48 T; 0 other;

Query Match 72.7%; Score 240; DB 21; Length 272;
Best Local Similarity 98.8%; Pred. No. 5.7e-62;
Matches 253; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 1 agccctgtgactccctcccaaccctcaaggagctcattgaggagctggtcaacatcacc 60
Db 17 agccctgtgactccctcccaaccctcaaggagctcattgaggagctggtcaacatcacc 76
QY 61 cagaatcaggcatccctctgcaacggcagcagcatggtgtggagcgtcaacctgaccgccggc 120
Db 77 cagaatcaggcatccctctgcaacggcagcagcatggtgtggagcgtcaacctgaccgccggc 136
QY 121 atgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgccatccaaagg 180
Db 137 atgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgccatccaaagg 196
QY 181 acccagagatgctgaaagcactgtgctctcaaaagcccgcgagcagg---gatttcaggt 237
Db 197 acccagagatgctgaaagcactgtgctctcaaaagcccgcgagcaggagatttcaggt 256
QY 238 gaacgcagcgagaca 253
Db 257 gaacgcagcgagaca 272

RESULT 14
Z55554
ID Z55554 standard; cDNA; 278 BP.
XX
AC Z55554;
XX
DT 14-MAR-2000 (first entry)
DE
XX Canine interleukin-13 (IL-13) cDNA probe.
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
XX
OS Canis familiaris.
XX
PN WO9961618-A2.
XX
PD 02-DEC-1999.
XX
PF 28-MAY-1999; 99WO-US11942.
XX
PR 29-MAY-1998; 98US-0087306.
XX
PA (HESK-) HESKA CORP.
XX
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;
XX
DR WPI; 2000-072623/06.
XX
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,
PT useful for treating or preventing e.g. tumors or autoimmune disease
XX
PS Claim 1i; Page 229; 264pp; English.
XX
CC Sequences Z55552-Z55560 and Z55561-Z55566 represent cDNA
CC sequences encoding canine interleukin-13 (IL-13) clones 80
CC and 78 respectively. The invention relates to canine
CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these
CC immunoregulatory proteins. The proteins, their associated
CC nucleic acids, specific antibodies and inhibitors may be used as
```





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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: May 13, 2001, 14:21:44 ; Search time 226.02 Seconds  
(without alignments)  
254.928 Million cell updates/sec

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Perfect score: 330  
Sequence: 1 agccctgtgactccctcccc.....atcgccatggaaatttcaga 330

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 302621 seqs, 87301344 residues

Total number of hits satisfying chosen parameters: 605242

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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4: /cgnl\_7/ptodata/1/ina/6B\_COMB.seq:\*  
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6: /cgnl\_7/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	187.4	56.8	336	1	US-08-371-121-24
2	187.4	56.8	1290	1	US-08-012-543-1
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4	187.4	56.8	1290	5	PCT-US93-07645-1
5	185.8	56.3	336	1	US-08-371-121-2
6	185.8	56.3	1297	1	US-08-371-121-15
7	184.2	55.8	384	1	US-08-371-121-17
8	182.6	55.3	425	1	US-08-594-469-4
9	182.6	55.3	425	2	US-08-906-957-4
10	182.6	55.3	4410	1	US-08-594-469-1
11	182.6	55.3	4410	2	US-08-906-957-1
12	151.4	45.9	447	1	US-08-371-121-26
13	151.4	45.9	1212	1	US-08-012-543-3
14	151.4	45.9	1212	5	PCT-US93-07645A-3
15	151.4	45.9	1212	5	PCT-US93-07645-3
16	33.4	10.1	1322	4	US-09-128-450-27
17	32.4	9.8	720	4	US-09-094-359-3
18	32.4	9.8	720	4	US-09-094-359-7
19	32.4	9.8	720	4	US-09-172-063-11
20	32.4	9.8	720	4	US-09-172-063-13
21	32.4	9.8	762	1	US-08-532-390-40
22	32.4	9.8	762	4	US-08-717-294-40
23	32.4	9.8	768	4	US-09-094-359-11
24	32.4	9.8	850	4	US-09-062-102-2
25	32.4	9.8	972	4	US-09-172-063-27
26	32.4	9.8	972	4	US-09-172-063-29
27	32.4	9.8	1095	4	US-09-085-305-5

28	32.4	9.8	1929	2	US-08-818-253-1	Sequence 1, Appli
29	32.4	9.8	1929	2	US-08-818-253-5	Sequence 5, Appli
30	32.4	9.8	1929	4	US-08-818-252-1	Sequence 1, Appli
31	32.4	9.8	1929	4	US-08-818-252-5	Sequence 5, Appli
32	32.4	9.8	1959	2	US-08-818-253-3	Sequence 3, Appli
33	32.4	9.8	1959	4	US-08-818-252-3	Sequence 3, Appli
34	32.4	9.8	1971	2	US-08-818-253-7	Sequence 7, Appli
35	32.4	9.8	1971	4	US-08-818-252-7	Sequence 7, Appli
36	32.4	9.8	7938	4	US-09-331-581-14	Sequence 14, Appl
37	32	9.7	1926	2	US-08-978-182-2	Sequence 2, Appli
38	32	9.7	1926	2	US-09-205-681-2	Sequence 2, Appli
39	31.8	9.6	35081	2	US-08-752-760A-1	Sequence 1, Appli
40	31.4	9.5	398	4	US-09-060-756-630	Sequence 630, App
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42	31.2	9.5	720	4	US-09-094-359-9	Sequence 9, Appli
43	31.2	9.5	720	4	US-09-172-063-12	Sequence 12, Appl
44	31.2	9.5	720	4	US-09-172-063-14	Sequence 14, Appl
45	31.2	9.5	720	4	US-09-172-063-17	Sequence 17, Appl

ALIGNMENTS

RESULT 1

US-08-371-121-24  
; Sequence 24, Application US/083711121  
; Patent No. 5652123  
; GENERAL INFORMATION:  
; APPLICANT: CAPUT, Daniel  
; APPLICANT: FERRARA, Pascual  
; APPLICANT: GUILLEMOT, Jean-Claude  
; APPLICANT: LEPLATOIS, Pascal  
; APPLICANT: MINTY, Adrian  
; APPLICANT: KAGHAD, Mourad  
; APPLICANT: LABIT-LE BOUTEILLER, Christine  
; APPLICANT: MAGAZIN, Marilyn  
; TITLE OF INVENTION: Protein having a cytokine type  
; TITLE OF INVENTION: activity, recombinant DNA coding for this protein,  
; TITLE OF INVENTION: transformed cells and microorganisms.  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FOLEY & LARDNER  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington, D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/371,121  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/938,161  
; FILING DATE: 30-NOV-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/FR92/00280  
; FILING DATE: 27-MAR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 91 00137  
; FILING DATE: 08-JAN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 91 03904  
; FILING DATE: 29-MAR-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SAXE, Bernhard D.  
; REGISTRATION NUMBER: 28,665  
; REFERENCE/DOCKET NUMBER: 16781/383  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 672-5300

```

; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 336 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-371-121-24

Query Match          56.8%; Score 187.4; DB 1; Length 336;
Best Local Similarity 76.9%; Pred. No. 2.1e-50;
Matches 256; Conservative 0; Mismatches 71; Indels 6; Gaps 2;

QY 2 gccctgtgactccctcccaaccctcaaggagctcatctgaggagctggtcaacatcaccc 61
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Db 2 GCCCTGTGCCTCCCTCTACAGCCCTCAGGGAGCTCATTTAGGAGCTGGTCAACATCACCC 61

QY 62 agaatc---aggcatccctctgcacaacggcagcatggtgtggagcgtcaacctgaccgcg 118
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Db 62 AGAACCCAGAAGGCTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAACCTGACAGCTG 121

QY 119 gcatgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgccatccaaa 178
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Db 122 GCATGTACTGTGCAGCCCTGGAATCCCTGATCAACGCTGCAGGCTGCAGTGCCATCGAGA 181

QY 179 ggaccagaggtgctgaagcactgtgctctcctcaaaagcccgcgagg---gatttcca 235
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Db 182 AGACCCAGAGGATGCTGAGCGGATTTCTGCCCGCACAAAGTCTCAGCTGGGCAGTTTCCA 241

QY 236 gtgaacgcagccgagacaccaaattgaagtgatccagttggtgaaaaaacctgctcacct 295
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Db 242 GCTTGCATGTCGAGACACCAAAATCGAGGTGGCCCAAGTTTGTAAAGGACCTGCTCTTAC 301

QY 296 atgtaagggagtttatgccatggaaatttca 328
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Db 302 ATTAAAGAAACTTTTTCGCGAGGGACGGTTCA 334

RESULT 2
US-08-012-543-1
; Sequence 1, Application US/08012543
; Patent No. 5596072
; GENERAL INFORMATION:
; APPLICANT: Culpepper, Janice
; APPLICANT: McKenzie, Andrew
; APPLICANT: Dang, Warren
; APPLICANT: de Waal Malefyt, Rene
; APPLICANT: Heath, Andrew
; APPLICANT: Aversa, Gregorio
; APPLICANT: Briere, Francine
; APPLICANT: Banchereau, Jacques
; APPLICANT: de Vries, Jan
; APPLICANT: Zurawski, Gerard
; TITLE OF INVENTION: Human Interleukin-13
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/012,543
; FILING DATE: 01-FEB-1993

```





APPLICATION NUMBER: FR 91 03904  
FILING DATE: 29-MAR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: SAXE, Bernhard D.  
REGISTRATION NUMBER: 28,665  
REFERENCE/DOCKET NUMBER: 16781/383  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 336 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-371-121-2

Query Match 56.3%; Score 185.8; DB 1; Length 336;  
Best Local Similarity 76.6%; Pred. No. 6.7e-50;  
Matches 255; Conservative 0; Mismatches 72; Indels 6; Gaps 2;

QY 2 gccctgtgactccctcccaaccctcaaggagctcattgaggagctggtcaacatcaccc 61  
Db 2 GCCCTGTGCCTCCCTCTACAGCCCTCAGGGAGCTCATTGAGGAGCTGGTCAACATCACCC 61  
QY 62 agaatc---aggcatccctctgcaacggcgagcatggttgaggcgtaacctgaccgcg 118  
Db 62 AGAACCCAGAGGCTCCGCTGCTGAATGGCAGCATGGTATGGAGCATCAACCTGACAGCTG 121  
QY 119 gcatgtactgcgcagctctagaatctctgatcaatgtctcgactgcagcgccatccaaa 178  
Db 122 ACATGTACTGTGCAGCCCTGGAATCCCTGATCAACGCTGTGAGGCTGCAGTGCCATCGAGA 181  
QY 179 ggaccagaggtgctgaaagcactgtgctctcaaaaagccggcgagg---gatttcca 235  
Db 182 AGACCCAGAGGATGCTGAGCGGATTCTGCCCGCACAGGTCTCAGCTGGGCAGTTTCCA 241  
QY 236 gtgaacgcagccgagacacacaaaattgaagtgtccagttggtgaaaaacctgctcacct 295  
Db 242 GCTTGCAATGTCGAGACACCAAAATCGAGGTGGCCCCAGTTTGTAAAGGACCTGCTCTTAC 301  
QY 296 atgtaaggggagtttatcgccatggaaatttca 328  
Db 302 ATTTAAAGAAACTTTTTCGAGGGGACGGTTCA 334

RESULT 6  
US-08-371-121-15  
Sequence 15, Application US/08371121  
Patent No. 5652123  
GENERAL INFORMATION:  
APPLICANT: CAPUT, Daniel  
APPLICANT: FERRARA, Pascual  
APPLICANT: GUILLEMOT, Jean-Claude  
APPLICANT: LEPLATOIS, Pascal  
APPLICANT: MINTY, Adrian  
APPLICANT: KAGHAD, Mourad  
APPLICANT: LABIT-LE BOUTEILLER, Christine  
APPLICANT: MAGAZIN, Marilyn  
TITLE OF INVENTION: Protein having a cytokine type  
TITLE OF INVENTION: activity, recombinant DNA coding for this protein,  
TITLE OF INVENTION: transformed cells and microorganisms.  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FOLEY & LARDNER  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington, D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/371,121  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/938,161  
FILING DATE: 30-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/FR92/00280  
FILING DATE: 27-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 91 00137  
FILING DATE: 08-JAN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 91 03904  
FILING DATE: 29-MAR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: SAXE, Bernhard D.  
REGISTRATION NUMBER: 28,665  
REFERENCE/DOCKET NUMBER: 16781/383  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1297 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 15..452  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 117..452  
US-08-371-121-15

Query Match 56.3%; Score 185.8; DB 1; Length 1297;  
Best Local Similarity 76.6%; Pred. No. 1.1e-49;  
Matches 255; Conservative 0; Mismatches 72; Indels 6; Gaps 2;

QY 2 gccctgtgactccctcccaaccctcaaggagctcattgaggagctggtcaacatcaccc 61  
Db 118 GCCCTGTGCCTCCCTCTACAGCCCTCAGGGAGCTCATTGAGGAGCTGGTCAACATCACCC 177  
QY 62 agaatc---aggcatccctctgcaacggcgagcatggttgaggcgtaacctgaccgcg 118  
Db 178 AGAACCCAGAGGCTCCGCTGCTGAATGGCAGCATGGTATGGAGCATCAACCTGACAGCTG 237  
QY 119 gcatgtactgcgcagctctagaatctctgatcaatgtctcgactgcagcgccatccaaa 178  
Db 238 ACATGTACTGTGCAGCCCTGGAATCCCTGATCAACGCTGTGAGGCTGCAGTGCCATCGAGA 297  
QY 179 ggaccagaggtgctgaaagcactgtgctctcaaaaagccggcgagg---gatttcca 235  
Db 298 AGACCCAGAGGATGCTGAGCGGATTCTGCCCGCACAGGTCTCAGCTGGSCAGTTTCCA 357  
QY 236 gtgaacgcagccgagacacacaaaattgaagtgtccagttggtgaaaaacctgctcacct 295  
Db 358 GCTTGCAATGTCGAGACACCAAAATCGAGGTGGCCCCAGTTTGTAAAGGACCTGCTCTTAC 417  
QY 296 atgtaaggggagtttatcgccatggaaatttca 328  
Db 418 ATTTAAAGAAACTTTTTCGAGGGGACGGTTCA 450







US-08-594-469-1

Query Match 55.3%; Score 182.6; DB 1; Length 4410;  
Best Local Similarity 76.0%; Pred. No. 1.8e-48;  
Matches 253; Conservative 0; Mismatches 74; Indels 6; Gaps 2;

Qy 2 gccctgtgactccctcccaaccctcaaggagctcattgaggagctggtcaacatcaccc 61  
Db 402 GCCCTGTGCTCCCTAGTACCTCCCTCAGGGAGCTCATTGAGGAGCTGGTCAACATCACCC 461  
Qy 62 agaatc---aggcatccctctgcaacggcagcatggtgtggagcgtcaacccgaccgccc 118  
Db 462 AGAACCCAGAGGCTCCCTCTGCAATGGCAGCATGGTATGGAGCATCAACCTGACAGCTG 521  
Qy 119 gcatgtactgcgagctctagaatctctgatcaatgtctccgactgcagcgcacatccaaa 178  
Db 522 GCATGTACTGTGCGCCCTGGAATCCCTGATCAACGTGTGAGGCTGCAGTGGCAGTTCGA 581  
Qy 179 ggacccagagatgctgaaagcactgtgtctctcaaaagcccgccgaggg---gatttcca 235  
Db 582 AGACCCAGAGGATGCTGAGCGGATTCTGCCCCGACAAAGTGTCAAGTGTGGCAGTTCGA 641  
Qy 236 gtgaacgcagccgagacacacaaattgaagtgtatccagttggtgaaacacccgtcacct 295  
Db 642 GCTTGCATGTCCGAGACACAAATCGAGGTGGCCCAAGTTGTAAAGGACCTGCTCTTAC 701  
Qy 296 atgtaaggggagtttatcgccatggaaatttca 328  
Db 702 ATTTAAAGAAACTTTTTCGCGAGGGACGGTTCA 734

RESULT 11

US-08-906-957-1  
; Sequence 1, Application US/08906957  
; Patent No. 5856142

GENERAL INFORMATION:  
; APPLICANT: LEGOUX, Richard  
; APPLICANT: MALDONADO, Paul  
; APPLICANT: SALOME, Marc  
; TITLE OF INVENTION: Method for the extraction of  
; TITLE OF INVENTION: periplasmic proteins of prokaryotic microorganisms in the  
; TITLE OF INVENTION: presence of arginine  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Bacon & Thomas  
; STREET: 625 Slaters Lane - Fourth Floor  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: USA  
; ZIP: 22314  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/906,957  
; FILING DATE: 06-AUG-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/594,469  
; FILING DATE:  
; APPLICATION NUMBER: FR 95 01083  
; FILING DATE: 31-JAN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: FICHTER, Richard E  
; REGISTRATION NUMBER: 26,382  
; REFERENCE/DOCKET NUMBER: REF/LEGOUX  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 683-0500  
; TELEFAX: (703) 683-1080  
; INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:  
; LENGTH: 4410 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-906-957-1

Query Match 55.3%; Score 182.6; DB 2; Length 4410;  
Best Local Similarity 76.0%; Pred. No. 1.8e-48;  
Matches 253; Conservative 0; Mismatches 74; Indels 6; Gaps 2;

Qy 2 gccctgtgactccctcccaaccctcaaggagctcattgaggagctggtcaacatcaccc 61  
Db 402 GCCCTGTGCTCCCTAGTACCTCCCTCAGGGAGCTCATTGAGGAGCTGGTCAACATCACCC 461  
Qy 62 agaatc---aggcatccctctgcaacggcagcatggtgtggagcgtcaacccgaccgccc 118  
Db 462 AGAACCCAGAGGCTCCCTCTGCAATGGCAGCATGGTATGGAGCATCAACCTGACAGCTG 521  
Qy 119 gcatgtactgcgagctctagaatctctgatcaatgtctccgactgcagcgcacatccaaa 178  
Db 522 GCATGTACTGTGCGCCCTGGAATCCCTGATCAACGTGTGAGGCTGCAGTGGCAGTTCGA 581  
Qy 179 ggacccagagatgctgaaagcactgtgtctctcaaaagcccgccgaggg---gatttcca 235  
Db 582 AGACCCAGAGGATGCTGAGCGGATTCTGCCCCGACAAAGTGTCAAGTGTGGCAGTTCGA 641  
Qy 236 gtgaacgcagccgagacacacaaattgaagtgtatccagttggtgaaacacccgtcacct 295  
Db 642 GCTTGCATGTCCGAGACACAAATCGAGGTGGCCCAAGTTGTAAAGGACCTGCTCTTAC 701  
Qy 296 atgtaaggggagtttatcgccatggaaatttca 328  
Db 702 ATTTAAAGAAACTTTTTCGCGAGGGACGGTTCA 734

RESULT 12

US-08-371-121-26  
; Sequence 26, Application US/08371121  
; Patent No. 5652123

GENERAL INFORMATION:  
; APPLICANT: CAPUT, Daniel  
; APPLICANT: FERRARA, Pascual  
; APPLICANT: GUILLEMOT, Jean-Claude  
; APPLICANT: LEPLATOIS, Pascal  
; APPLICANT: MINTY, Adrian  
; APPLICANT: KAGHAD, Mourad  
; APPLICANT: LABIT-LE BOUTEILLER, Christine  
; APPLICANT: MAGAZIN, Marilyn  
; TITLE OF INVENTION: Protein having a cytokine type  
; TITLE OF INVENTION: activity, recombinant DNA coding for this protein,  
; TITLE OF INVENTION: transformed cells and microorganisms.  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FOLEY & LARDNER  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington, D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/371,121  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/938,161  
; FILING DATE: 30-NOV-1992



; TITLE OF INVENTION: Human Interleukin-13
; NUMBER OF SEQUENCES: 6
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.5
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07645A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/012543
; FILING DATE: 01-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/010977
; FILING DATE: 29-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/933416
; FILING DATE: 21-AUG-1992
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1212 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
PCT-US93-07645A-3

Query Match 45.9%; Score 151.4; DB 5; Length 1212;
Best Local Similarity 68.8%; Pred. No. 8.5e-39;
Matches 225; Conservative 0; Mismatches 96; Indels 6; Gaps 1;

QY 1 agccctgtgactccctcccaacctcaaggagctcattgaggagctgggtcaacatcacc 60
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Db 142 AGATCTGTGCTCTCCCTCTGACCCCTTAAGGAGCTTATTGAGGAGCTGAGCAACATCACA 201

QY 61 cagaatcaggcatccctctgcaacggcagcatgggtgtggagcgtcaaacctgaccgccggc 120
|| ||||| ||| | | ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 202 CAAGACCAGACTCCCTGTGCAACGGCAGCATGGTATGGAGTGTGGACCTGGCCGTGGC 261

QY 121 atgtactgcgcagctctagaaatctctgatcaatgtctcgcagctgcagcgccatccaaagg 180
|| ||||| ||| | | ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 262 GGGTTCTGTAGCCCTGGATTCCCTTGACCAACATCTCCAATTGCAATGCCATCTACAGG 321

QY 181 acccagaggatgctgaaagcactgtgtctctcaaaagcccgcgagggtattccagttaa 240
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Db 322 ACCCAGAGGATATTGCATGGCCTCTGTAAACCGCAAGGCCCCCACTACGGTCTCCA----- 376

QY 241 cgcagccgagacacaccaaattgaagtgatccagttggtgaaaaaacctgctcacctatgta 300
|| || | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 377 -GCCTCCCCGATACCAAAATCGAAGTAGCCCACTTTATATAACAAAACTGCTCAGCTACACA 435

QY 301 aggggagtttatcgccatggaaaatttc 327
|| | | | ||||| || |||
Db 436 AAGCAACTGTTTCGCCACGGCCCCCTTC 462

RESULT 15
PCT-US93-07645-3
; Sequence 3, Application PC/TUS9307645
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Human Interleukin-13
; NUMBER OF SEQUENCES: 6
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.5
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07645
; FILING DATE: 19930818
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/012543
; FILING DATE: 01-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/010977
; FILING DATE: 29-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/933416
; FILING DATE: 21-AUG-1992
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1212 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
PCT-US93-07645-3

Query Match 45.9%; Score 151.4; DB 5; Length 1212;
Best Local Similarity 68.8%; Pred. No. 8.5e-39;
Matches 225; Conservative 0; Mismatches 96; Indels 6; Gaps 1;

QY 1 agccctgtgactccctcccaacctcaaggagctcattgaggagctgggtcaacatcacc 60
|| ||||| ||| | | ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 142 AGATCTGTGCTCTCCCTCTGACCCCTTAAGGAGCTTATTGAGGAGCTGAGCAACATCACA 201

QY 61 cagaatcaggcatccctctgcaacggcagcatgggtgtggagcgtcaaacctgaccgccggc 120
|| ||||| ||| | | ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 202 CAAGACCAGACTCCCTGTGCAACGGCAGCATGGTATGGAGTGTGGACCTGGCCGTGGC 261

QY 121 atgtactgcgcagctctagaaatctctgatcaatgtctcgcagctgcagcgccatccaaagg 180
|| ||||| ||| | | ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 262 GGGTTCTGTAGCCCTGGATTCCCTTGACCAACATCTCCAATTGCAATGCCATCTACAGG 321

QY 181 acccagaggatgctgaaagcactgtgtctctcaaaagcccgcgagggtattccagttaa 240
|| ||||| ||| | | ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 322 ACCCAGAGGATATTGCATGGCCTCTGTAAACCGCAAGGCCCCCACTACGGTCTCCA----- 376

QY 241 cgcagccgagacacaccaaattgaagtgatccagttggtgaaaaaacctgctcacctatgta 300
|| || | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 377 -GCCTCCCCGATACCAAAATCGAAGTAGCCCACTTTATATAACAAAACTGCTCAGCTACACA 435

QY 301 aggggagtttatcgccatggaaaatttc 327
|| | | | ||||| || |||
Db 436 AAGCAACTGTTTCGCCACGGCCCCCTTC 462

Search completed: May 13, 2001, 14:21:47
Job time: 17858 sec





GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic-- nucleic search, using sw model

Run on: May 13, 2001, 11:40:52 ; Search time 5997.24 Seconds  
(without alignments)  
480.707 Million cell updates/sec

Title: US-09-451-527-104  
Perfect score: 330  
Sequence: 1.agcctgtgactccctcccc.....atcgccatggaaatttcaga 330

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 9623517 seqs, 4368049070 residues

Total number of hits satisfying chosen parameters: 19247034

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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188: em_gss_inv3:*
189: em_gss_other:*

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196: em_gss_rod4:*
197: em_gss_rod5:*
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230: gb_gss30:*
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232: gb_gss32:*
233: gb_gss33:*
234: gb_gss34:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	39	11.8	477	218	AZ261971	AZ261971 RPCI-23-1
2	39	11.8	521	215	AZ027551	AZ027551 RPCI-23-3
3	36.4	11.0	277	137	BE593226	BE593226 WSL_99_B0
4	36.4	11.0	537	166	BE357229	BE357229 DGL_147_B
5	35.2	10.7	757	174	BG260311	BG260311 602371427
6	34.4	10.4	462	143	BF039993	BF039993 BP250023B
7	34.4	10.4	507	138	BE705147	BE705147 SC02_08f0
8	34.2	10.4	535	161	BE032541	BE032541 131940 MA
9	34.2	10.4	546	161	BE032543	BE032543 131942 MA
10	34.2	10.4	570	24	AI746678	AI746678 ul06b05.y
11	34.2	10.4	965	217	AZ201624	AZ201624 SP_0053_A
12	34.2	10.4	2275	14	AF034173	AF034173 AF034173
13	34	10.3	370	166	BE363650	BE363650 WSL_64_G1
14	34	10.3	562	166	BE361027	BE361027 DGL_69_A0
15	33.8	10.2	341	163	BE127683	BE127683 DEPA1432
16	33.8	10.2	498	150	BF606532	BF606532 273595 MA
17	33.6	10.2	577	166	BE402120	BE402120 CSB004F06
18	33.6	10.2	714	166	BE414190	BE414190 SCU007.CO

19 33.6 10.2 727 164 BE216356  
c 20 33.4 10.1 177 103 AI909438  
21 33.4 10.1 544 13 AA880435  
22 33.4 10.1 700 113 AW318852  
23 33.4 10.1 712 115 AW475303  
24 33.4 10.1 1056 144 BF143984  
25 33.2 10.1 462 164 BE228410  
26 33.2 10.1 616 15 AI062250  
27 33.2 10.1 621 175 C97983  
28 33.2 10.1 683 15 AI064071  
29 33.2 10.1 712 107 AU092344  
30 33.2 10.1 1100 140 BE871785  
31 33 10.0 600 146 BF312933  
32 33 10.0 779 231 CNS03LV7  
33 32.6 9.9 285 6 AA360834  
34 32.6 9.9 335 6 AA361196  
c 35 32.6 9.9 452 158 W80370  
36 32.6 9.9 468 107 AU129052  
37 32.6 9.9 484 121 AW862698  
38 32.6 9.9 531 121 AW927591  
c 39 32.6 9.9 662 107 AU162975  
40 32.6 9.9 805 15 AI068702  
41 32.6 9.9 891 151 BF685554  
c 42 32.4 9.8 448 166 BE380347  
43 32.4 9.8 546 120 AW786287  
44 32.4 9.8 576 141 BE907816  
45 32.4 9.8 598 167 BE441993

ALIGNMENTS

RESULT 1  
AZ261971  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
FEATURES  
Source

AZ261971 477 bp DNA  
RPCI-23-123P23.TV RPCI-23 Mus musculus genomic clone  
DNA sequence.  
AZ261971.1 GI:9470858  
GSS.  
house mouse.  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 477)  
Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S., Akinret  
,B., Levins,M., McGann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P.  
and Fraser,C.M.  
Mouse BAC End Sequences from Library RPCI-23  
Unpublished (1999)  
Other\_GSSs: RPCI-23-123P23.TJ  
Contact: Shaying Zhao  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: szhao@tigr.org  
Clones are derived from the mouse BAC library RPCI-23. For BAC  
library availability, please contact Pieter de Jong  
(pieter@dejong.med.buffalo.edu). Clones may be purchased from  
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)  
or from Resea ch Genetics (info@resgen.com). BAC end page:  
http://www.tigr.org/tdb/bac\_ends/mouse/bac\_end\_intro.html  
Plate: 123 row: P column: 23  
Seq primer: T7  
Class: BAC ends.  
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/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
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AI909438 IL-BT208-  
AA880435 vW89F07.r  
AW318852 un08d12.y  
AW475303 un64b04.y  
BF143984 601791238  
BE228410 98AS2556  
AI062250 GH01393.5  
C97983 C97983 Rice  
AI064071 GH04331.5  
AU092344 AU092344  
BE871785 601448347  
BF312933 601896391  
AL249964 Tetraodon  
AA360834 EST70082  
AA361196 EST70439  
W80370 zh50f02.s1  
AU129052 AU129052  
AW862698 945006D06  
AW927591 945006D06  
AU162975 AU162975  
AI068702 mgae0003d  
BF685554 602140603  
BE380347 601270411  
AW786287 119229 MA  
BE907816 601501924  
BE441993 925010B01

/clone\_lib="RPCI-23"  
/sex="Female"  
/lab\_host="DH10B"  
/note="Organ: Kidney/Brain; Vector: pBACE3.6; Site\_1:  
EcoRI; Site\_2: EcoRI; Female C57BL/6J mouse kidney and/or  
brain genomic DNA was isolated and partially digested  
with a combination of EcoRI and EcoRI Methylase. Size  
selected DNA was cloned into the pBACE3.6 vector at the  
EcoRI sites. The ligation products were transformed into  
DH10B electrocompetent cells (BRL Life Technologies)."  
BASE COUNT 129 a 121 c 113 g 114 t  
ORIGIN  
Query Match 11.8%; Score 39; DB 218; Length 477;  
Best Local Similarity 52.1%; Pred. No. 0.66;  
Matches 87; Conservative 0; Mismatches 80; Indels 0; Gaps 0;  
QY 95 tgtggagcgtcaacctgaccgcccggcatgtactgcgcagctctagaatctctgataatg 154  
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Db 273 TGGCTAGCTTCAGTCACATGGTCAGACTGGACTGGATGGATCATTCTGAATAAT 332  
QY 155 tctccgactgcagcgccatccaaaggaccagagagatgctgaaagcactgtgctcaaaa 214  
| ||||| | | | | | | | | | | | ||||| ||  
Db 333 ATGGCAGCTGGAGCGTACTGGGATAGACAGTGGGCAACTGAGAACACTGTGGTCACAAA 392  
QY 215 agcccgcgcagggaatttccagtgaaacgcagccgagacacacaaaatt 261  
||| ||| | | | | | | | | | | | | | | |  
Db 393 AGCTAGCAGTCTGTCTGTGCTGAGATGGCAGTCTGCATATCCTGATT 439  
RESULT 2  
AZ027551  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
FEATURES  
Source

AZ027551 521 bp DNA  
RPCI-23-343M24.TJ RPCI-23 Mus musculus genomic clone  
DNA sequence.  
AZ027551  
AZ027551.1 GI:7102935  
GSS.  
house mouse.  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 521)  
Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S., Akinret  
,B., Levins,M., McGann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P.  
and Fraser,C.M.  
Mouse BAC End Sequences from Library RPCI-23  
Unpublished (1999)  
Contact: Shaying Zhao  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: szhao@tigr.org  
Clones are derived from the mouse BAC library RPCI-23. For BAC  
library availability, please contact Pieter de Jong  
(pieter@dejong.med.buffalo.edu). Clones may be purchased from  
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)  
or from Resea ch Genetics (info@resgen.com). BAC end page:  
http://www.tigr.org/tdb/bac\_ends/mouse/bac\_end\_intro.html  
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Seq primer: SP6  
Class: BAC ends.  
Location/Qualifiers  
1. .521  
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/strain="C57BL/6J"  
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/clone="RPCI-23-343M24"  
/clone\_lib="RPCI-23"  
/sex="Female"





Db 309 CGACGCCGCCGAGTGGGTCAACGGCCAGGTGTCATCCGGCCCAACGGCGGTACGTGTGATG 368

QY 144 tctgatcaatgtctccgactgc 165

Db 369 TCTGATCTTTAGCTTCTACAGC 390

RESULT 5

BG260311/c

LOCUS

DEFINITION BG260311 757 bp mRNA EST 13-FEB-2001

602371427F1 NIH\_MGC\_93 Homo sapiens cDNA clone IMAGE:4479367 5', mRNA sequence.

ACCESSION BG260311

VERSION BG260311.1 GI:12770127

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 757)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.  
Tel: (301) 496-1550  
Email: Robert\_Strausberg@nih.gov  
Tissue Procurement: ATCC  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Plate: LLAM10311 row: f column: 08  
High quality sequence stop: 736.  
Location/Qualifiers

1. 757

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/db\_xref="taxon:9606"  
/clone="IMAGE:4479367"  
/clone\_lib="NIH\_MGC\_93"  
/tissue\_type="transitional cell papilloma, cell line"  
/lab\_host="DH10B (phage-resistant)",  
/note="Organ: bladder; Vector: pCMV-SPORT6; Site\_1: NotI; Site\_2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.7 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH\_MGC Library."  
186 a 200 c 201 g 170 t

BASE COUNT

ORIGIN

Query Match 10.7%; Score 35.2; DB 174; Length 757;  
Best Local Similarity 49.0%; Pred. No. 9.5;  
Matches 94; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

QY 137 tagaatctctgatcaatgtctccgactgcagcgcccatccaaaggaccagagagatgctga 196

Db 688 TGAAGCCCTCATGAGTGCCAGGGCCCGCCACTTTGTCCAGAGGGCCCCAACGACTGGGGT 629

QY 197 aagcactgtgctctcaaaaagcccgccgagggatttccagtgaaacgcagccagacacca 256

Db 628 ATGTACTTTGACCCCAACAAGCCATCTGGGATGAGCCCGCTTTTCAGCCACCATGTCTCAA 569

QY 257 aaattgaagtgatccagttggtgaaaaaacctgctcacctatgtaaggggagtttatcgcc 316

Db 568 ATTCATCAGCATTGAACCTTGGTGAAGCCCCCACTTCTTTGAGATGTGGATCTTCTGGCGGC 509

QY 317 atggaaatttca 328

Db 508 CAGGAAACTTGA 497

us-09-451-527-104.rst

RESULT 6

BF039993

LOCUS

DEFINITION BF039993 462 bp mRNA EST 10-OCT-2000

BP250023B10D12 Soares normalized bovine placenta Bos taurus cDNA clone BP250023B10D12 5', mRNA sequence.

ACCESSION BF039993

VERSION BF039993.1 GI:10757048

KEYWORDS EST.

SOURCE cow.

ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 462)

AUTHORS Lewin,H.A., Soares,M.B., Rebeiz,M., Pardinas,J., Liu,L. and Larson,J.H.

TITLE Bovine ESTs

JOURNAL Unpublished (2000)

COMMENT Contact: Lewin, H. A.  
W. M. Keck Center for Comparative and Functional Genomics  
University of Illinois at Urbana-Champaign  
340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL 61801, USA  
Tel: 217 333 5998  
Fax: 217 244 5617  
Email: h-lewin@uiuc.edu  
Funding for cattle EST sequencing was provided by the USDA National Research Initiative, Animal Genome Resource Grant AG 99-3205-8534 to H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED from Washington University Genome Center. Vector Trimmi g:  
Cross\_match from Washington University Genome Center PHRAP suite.  
This sequence is vector free and at least 200 bp in length.  
PCR Primers  
FORWARD: TAATACGACTCACTATAGGG  
BACKWARD: ATTAACCCCTCACTAAAG  
Insert Length: 462 Std Error: 0.00  
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High quality sequence stop: 462.  
Location/Qualifiers

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/clone\_lib="Soares normalized bovine placenta"  
/sex="female"  
/lab\_host="DH10B"  
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110 a 153 c 123 g 73 t 3 others

BASE COUNT

ORIGIN

Query Match 10.4%; Score 34.4; DB 143; Length 462;  
Best Local Similarity 49.7%; Pred. No. 14;  
Matches 86; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

QY 25 ctcaaggagctcattgaggagctggtcaacatcacccagaatcaggcatccctctgcaac 84

Db 113 CTGATGGAGTTCAGTGAGCACCTGGCCATCATCTCTGGAGGACGACCGCTCCGACATCAGC 172

QY 85 ggcagcatggtgtggagcgctcaacctgaccgcccggcatgtactgcgagctctagaatct 144

Db 173 TCCACCTGCGCCAACAACATCAACCAACACGGAGCTGCTGCCCTCGAGCTGGACACC 232

QY 145 ctgatcaatgtctccgactgcagcgcccatccaaaggaccagagatgctgaa 197

Db 233 CTGGTGGCAAGGGGGCGCTTCGCGCGAGNTCTACAAGGCCAAGCTGAAGCAGAA 285













GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 13, 2001, 14:25:22 ; Search time 9342.78 Seconds  
(without alignments)  
520.915 Million cell updates/sec

Title: US-09-451-527-106  
Perfect score: 330  
Sequence: 1 tctgaaatttccatggcgat.....ggggaggaggtcacagggct 330

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1283235 seqs, 7373929652 residues

Total number of hits satisfying chosen parameters: 2566470

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

- GenEmbl:\*
- 1: gb\_ba1:\*
  - 2: gb\_ba2:\*
  - 3: gb\_ba3:\*
  - 4: gb\_in1:\*
  - 5: gb\_in2:\*
  - 6: gb\_in3:\*
  - 7: gb\_om:\*
  - 8: gb\_ov:\*
  - 9: gb\_pat1:\*
  - 10: gb\_pat2:\*
  - 11: gb\_ph:\*
  - 12: gb\_pl1:\*
  - 13: gb\_pl2:\*
  - 14: gb\_pl3:\*
  - 15: gb\_pl4:\*
  - 16: em\_ba1:\*
  - 17: em\_ba2:\*
  - 18: em\_fun:\*
  - 19: em\_htgo\_hum:\*
  - 20: em\_htgo\_inv:\*
  - 21: em\_htgo\_rod:\*
  - 22: em\_htg\_hum1:\*
  - 23: em\_htg\_hum2:\*
  - 24: em\_htg\_hum3:\*
  - 25: em\_htg\_hum4:\*
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  - 29: em\_htg\_hum8:\*
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  - 33: em\_htg\_rod:\*
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  - 39: em\_hum6:\*
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- 48: em\_ro:\*
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- 91: gb\_pr7:\*
- 92: gb\_pr8:\*
- 93: gb\_pr9:\*
- 94: gb\_rol:\*
- 95: gb\_ro2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	DB	ID	Description
C 1	317	96.1	1302	7	AF244915	AF244915 Canis fam
C 2	187.4	56.8	336	9	A29931	A29931 Sequence co
C 3	187.4	56.8	336	10	I58494	I58494 Sequence 24
C 4	187.4	56.8	1270	93	HUMIL13A	L06801 Homo sapien
C 5	187.4	56.8	1282	92	HSNC30	X69079 H.sapiens i
C 6	187.4	56.8	1290	10	I34548	I34548 Sequence 1
C 7	185.8	56.3	336	9	A29930	A29930 Sequence co
C 8	185.8	56.3	336	10	I58481	I58481 Sequence 2
C 9	185.8	56.3	417	88	AF043334	AF043334 Homo sapi
C 10	185.8	56.3	1297	9	A29948	A29948 Coding sequ
C 11	185.8	56.3	1297	10	I58488	I58488 Sequence 15

C 12	184.2	55.8	384	9	A29950	A29950 Nucleic aci
C 13	184.2	55.8	384	10	I58489	I58489 Sequence 17
C 14	182.6	55.3	425	9	AR027065	AR027065 Sequence
C 15	182.6	55.3	425	10	I86198	I86198 Sequence 4
C 16	182.6	55.3	4410	9	A52326	A52326 Sequence 1
C 17	182.6	55.3	4410	9	AR027062	AR027062 Sequence
C 18	182.6	55.3	4410	10	I86195	I86195 Sequence 1
C 19	163	49.4	343	7	AF072807	AF072807 Bos tauru
C 20	151.4	45.9	447	10	I58495	I58495 Sequence 26
C 21	151.4	45.9	1207	94	MUSSTCPE	M23504 Mus musculus
C 22	151.4	45.9	1212	10	I34549	I34549 Sequence 3
C 23	140.8	42.7	443	94	RATIL13A	L26913 Rattus Norv
C 24	106.4	32.2	213343	78	AF276990	AF276990 Canis fam
C 25	71.4	21.6	3714	93	HUM11DC992	L42080 Homo sapien
C 26	71.4	21.6	4600	93	HUMIL13B	L13029 Human inter
C 27	71.4	21.6	4740	93	HSU10307	U10307 Human inter
C 28	71.4	21.6	5670	93	HSU31120	U31120 Human inter
C 29	71.4	21.6	50282	85	AC004039	AC004039 Homo sapi
C 30	71.4	21.6	78469	75	AC074127	AC074127 Homo sapi
C 31	71	21.5	3395	93	HUM11DC98Z	L42079 Homo sapien
C 32	70	21.2	3520	7	BTA132441	AJ132441 Bos tauru
C 33	58.4	17.7	78469	75	AC074127	AC074127 Homo sapi
C 34	51.6	15.6	4376	94	MUSIL13A	L13028 Mouse inter
C 35	49.4	15.0	142732	88	AC084392	AC084392 Homo sapi
C 36	49.4	15.0	159500	94	AC005742	AC005742 Mus muscu
C 37	49.4	15.0	237823	66	AC020886	AC020886 Mus muscu
C 38	40.8	12.4	38390	3	SC2H12	AL359215 Streptomy
C 39	39	11.8	13684	94	MUSGABAT	M92377 Mus musculus
C 40	37	11.2	39739	3	SCD16A	AL078618 Streptomy
C 41	36.8	11.2	185300	2	AP000063	AP000063 Aeropyrum
C 42	36.6	11.1	51440	12	AB025632	AB025632 Arabidops
C 43	36.4	11.0	2437	3	SAAJ3310	AJ223310 Streptomy
C 44	36.4	11.0	2437	3	SAU77894	U77894 Streptomyce
C 45	36.2	11.0	3073	94	AF195788	AF195788 Rattus no

ALIGNMENTS

RESULT 1	AF244915/c	AF244915	1302 bp	mRNA	MAM	16-OCT-2000
LOCUS	Canis familiaris interleukin-13 mRNA, complete cds.					
DEFINITION	Canis familiaris interleukin-13 mRNA, complete cds.					
ACCESSION	AF244915					
VERSION	AF244915.1	GI:7528273				
KEYWORDS						
SOURCE	dog.					
ORGANISM	Canis familiaris					
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.					
AUTHORS	Yang, S., Boroughs, K.L. and McDermott, M.J.					
TITLE	Canine interleukin-13: molecular cloning of full-length cDNA and expression of biologically active recombinant protein					
JOURNAL	J. Interferon Cytokine Res. 20 (9), 779-785 (2000)					
MEDLINE	20485146					
PUBMED	11032397					
REFERENCE	2 (bases 1 to 1302)					
AUTHORS	Yang, S.					
TITLE	Direct Submission					
JOURNAL	Submitted (13-MAR-2000) Allergy and Immunology, Heska Corporation, 1613 Prospect Parkway, Fort Collins, CO 80525, USA					
FEATURES	Location/Qualifiers					
source	1. .1302					
	/organism="Canis familiaris"					
	/db_xref="taxon:9615"					
	1. .51					
	52. .447					
	/codon_start=1					
	/product="interleukin-13"					
	/protein_id="AAF63204.1"					
	/db_xref="GI:7528274"					
	/translation="MALWLTVVIALTCLGGLASPSVTPSPPTLKELIEELVNITQNA					
5'UTR						
CDS						

3'UTR	SILNGSMVWSVNLTAGMYCALESILNVSDCSAIQRTQRLKALCSQKPAAGQISSER					
BASE COUNT	337 a	318 c	340 g	307 t		
ORIGIN	SRDKIEIVQLVKNLLTYVRGVYRHGFR"					
	448. .1302					
Query Match	96.1%;	Score 317;	DB 7;	Length 1302;		
Best Local Similarity	99.1%;	Pred. No. 1.1e-72;				
Matches 330;	Conservative 0;	Mismatches 0;	Indels 3;	Gaps 1;		
QY 1	tctgaaatttccatgctgataaaactcccttaccactgagcaggtttttccaccaactg	60				
Db 444	TCTGAAATTTCCATGGCGATAAACTCCCTTACATAGGTGAGCAGGTTTTCACCAACTG	385				
QY 61	gatcacttcaatttgggtctcggctgcgttccactggaat---ccctgcgcgggctt	117				
Db 384	GATCACTTCAATTTGGTGTCTCGGCTGCGTTCAGTGGAAATCTGCCCTGCCGGGGCTT	325				
QY 118	ttgagagcacagctgtttcagcatcctctgggtccttggatggcgtcagtcggagac	177				
Db 324	TTGAGAGCACAGTCTTTCAGCATCTCTGGTCTCTTGGATGGCGCTGCAGTCGGAGAC	265				
QY 178	attgatcagagattctagagctgcgcagtagtaccggtcaggttgcagctccacac	237				
Db 264	ATTGATCAGAGATTCTAGAGCTGCGCAGTACATGCGCGGTCAGGTTGACGCTCCACAC	205				
QY 238	catgctgccttgcagagggatgcctgattctgggtgatgttgaccagctcctcaatgag	297				
Db 204	CATGCTGCCGTGCAGAGGGATGCTGTGATTTCTGGGTGATGTTGACCAAGTCTCAATGAG	145				
QY 298	ctccttgaggggtgggaggaggtcacagggt 330					
Db 144	CTCCTTGAGGGTTGGGGAGGGAGTCAACAGGGCT 112					

RESULT 2

A29931/c	A29931	336 bp	DNA	PAT	23-JUN-1995
LOCUS	Sequence coding for the mature cytokine like protein.				
DEFINITION	A29931				
ACCESSION	A29931.1	GI:1249019			
VERSION					
KEYWORDS	synthetic construct.				
SOURCE	synthetic construct				
ORGANISM	artificial sequence.				
REFERENCE	1 (bases 1 to 336)				
AUTHORS	Caput, D., Ferrara, P., Guillemot, J.C., Kaghad, M., Labit-le				
	Bouteiller, C., Lepoint, P., Magazin, M. and Minty, A.				
TITLE	Protein having cytokin type activity, recombinant DNA coding for				
JOURNAL	this protein, transformed cells and microorganisms				
	Patent: EP 0506574-A 3 30-SEP-1992;				
	ELF SANOFI				
FEATURES	Location/Qualifiers				
source	1. .336				
	/organism="synthetic construct"				
	/db_xref="taxon:32630"				
BASE COUNT	80 a	95 c	90 g	71 t	
ORIGIN					
Query Match	56.8%;	Score 187.4;	DB 9;	Length 336;	
Best Local Similarity	76.9%;	Pred. No. 9.3e-39;			
Matches 256;	Conservative 0;	Mismatches 71;	Indels 6;	Gaps 2;	
QY 3	tgaatttccatgctgataaaactcccttaccactgagcaggtttttccaccaactgga	62			
Db 334	TGAACCGTCCCTCGCGAAAGTTTCTTAATGTAAAGACAGGTCCTTTACAAACTGGG	275			
QY 63	tcacttcaatttgggtctcggctgcgttccactggaat---tccctgcgcgggctttt	119			
Db 274	CCACCTCGATTTGGTGTCTCGGACATGCAAGCTGGAAACTGCCACGCTGAGACCTTGT	215			



Qy	120	gagagcacagtgttccatccctctgcagcatccctctgggtccttggatggcgctgcagtcgagacat	179
Db	214	GCGGCAGATCCGCTCAGCATCCTCTGGGTCTTCTCGATGGCACTGCAGCCTGACACGT	155
Qy	180	tgatcagagattctagagctgcgcagttacatgccggcggtcaggttgacgctccacacca	239
Db	154	TGATCAGGGATTCCAGGGCTGCACAGTACATGCCAGCTGTCAGGTTGATGCTCCATACCA	95
Qy	240	tgctgccgttgacagagggatgc---ctgattctgggtgatgttgaccagctcctcaatga	296
Db	94	TGCTGCCATTGCAGAGCGGAGCCTTCTGGTTCTGGGTGATGTTGACCAGCTCCTCAATGA	35
Qy	297	gctccttgaggttggggagggaggtcacagggc	329
Db	34	GCTCCCTGAGGGCTGTAGAGGGAGGCACAGGGC	2
RESULT	3		
LOCUS	I58494	336 bp	DNA
DEFINITION	Sequence 24 from patent US 5652123.	PAT	07-OCT-1997
ACCESSION	I58494		
VERSION	I58494.1	GI:2477732	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 336)		
AUTHORS	Caput,D., Ferrara,P., Guillemot,J., Kaghad,M., Labit-Le Bouteiller,C., Leplatouis,P., Magazin,M. and Minty,A.		
TITLE	Protein having interleukin 13 activity, recombinant DNA coding for this protein, transformed cells and microorganisms		
JOURNAL	Patent: US 5652123-A 24 29-JUL-1997;		
FEATURES	Location/Qualifiers		
source	1..336		
BASE COUNT	80 a 95 c 90 g	71 t	
ORIGIN	/organism="unknown"		
Query Match	56.8%;	Score 187.4;	DB 10; Length 336;
Best Local Similarity	76.9%;	Pred. No. 9.3e-39;	
Matches	256;	Conservative 0;	Mismatches 71; Indels 6; Gaps 2;
Qy	3	tgaatttccatggcgataaaactcccccttacatagtgagcaggtttttcaccaactgga	62
Db	334	TGAACCGTCCCTCGGAAAAAGTTTCTTTAAATGTAAGACAGAGGTCTTTACAAACTGGG	275
Qy	63	tcacttcaatttgggtgtctcggtgcgttcactgaaaa---tcctgcccgggctttt	119
Db	274	CCACCTCGATTTTGGTGTCTCGGACATGCAAGCTGGAAAACTGCCCAGCTGAGACCTTGT	215
Qy	120	gagagcacagtgttccatccctctgcagcatccctctgggtccttggatggcgctgcagtcgagacat	179
Db	214	GCGGCAGAAATCCGCTCAGCATCCTCTGGGTCTTCTCGATGGCACTGCAGCCTGACACGT	155
Qy	180	tgatcagagattctagagctgcgcagttacatgccggcggtcaggttgacgctccacacca	239
Db	154	TGATCAGGGATTCCAGGGCTGCACAGTACATGCCAGCTGTCAGGTTGATGCTCCATACCA	95
Qy	240	tgctgccgttgacagagggatgc---ctgattctgggtgatgttgaccagctcctcaatga	296
Db	94	TGCTGCCATTGCAGAGCGGAGCCTTCTGGTTCTGGGTGATGTTGACCAGCTCCTCAATGA	35
Qy	297	gctccttgaggttggggagggaggtcacagggc	329
Db	34	GCTCCCTGAGGGCTGTAGAGGGAGGCACAGGGC	2
RESULT	4		
LOCUS	HUMIL13A	1270 bp	mRNA
DEFINITION	Homo sapiens interleukin 13 mRNA, complete cds.	PRI	22-JUL-1993

ACCESSION	L06801		
VERSION	L06801.1	GI:186275	
KEYWORDS	cytokine; growth factor; interleukin 13; regulatory protein.		
SOURCE	Homo sapiens cDNA to mRNA.		
ORGANISM	Homo sapiens		
REFERENCE	1 (bases 1 to 1270)		
AUTHORS	McKenzie,A.N.J., Culpepper,J.A., de Waal Malefyt,R., Briere,F., Punnonen,J., Aversa,G., Sato,A., Dang,W., Cocks,B.G., Menon,S., de Vries,J.E., Banchereau,J. and Zurawski,G.R.		
TITLE	Interleukin-13, a T cell-derived cytokine that regulates human monocyte and B cell function		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 90, 3735-3739 (1993)		
MEDLINE	93234572		
FEATURES	Location/Qualifiers		
source	1..1270		
CDS	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	45..443		
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	/product="interleukin 13"		
	/protein_id="AAA36107.1"		
	/db_xref="GI:186276"		
	/translation="MALLLTIVIALTCLGGFASPGVPPPTALRELIELVNITQNK APLCNGSMVWSINLTAGMYCAALESLINVSGCSAIEKTQRLMSGFCHKVSAGQFSSL HVRDTKIEVAQFVKDLLLHLKLFREGRFN"		
polyA_site	1270		
BASE COUNT	288 a 335 c 336 g	311 t	
ORIGIN			
Query Match	56.8%;	Score 187.4;	DB 93; Length 1270;
Best Local Similarity	76.9%;	Pred. No. 8.5e-39;	
Matches	256;	Conservative 0;	Mismatches 71; Indels 6; Gaps 2;
Qy	3	tgaatttccatggcgataaaactcccccttacatagtgagcaggtttttcaccaactgga	62
Db	438	TGAACCGTCCCTCGGAAAAAGTTTCTTTAAATGTAAGACAGAGGTCTTTACAAACTGGG	379
Qy	63	tcacttcaatttgggtgtctcggtgcgttcactgaaaa---tcctgcccgggctttt	119
Db	378	CCACCTCGATTTTGGTGTCTCGGACATGCAAGCTGGAAAACTGCCCAGCTGAGACCTTGT	319
Qy	120	gagagcacagtgttccatccctctgcagcatccctctgggtccttggatggcgctgcagtcgagacat	179
Db	318	GCGGCAGAAATCCGCTCAGCATCCTCTGGGTCTTCTCGATGGCACTGCAGCCTGACACGT	259
Qy	180	tgatcagagattctagagctgcgcagttacatgccggcggtcaggttgacgctccacacca	239
Db	258	TGATCAGGGATTCCAGGGCTGCACAGTACATGCCAGCTGTCAGGTTGATGCTCCATACCA	199
Qy	240	tgctgccgttgacagagggatgc---ctgattctgggtgatgttgaccagctcctcaatga	296
Db	198	TGCTGCCATTGCAGAGCGGAGCCTTCTGGTTCTGGGTGATGTTGACCAGCTCCTCAATGA	139
Qy	297	gctccttgaggttggggagggaggtcacagggc	329
Db	138	GCTCCCTGAGGGCTGTAGAGGGAGGCACAGGGC	106
RESULT	5		
HSNC30/c	HSNC30	1282 bp	mRNA
LOCUS	H.sapiens interleukin-13 mRNA.		
DEFINITION	X69079		
ACCESSION	X69079.1	GI:297787	
VERSION	lymphokine.		
KEYWORDS	human.		
SOURCE	Homo sapiens		
ORGANISM	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1 (bases 1 to 1282)	PRI	17-FEB-1997



Db 138 GCTCCCTGAGGGCTGTAGAGGGAGGCACAGGGC 106

RESULT 7

A29930/c

LOCUS A29930 336 bp DNA PAT 23-JUN-1995

DEFINITION Sequence coding for the mature cytokine like protein.

ACCESSION A29930

VERSION A29930.1 GI:1249018

KEYWORDS synthetic construct.

SOURCE synthetic construct.

ORGANISM artificial sequence.

REFERENCE 1 (bases 1 to 336)

AUTHORS Caput,D., Ferrara,P., Guillemot,J.C., Kaghad,M., Labit-le Bouteiller,C., Leplatols,P., Magazin,M. and Minty,A.

TITLE Protein having cytokin type activity, recombinant DNA coding for this protein, transformed cells and microorganisms

JOURNAL Patent: EP 0506574-A 2 30-SEP-1992;

ELF SANOFI

FEATURES

source Location/Qualifiers

1. .336

/organism="synthetic construct"

/db\_xref="taxon:32630"

BASE COUNT 81 a 95 c 89 g 71 t

ORIGIN

Query Match 56.3%; Score 185.8; DB 9; Length 336;

Best Local Similarity 76.6%; Pred. No. 2.4e-38;

Matches 255; Conservative 0; Mismatches 72; Indels 6; Gaps 2;

QY 3 tgaatattccatggcgataaaactcccccttacataggtgagcaggttttttaccacaaactgga 62

Db 334 TGAACCGTCCCTCGCGAAAAAGTTCTTTAAATGTAAGAGCAGGTCCTTTACAAACTGGG 275

QY 63 tcaattcaatttgggtctcggtcgttcactggaaa---tccctgccgcgggctttt 119

Db 274 CCACCTCGATTTTGGTGCTCTCGGACATGCAAGCTGGAAAACTGCCCCAGCTGAGACCTTGT 215

QY 120 gagagcacagtgcttttcagcatcctctgggtccttggatggcgctgcagtcggagacat 179

Db 214 GCGGCGAGAATCCGCTCAGCATCCTCTGGGTCTTCTCGATGGCAGCTGCAGCCTGACACGT 155

QY 180 tgatcagagattcttagagctgcgcagtagacatgccggcggtcaggttgacgcgtccacacca 239

Db 154 TGATCAGGGATTCCAGGGCTGCACAGTACATGTCTCGATGGCAGCTGCAGCCTGACACGT 155

QY 240 tgctgccgttgacagaggatgc---ctgattctgggtgatgttgaccagctcctcaatga 296

Db 94 TGCTGCCATTGCAGAGCGGAGCCTTCTGGTTCTGGGTGATGTTGACAGCTCCTCAATGA 35

QY 297 gctccttgagggttggggaggaggtcacagggc 329

Db 34 GCTCCCTGAGGGCTGTAGAGGGAGGCACAGGGC 2

RESULT 8

I58481/c

LOCUS I58481 336 bp DNA PAT 07-OCT-1997

DEFINITION Sequence 2 from patent US 5652123.

ACCESSION I58481

VERSION I58481.1 GI:2477719

KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 336)

AUTHORS Caput,D., Ferrara,P., Guillemot,J., Kaghad,M., Labit-Le Bouteiller,C., Leplatols,P., Magazin,M. and Minty,A.

TITLE Protein having interleukin 13 activity, recombinant DNA coding for this protein, transformed cells and microorganisms

JOURNAL Patent: US 5652123-A 2 29-JUL-1997;

FEATURES

source Location/Qualifiers

1. .336

/organism="unknown"

BASE COUNT 81 a 95 c 89 g 71 t

ORIGIN

Query Match 56.3%; Score 185.8; DB 10; Length 336;

Best Local Similarity 76.6%; Pred. No. 2.4e-38;

Matches 255; Conservative 0; Mismatches 72; Indels 6; Gaps 2;

QY 3 tgaatattccatggcgataaaactcccccttacataggtgagcaggttttttaccacaaactgga 62

Db 334 TGAACCGTCCCTCGCGAAAAAGTTCTTTAAATGTAAGAGCAGGTCCTTTACAAACTGGG 275

QY 63 tcaattcaatttgggtctcggtcgttcactggaaa---tccctgccgcgggctttt 119

Db 274 CCACCTCGATTTTGGTGCTCTCGGACATGCAAGCTGGAAAACTGCCCCAGCTGAGACCTTGT 215

QY 120 gagagcacagtgcttttcagcatcctctgggtccttggatggcgctgcagtcggagacat 179

Db 214 GCGGCGAGAATCCGCTCAGCATCCTCTGGGTCTTCTCGATGGCAGCTGCAGCCTGACACGT 155

QY 180 tgatcagagattcttagagctgcgcagtagacatgccggcggtcaggttgacgcgtccacacca 239

Db 154 TGATCAGGGATTCCAGGGCTGCACAGTACATGTCTCGATGGCAGCTGCAGCCTGACACGT 155

QY 240 tgctgccgttgacagaggatgc---ctgattctgggtgatgttgaccagctcctcaatga 296

Db 94 TGCTGCCATTGCAGAGCGGAGCCTTCTGGTTCTGGGTGATGTTGACAGCTCCTCAATGA 35

QY 297 gctccttgagggttggggaggaggtcacagggc 329

Db 34 GCTCCCTGAGGGCTGTAGAGGGAGGCACAGGGC 2

RESULT 9

AF043334/c

LOCUS AF043334 417 bp mRNA PRI 21-FEB-1998

DEFINITION Homo sapiens interleukin 13 precursor (IL13) mRNA, complete cds.

ACCESSION AF043334

VERSION AF043334.1 GI:2905619

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 417)

AUTHORS Jang,J.S. and Kim,B.E.

TITLE Direct Submission

JOURNAL Submitted (15-JAN-1998) Protein Engineering, General Institute of Technology, Hyundai Pharm. Ind. Co., Ltd., 213 Sosa Bon 1-dong, Sosa-gu, Bucheon 422-231, Korea

COMMENT

Nested PCR:

1) first PCR :

forward primer (5'-ctcaatcctctcctctgttgga-3')

reverse primer (5'-tagtcaggtcctgtctctgc-3')

2) second PCR :

forward primer (5'-ctcatggcgcttttggtagaccagc-3')

reverse primer (5'-gatgctttcgaagtttcagttgaa-3').

FEATURES

source Location/Qualifiers

1. .417

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/cell\_type="PHA-treated peripheral blood leukocyte"

gene 1. .417

/gene="IL13"

primer\_bind 1. .24

/gene="IL13"

/note="second PCR"

/PCR\_conditions="94C-1min, 50C-1min, 72C-3min, 30 cycles; DeltaCycler II from Ericomp"

CDS 4. .402







Best Local SImilarity 76.0%; Pred. No. 1.6e-37;									
Matches 253;		Conservative 0;		Mismatches 74;		Indels 6;		Gaps 2;	
QY	3	tgaaatttccatggcgataaaactcccccttacataggtgagcaggtttttccaccaactgga	62						
Db	397	TGAACCGTCCCTCGCGAAAAAGTTTCTTTAAATGTAAGAGCAGGTCCTTTACAAACTGGG	338						
QY	63	tcacttcaattttggtgtctcgggtgcgttcactggaaa---tccctgccgcgggctttt	119						
Db	337	CCACCTCGATTTTGGTGTCTCGGACATGCAAGCTGGAAACTGCCCAGCTGAGACCTTGT	278						
QY	120	gagagcacagtgtctttcagcatcctctgggtccttttgatggcgctgcagtcggagacat	179						
Db	277	GCGGGCAGAATCCGCTCAGCATCCTCTGGGTCTTCTCGATGGCACTGCAGCCTGACACGT	218						
QY	180	tgatcagagattctagagctgcgcagtagcatatcccgccggtcaggttgacgctccacacca	239						
Db	217	TGATCAGGGATTCCAGGGCTGCACAGTACATGCCAGCTGTCAAGTTGATGCTCCATACCA	158						
QY	240	tgctgccgttgccagagggatgc---ctgattctcgggtgatgtgaccagctcctcaatga	296						
Db	157	TGCTGCCATTGCAGAGCGGAGCCTTCTGGTTCTGGGTGATGTTGACCAGCTCCTCAATGA	98						
QY	297	gctccttgagggttggggagggaggtcacagggc	329						
Db	97	GCTCCCTGAGGGCAGTACTGGGAGGCACAGGGC	65						
RESULT 15									
I86198/c									
LOCUS		I86198		425 bp		DNA		PAT 10-JUN-1998	
DEFINITION		Sequence 4 from patent US 5700665.							
ACCESSION		I86198							
KEYWORDS		I86198.1 GI:3205916							
SOURCE		Unknown.							
ORGANISM		Unknown.							
REFERENCE		1 (bases 1 to 425)							
AUTHORS		Legoux,R., Maldonado,P. and Salome,M.							
TITLE		Method for the extraction of periplasmic proteins from prokaryotic microorganisms in the presence of arginine							
JOURNAL		Patent: US 5700665-A 4 23-DEC-1997;							
FEATURES		Location/Qualifiers							
source		1..425							
BASE COUNT		100 a		116 c		110 g		99 t	
ORIGIN									
Query Match 55.3%; Score 182.6; DB 10; Length 425;									
Best Local Similarity 76.0%; Pred. No. 1.6e-37;		Matches 253;		Conservative 0;		Mismatches 74;		Indels 6; Gaps 2;	
QY	3	tgaaatttccatggcgataaaactcccccttacataggtgagcaggtttttccaccaactgga	62						
Db	397	TGAACCGTCCCTCGCGAAAAAGTTTCTTTAAATGTAAGAGCAGGTCCTTTACAAACTGGG	338						
QY	63	tcacttcaattttggtgtctcgggtgcgttcactggaaa---tccctgccgcgggctttt	119						
Db	337	CCACCTCGATTTTGGTGTCTCGGACATGCAAGCTGGAAACTGCCCAGCTGAGACCTTGT	278						
QY	120	gagagcacagtgtctttcagcatcctctgggtccttttgatggcgctgcagtcggagacat	179						
Db	277	GCGGGCAGAATCCGCTCAGCATCCTCTGGGTCTTCTCGATGGCACTGCAGCCTGACACGT	218						
QY	180	tgatcagagattctagagctgcgcagtagcatatcccgccggtcaggttgacgctccacacca	239						
Db	217	TGATCAGGGATTCCAGGGCTGCACAGTACATGCCAGCTGTCAAGTTGATGCTCCATACCA	158						
QY	240	tgctgccgttgccagagggatgc---ctgattctcgggtgatgtgaccagctcctcaatga	296						
Db	157	TGCTGCCATTGCAGAGCGGAGCCTTCTGGTTCTGGGTGATGTTGACCAGCTCCTCAATGA	98						

QY 297 gctccttgaggggttggggagggaggtcacagggc 329  
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Db 97 GCTCCCTGAGGGGCAGTACTGGGAGGCACAGGGC 65

Search completed: May 13, 2001, 14:25:24  
Job time: 19404 sec

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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: May 13, 2001, 14:30:26 ; Search time 472.02 Seconds  
(without alignments)  
408.135 Million cell updates/sec

Title: US-09-451-527-106  
Perfect score: 330  
Sequence: 1 tctgaaatttcctatggcgat.....ggggagggtcacagggt 330

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 678276 seqs, 291890651 residues

Total number of hits satisfying chosen parameters: 1356552

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /cgnl\_8/gcgdata/geneseq/geneseq/NA1981.DAT: \*  
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4: /cgnl\_8/gcgdata/geneseq/geneseq/NA1983.DAT: \*  
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19: /cgnl\_8/gcgdata/geneseq/geneseq/NA1998.DAT: \*  
20: /cgnl\_8/gcgdata/geneseq/geneseq/NA1999.DAT: \*  
21: /cgnl\_8/gcgdata/geneseq/geneseq/NA2000.DAT: \*  
22: /cgnl\_8/gcgdata/geneseq/geneseq/NA2001.DAT: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match	Length	ID	Description
C 1	330	100.0	330	21	Canine mature inte
2	330	100.0	330	21	Canine mature inte
C 3	330	100.0	390	21	Canine interleukin
4	330	100.0	390	21	Canine interleukin
C 5	330	100.0	1269	21	Canine interleukin
6	330	100.0	1269	21	Canine interleukin
C 7	317	96.1	333	21	Canine mature inte
8	317	96.1	333	21	Canine mature inte
C 9	317	96.1	393	21	Canine interleukin
10	317	96.1	393	21	Canine interleukin
C 11	317	96.1	1302	21	Canine interleukin

C 12	317	96.1	1302	21	255556	Canine interleukin
C 13	240	72.7	272	21	255553	Canine interleukin
C 14	218	66.1	278	21	255554	Canine interleukin
C 15	187.4	56.8	336	13	Q28944	Gly41-Cytokine cod
C 16	187.4	56.8	1270	21	F21334	Human low adenosin
C 17	187.4	56.8	1270	21	A35212	Human adenosine re
C 18	187.4	56.8	1282	21	F21332	Human low adenosin
C 19	187.4	56.8	1282	21	A35210	Human adenosine re
C 20	187.4	56.8	1290	15	Q56692	Sequence encoding
C 21	187.4	56.8	6952	21	F21333	Human low adenosin
C 22	187.4	56.8	6952	21	A35211	Human adenosine re
C 23	187.4	56.8	14978	21	F21338	Human low adenosin
C 24	187.4	56.8	14978	21	A35216	Human adenosine re
C 25	185.8	56.3	336	13	Q28943	Asp41-Cytokine cod
C 26	185.8	56.3	1297	13	Q28947	Cytokine NC30. Q
C 27	151.4	45.9	1212	15	Q56693	Sequence encoding
C 28	71.4	21.6	5670	21	F21331	Human low adenosin
C 29	71.4	21.6	5670	21	F21337	Human low adenosin
C 30	71.4	21.6	5670	21	A35209	Human adenosine re
C 31	71.4	21.6	5670	21	A35215	Human adenosine re
C 32	39	11.8	166	21	255552	Canine interleukin
C 33	34	10.3	479	21	C38383	Zea mays DNA fragm
C 34	34	10.3	1896	21	Z48297	S. coelicolor YesW
C 35	33.8	10.2	2792	20	X78074	Rat DTDST cDNA. R
C 36	33.4	10.1	66	20	Z32227	Human interleukin
C 37	33.4	10.1	772	19	V48405	Dominant-negative
C 38	32.4	9.8	717	21	A93373	Enhanced green flu
C 39	32.4	9.8	717	21	A93374	Enhanced blue fluo
C 40	32.4	9.8	717	21	A93375	Enhanced cyan fluo
C 41	32.4	9.8	717	21	A27573	DNA encoding EGFP
C 42	32.4	9.8	717	21	A27574	DNA encoding EBFP
C 43	32.4	9.8	717	21	A27575	DNA encoding ECFP
C 44	32.4	9.8	720	21	C62377	CDNA encoding a gr
C 45	32.4	9.8	720	21	Z45644	DNA encoding the m

ALIGNMENTS

RESULT 1  
Z55565/c  
ID Z55565 standard; cDNA; 330 BP.  
XX  
AC Z55565;  
XX  
DT 14-MAR-2000 (first entry)  
XX  
DE Canine mature interleukin-13 (IL-13) clone 78 cDNA.  
XX  
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;  
immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.  
XX  
OS Canis familiaris.  
XX  
PN WO9961618-A2.  
XX  
PD 02-DEC-1999.  
XX  
PF 28-MAY-1999; 99WO-US11942.  
XX  
PR 29-MAY-1998; 98US-0087306.  
XX  
(HESK-) HESKA CORP.  
XX  
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;  
XX  
DR WPI; 2000-072623/06.  
XX  
PT P-PSDB; Y58224.  
XX  
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
useful for treating or preventing e.g. tumors or autoimmune disease  
XX  
PS Claim 1i; Page 239-240; 264pp; English.



```
XX Sequences Z55552-Z55560 and Z55561-Z55566 represent cDNA
CC sequences encoding canine interleukin-13 (IL-13) clones 80
CC and 78 respectively. The invention relates to canine
CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these
CC immunoregulatory proteins. The proteins, their associated
CC nucleic acids, specific antibodies and inhibitors may be used as
CC vaccines for therapeutic or prophylactic regulation of an immune
CC response in animals (particularly cats, dogs, horses and humans).
CC They may be used to treat autoimmune or infectious diseases including
CC allergies, tumours, inflammation and graft rejection, and to increase
CC the response from a co-administered antigen. The nucleotide sequences
CC can also be used for the recombinant production of a protein, while
CC nucleotide fragments are useful as probes, as amplification primers and
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
CC The proteins may be used to raise antibodies and to screen for
CC modulators of activity, while the antibodies may be used in detection,
CC and in drug targeting.
XX Sequence 330 BP; 88 A; 96 C; 82 G; 64 T; 0 other;

Query Match      100.0%; Score 330; DB 21; Length 330;
Best Local Similarity 100.0%; Pred. No. 1.3e-88;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctgaaatttccatggcgataaaactcccttacataggtgagcaggtttttcaccaactg 60
Db 330 TCTGAATTTCCATGGCGATAAACTCCCTTACATAGGTGAGCAGGTTTTCACCAACTG 271

QY 61 gatcacttcaatttgggtgtctcggtcggttcactggaatccctgccgcgggttttg 120
Db 270 GATCACTTCAATTTGGTGTCTCGGCTGCGTTCACTGGAAATCCCTGCCGGGGCTTTTG 211

QY 121 agagcacagtgttttcagcatcctctgtggtccttggatggcgctgcagtcggagacatt 180
Db 210 AGAGCACAGTGCTTTTCAGCATCCTCTGTGGTCTCTTGGATGGCGCTGCAGTCGGAGACATT 151

QY 181 gatcagagattctagagctgcgcagtagcatgcgcggcggtcaggttgacgtccacacccat 240
Db 150 GATCAGAGATTCTAGAGCTGCGCAGTACATGCCGGCGGTGAGGTTGACGCTCCACACCAT 91

QY 241 gctgccgttgcagagggatgcctgattctgtggtgatgttgaccagctcctcaatgagctc 300
Db 90 GCTGCCGTTGCAGAGGGATGCCTGATTCTGGGTGATGTGACCAGCTCCTCAATGAGCTC 31

QY 301 cttgaggggttgggagggagtcacagggct 330
Db 30 CTTGAGGGTTGGGGAGGGAGTCACAGGGCT 1

RESULT 2
Z55566
ID Z55566 standard; cDNA; 330 BP.
XX
AC Z55566;
XX
DT 14-MAR-2000 (first entry)
XX
DE Canine mature interleukin-13 (IL-13) clone 78 cDNA complement.
XX
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;
XX immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
XX
OS Canis familiaris.
XX
PN WO9961618-A2.
XX
PD 02-DEC-1999.
XX
```

```
PF 28-MAY-1999; 99WO-US11942.
XX
PR 29-MAY-1998; 98US-0087306.
XX
PA (HESK-) HESKA CORP.
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;
XX
DR WPI; 2000-072623/06.
DR P-PSDB; Y58224.
XX
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,
PT useful for treating or preventing e.g. tumors or autoimmune disease
XX
PS Claim 1i; Page 241; 264pp; English.
XX
CC Sequences Z55552-Z55560 and Z55561-Z55566 represent cDNA
CC sequences encoding canine interleukin-13 (IL-13) clones 80
CC and 78 respectively. The invention relates to canine
CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these
CC immunoregulatory proteins. The proteins, their associated
CC nucleic acids, specific antibodies and inhibitors may be used as
CC vaccines for therapeutic or prophylactic regulation of an immune
CC response in animals (particularly cats, dogs, horses and humans).
CC They may be used to treat autoimmune or infectious diseases including
CC allergies, tumours, inflammation and graft rejection, and to increase
CC the response from a co-administered antigen. The nucleotide sequences
CC can also be used for the recombinant production of a protein, while
CC nucleotide fragments are useful as probes, as amplification primers and
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
CC The proteins may be used to raise antibodies and to screen for
CC modulators of activity, while the antibodies may be used in detection,
CC and in drug targeting.
XX
SQ Sequence 330 BP; 64 A; 82 C; 96 G; 88 T; 0 other;

Query Match      100.0%; Score 330; DB 21; Length 330;
Best Local Similarity 100.0%; Pred. No. 1.3e-88;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctgaaatttccatggcgataaaactcccttacataggtgagcaggtttttcaccaactg 60
Db 1 tctgaaatttccatggcgataaaactcccttacataggtgagcaggtttttcaccaactg 60

QY 61 gatcacttcaatttgggtgtctcggtcggttcactggaatccctgccgcgggttttg 120
Db 61 gatcacttcaatttgggtgtctcggtcggttcactggaatccctgccgcgggttttg 120

QY 121 agagcacagtgttttcagcatcctctgtggtccttggatggcgctgcagtcggagacatt 180
Db 121 agagcacagtgttttcagcatcctctgtggtccttggatggcgctgcagtcggagacatt 180

QY 181 gatcagagattctagagctgcgcagtagcatgcgcggcggtcaggttgacgtccacacccat 240
Db 181 gatcagagattctagagctgcgcagtagcatgcgcggcggtcaggttgacgtccacacccat 240

QY 241 gctgccgttgcagagggatgcctgattctgtggtgatgttgaccagctcctcaatgagctc 300
Db 241 gctgccgttgcagagggatgcctgattctgtggtgatgttgaccagctcctcaatgagctc 300

QY 301 cttgaggggttgggagggagtcacagggct 330
Db 301 cttgaggggttgggagggagtcacagggct 330

RESULT 3
Z55563/c
ID Z55563 standard; cDNA; 390 BP.
XX
```

AC Z55563;  
XX  
DT 14-MAR-2000 (first entry)  
XX  
DE Canine interleukin-13 (IL-13) clone 78 cDNA coding region.  
XX  
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;  
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.  
XX  
OS Canis familiaris.  
XX  
PN WO9961618-A2.  
XX  
PD 02-DEC-1999.  
XX  
PF 28-MAY-1999; 99WO-US11942.  
XX  
PR 29-MAY-1998; 98US-0087306.  
XX  
PA (HESK-) HESKA CORP.  
XX  
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;  
XX  
DR WPI; 2000-072623/06.  
DR P-PSDB; Y58223.  
XX  
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
PT useful for treating or preventing e.g. tumors or autoimmune disease  
XX  
PS Claim 11; Page 238-239; 264pp; English.  
XX  
CC Sequences 255552-255560 and 255561-255566 represent cDNA  
CC sequences encoding canine interleukin-13 (IL-13) clones 80  
CC and 78 respectively. The invention relates to canine  
CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or  
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline  
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage  
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these  
CC immunoregulatory proteins. The proteins, their associated  
CC nucleic acids, specific antibodies and inhibitors may be used as  
CC vaccines for therapeutic or prophylactic regulation of an immune  
CC response in animals (particularly cats, dogs, horses and humans).  
CC They may be used to treat autoimmune or infectious diseases including  
CC allergies, tumours, inflammation and graft rejection, and to increase  
CC the response from a co-administered antigen. The nucleotide sequences  
CC can also be used for the recombinant production of a protein, while  
CC nucleotide fragments are useful as probes, as amplification primers and  
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
CC The proteins may be used to raise antibodies and to screen for  
CC modulators of activity, while the antibodies may be used in detection,  
CC and in drug targeting.  
XX  
SQ Sequence 390 BP; 92 A; 117 C; 99 G; 82 T; 0 other;  
  
Query Match 100.0%; Score 330; DB 21; Length 390;  
Best Local Similarity 100.0%; Pred. No. 1.4e-88;  
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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DB 390 TCTGAATTTCCATGGCGATAAACTCCCTTACATAGGTGAGCAGGTTTTTCACCAACTG 331  
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QY 61 gatcaattcaatttgggtgtctcggtcggttcactggaaatccctgcgcggggttttg 120  
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DB 330 GATCACTTCANTTTGGTGTCTCGGCTGGGTTCACTGGAAATCCCTGCCGGGGCTTTTG 271  
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QY 121 agagcacagtgttttcagcatcctctgtggtccttggatggcgctgcagtcggagacatt 180  
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DB 270 AGAGCACAGTGTCTTCAGCATCCTCTGGGTCTTTGGATGGCGCTGCAGTCGAGACATT 211  
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QY 181 gatcagagattctagactgcgcagtcacatgccggcggtcaggttgacgtctcacacatt 240  
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Db 210 GATCAGAGATTCTAGAGCTGGCGAGTACATGCCGGGGTGAGGTTGACGCTCCACACCAT 151  
QY 241 gctgcggttcagagaggtgctgattctgtggtgatgttgaccagctcctcaatgagctc 300  
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Db 150 GCTGCGGTTGCAGAGGGGATGCTGATCTGGGTGATGTTGACCAAGCTCCTCAATGAGCTC 91  
QY 301 ctgaggggtgggagggaggtcacagggct 330  
|||||  
Db 90 CTTGACGGTTGGGAGGGAGTGCACAGGGCT 61  
  
RESULT 4  
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ID Z55564 standard; cDNA; 390 BP.  
XX  
AC Z55564;  
XX  
DT 14-MAR-2000 (first entry)  
XX  
DE Canine interleukin-13 (IL-13) clone 78 cDNA coding region complement.  
XX  
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;  
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.  
XX  
OS Canis familiaris.  
XX  
PN WO9961618-A2.  
XX  
PD 02-DEC-1999.  
XX  
PF 28-MAY-1999; 99WO-US11942.  
XX  
PR 29-MAY-1998; 98US-0087306.  
XX  
PA (HESK-) HESKA CORP.  
XX  
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;  
XX  
DR WPI; 2000-072623/06.  
DR P-PSDB; Y58223.  
XX  
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
PT useful for treating or preventing e.g. tumors or autoimmune disease  
XX  
PS Claim 11; Page 239; 264pp; English.  
XX  
CC Sequences 255552-255560 and 255561-255566 represent cDNA  
CC sequences encoding canine interleukin-13 (IL-13) clones 80  
CC and 78 respectively. The invention relates to canine  
CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or  
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline  
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage  
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these  
CC immunoregulatory proteins. The proteins, their associated  
CC nucleic acids, specific antibodies and inhibitors may be used as  
CC vaccines for therapeutic or prophylactic regulation of an immune  
CC response in animals (particularly cats, dogs, horses and humans).  
CC They may be used to treat autoimmune or infectious diseases including  
CC allergies, tumours, inflammation and graft rejection, and to increase  
CC the response from a co-administered antigen. The nucleotide sequences  
CC can also be used for the recombinant production of a protein, while  
CC nucleotide fragments are useful as probes, as amplification primers and  
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
CC The proteins may be used to raise antibodies and to screen for  
CC modulators of activity, while the antibodies may be used in detection,  
CC and in drug targeting.  
XX  
SQ Sequence 390 BP; 82 A; 99 C; 117 G; 92 T; 0 other;

Query Match 100.0%; Score 330; DB 21; Length 390;  
Best Local Similarity 100.0%; Pred. No. 1.4e-88;  
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctgaaatttccatggcgataaaactccccttacataggtgagcaggtttttcaccacactg 60  
|||||  
Db 1 tctgaaatttccatggcgataaaactccccttacataggtgagcaggtttttcaccacactg 60  
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QY 61 gatcacttcaattttgtgtctcggtcgctgcgttcaactggaataccctgccgcgggttttg 120  
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|||||  
QY 121 agagcacagtgttttcagcatcctctggttccttttgatggcgctgcagtcggagacatt 180  
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Db 121 agagcacagtgttttcagcatcctctggttccttttgatggcgctgcagtcggagacatt 180  
|||||  
QY 181 gatcagagattctagagctgcgcagtcacatgccggcggtcaggttgacgctccacacatt 240  
|||||  
Db 181 gatcagagattctagagctgcgcagtcacatgccggcggtcaggttgacgctccacacatt 240  
|||||  
QY 241 gctgccgttcagagggatgcctgattctggtgatgttgaccagctcctcaatgagctc 300  
|||||  
Db 241 gctgccgttcagagggatgcctgattctggtgatgttgaccagctcctcaatgagctc 300  
|||||  
QY 301 cttgaggggttggggagggagtcacagggct 330  
|||||  
Db 301 cttgaggggttggggagggagtcacagggct 330  
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RESULT 5  
Z55561/c  
ID Z55561 standard; cDNA; 1269 BP.  
XX  
AC Z55561;  
XX  
DT 14-MAR-2000 (first entry)  
XX  
DE Canine interleukin-13 (IL-13) clone 78 cDNA.  
XX  
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;  
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.  
OS Canis familiaris.  
XX  
FH Key Location/Qualifiers  
FT CDS 57..449  
FT /\*tag= a  
FT /product= "Canine IL-13 clone 78"

XX  
PN WO9961618-A2.  
XX  
PD 02-DEC-1999.  
XX  
PF 28-MAY-1999; 99WO-US11942.  
XX  
PR 29-MAY-1998; 98US-0087306.  
XX  
PA (HESK-) HESKA CORP.  
XX  
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;  
XX  
DR WPI; 2000-072623/06.  
XX  
PT P-PSDB; Y58223.  
PT  
PS Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
PT useful for treating or preventing e.g. tumors or autoimmune disease  
XX  
PS Claim 11; Page 235-236; 264pp; English.  
XX  
CC Sequences Z55552-Z55560 and Z55561-Z55566 represent cDNA  
CC sequences encoding canine interleukin-13 (IL-13) clones 80  
CC and 78 respectively. The invention relates to canine  
CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or  
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline  
CC interferon-alpha (IFN-alpha), and feline granulocyte macrophage  
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these

CC immunoregulatory proteins. The proteins, their associated  
CC nucleic acids, specific antibodies and inhibitors may be used as  
CC vaccines for therapeutic or prophylactic regulation of an immune  
CC response in animals (particularly cats, dogs, horses and humans).  
CC They may be used to treat autoimmune or infectious diseases including  
CC allergies, tumours, inflammation and graft rejection, and to increase  
CC the response from a co-administered antigen. The nucleotide sequences  
CC can also be used for the recombinant production of a protein, while  
CC nucleotide fragments are useful as probes, as amplification primers and  
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
CC The proteins may be used to raise antibodies and to screen for  
CC modulators of activity, while the antibodies may be used in detection,  
CC and in drug targeting.  
XX  
SQ Sequence 1269 BP; 302 A; 320 C; 340 G; 307 T; 0 other;  
Query Match 100.0%; Score 330; DB 21; Length 1269;  
Best Local Similarity 100.0%; Pred. No. 2.1e-88;  
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 tctgaaatttccatggcgataaaactccccttacataggtgagcaggtttttcaccacactg 60  
|||||  
Db 446 TCTGAAATTTCCATGGCGATAAAACTCCCTTACATAGGTGAGCAGGTTTTCACCAACTG 387  
|||||  
QY 61 gatcacttcaattttgtgtctcggtcgctgcgttcaactggaaatccctgccgcgggttttg 120  
|||||  
Db 386 GATCACTTCAATTTTGGTGTCTCGGCTCGGTCACTGGAATCCCTGCCGGGGCTTTTG 327  
|||||  
QY 121 agagcacagtgttttcagcatcctctggttccttttgatggcgctgcagtcggagacatt 180  
|||||  
Db 326 AGAGCACAGTGTCTTTCAGCATCCTCTGGGTCTTGGATGGCGCTGCAGTCGGAGACATT 267  
|||||  
QY 181 gatcagagattctagagctgcgcagtcacatgccggcggtcaggttgacgctccacacatt 240  
|||||  
Db 266 GATCAGAGATTCTAGAGCTGCCAGTACATGCCGGGGCTCAGGTGACCGTCCACACCAT 207  
|||||  
QY 241 gctgccgttcagagggatgcctgattctggtgatgttgaccagctcctcaatgagctc 300  
|||||  
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QY 301 cttgaggggttggggagggagtcacagggct 330  
|||||  
Db 146 CTTGAGGGTTGGGAGGGGAGTCACAGGGCT 117  
|||||  
RESULT 6  
Z55562  
ID Z55562 standard; cDNA; 1269 BP.  
XX  
AC Z55562;  
XX  
DT 14-MAR-2000 (first entry)  
XX  
DE Canine interleukin-13 (IL-13) clone 78 cDNA complement.  
XX  
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;  
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.  
OS Canis familiaris.  
XX  
FH Key Location/Qualifiers  
FT CDS complement (821..1213)  
FT /\*tag= a  
FT /product= "Canine IL-13 clone 78"  
XX  
PN WO9961618-A2.  
XX  
PD 02-DEC-1999.  
XX  
PF 28-MAY-1999; 99WO-US11942.  
XX  
PR 29-MAY-1998; 98US-0087306.







|||||  
Db 93 CATGCTGCCGTTGCAGAGGATGCTGATCTGGGTGATGTTGACCAAGCTCCTCAATGAG 34  
QY 298 ctccttgagggttgaggaggtcacagggt 330  
Db 33 CTCCTTGAGCGTTGGCGAGGAGTCACAGGGCT 1  
RESULT 8  
Z55560  
ID Z55560 standard; cDNA; 333 BP.  
XX  
AC Z55560;  
XX  
DT 14-MAR-2000 (first entry)  
XX  
DE Canine mature interleukin-13 (IL-13) clone 80 cDNA complement.  
XX  
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;  
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.  
XX  
OS Canis familiaris.  
XX  
PN WO9961618-A2.  
XX  
PD 02-DEC-1999.  
XX  
PF 28-MAY-1999; 99WO-US11942.  
XX  
PR 29-MAY-1998; 98US-0087306.  
XX  
PA (HESK-) HESKA CORP.  
XX  
PI Sim G, Yang S, Drelitz MJ, Wonderling RS;  
XX  
DR WPI; 2000-072623/06.  
DR P-PSDB; Y58222.  
XX  
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
PT useful for treating or preventing e.g. tumors or autoimmune disease  
XX  
PS Claim 1i; Page 235; 264pp; English.  
XX  
CC Sequences Z55552-Z55560 and Z55561-Z55566 represent cDNA  
CC sequences encoding canine interleukin-13 (IL-13) clones 80  
CC and 78 respectively. The invention relates to canine  
CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or  
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline  
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage  
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these  
CC immunoregulatory proteins. The proteins, their associated  
CC nucleic acids, specific antibodies and inhibitors may be used as  
CC vaccines for therapeutic or prophylactic regulation of an immune  
CC response in animals (particularly cats, dogs, horses and humans).  
CC They may be used to treat autoimmune or infectious diseases including  
CC allergies, tumours, inflammation and graft rejection, and to increase  
CC the response from a co-administered antigen. The nucleotide sequences  
CC can also be used for the recombinant production of a protein, while  
CC nucleotide fragments are useful as probes, as amplification primers and  
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
CC The proteins may be used to raise antibodies and to screen for  
CC modulators of activity, while the antibodies may be used in detection,  
CC and in drug targeting.  
XX  
SQ Sequence 333 BP; 64 A; 83 C; 97 G; 89 T; 0 other;  
Query Match 96.1%; Score 317; DB 21; Length 333;  
Best Local Similarity 99.1%; Pred. NO. 9.1e-85;  
Matches 330; Conservative 0; Mismatches 0; Indels 3; Gaps 1;  
QY 1 tctgaaatttccatggcgataaaactcccccttacataggtgagcaggtttttccaccaactg 60  
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Db 1 tctgaaatttccatggcgataaaactcccccttacataggtgagcaggtttttccaccaactg 60  
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Db 61 gatcacttcaattttgtgtctcggtcgcttcactggaatctgccctgcccgggctt 120  
QY 118 ttgagagcacagtgttttcagcatcctctgggtcctttggatggcgctgcagtcggagac 177  
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Db 121 ttgagagcacagtgttttcagcatcctctgggtcctttggatggcgctgcagtcggagac 180  
QY 178 attgatcagagattctagagctgcgcagtagcatccggcggtcaggttgacgtccacac 237  
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Db 181 attgatcagagattctagagctgcgcagtagcatccggcggtcaggttgacgtccacac 240  
QY 238 catgctgccgttgagagggatgcctgattcttggtgatgttgaccagctcctcaatgag 297  
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Db 241 catgctgccgttgagagggatgcctgattcttggtgatgttgaccagctcctcaatgag 300  
QY 298 ctccttgagggttgaggagggaggtcacagggt 330  
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RESULT 9  
Z55557/C  
ID Z55557 standard; cDNA; 393 BP.  
XX  
AC Z55557;  
XX  
DT 14-MAR-2000 (first entry)  
XX  
DE Canine interleukin-13 (IL-13) clone 80 cDNA coding region.  
XX  
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;  
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.  
XX  
OS Canis familiaris.  
XX  
PN WO9961618-A2.  
XX  
PD 02-DEC-1999.  
XX  
PF 28-MAY-1999; 99WO-US11942.  
XX  
PR 29-MAY-1998; 98US-0087306.  
XX  
PA (HESK-) HESKA CORP.  
PI Sim G, Yang S, Drelitz MJ, Wonderling RS;  
XX  
DR WPI; 2000-072623/06.  
DR P-PSDB; Y58221.  
XX  
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
PT useful for treating or preventing e.g. tumors or autoimmune disease  
XX  
PS Claim 1i; Page 232-233; 264pp; English.  
XX  
CC Sequences Z55552-Z55560 and Z55561-Z55566 represent cDNA  
CC sequences encoding canine interleukin-13 (IL-13) clones 80  
CC and 78 respectively. The invention relates to canine  
CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or  
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline  
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage  
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these  
CC immunoregulatory proteins. The proteins, their associated  
CC nucleic acids, specific antibodies and inhibitors may be used as  
CC vaccines for therapeutic or prophylactic regulation of an immune  
CC response in animals (particularly cats, dogs, horses and humans).  
CC They may be used to treat autoimmune or infectious diseases including  
CC allergies, tumours, inflammation and graft rejection, and to increase  
CC the response from a co-administered antigen. The nucleotide sequences  
CC can also be used for the recombinant production of a protein, while

```
CC nucleotide fragments are useful as probes, as amplification primers and
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
CC The proteins may be used to raise antibodies and to screen for
CC modulators of activity, while the antibodies may be used in detection,
CC and in drug targeting.
XX
SQ Sequence 393 BP; 93 A; 118 C; 100 G; 82 T; 0 other;

Query Match          96.1%; Score 317; DB 21; Length 393;
Best Local Similarity 99.1%; Pred. No. 9.7e-85;
Matches 330; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 1 tctgaaattccatggcgataaaactcccttacataggtgagcagggtttttcaccactg 60
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Db ATTGATCAGAGATTCTAGAGCTGCGCAGTACATGCCGCGGTTCAGTTGACGCTCCACAC 154
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ID Z55558 standard; cDNA; 393 BP.
XX
AC Z55558;
XX
DT 14-MAR-2000 (first entry)
XX
DE Canine interleukin-13 (IL-13) clone 80 cDNA coding region complement.
XX
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
XX
OS Canis familiaris.
XX
PN WO9961618-A2.
XX
PD 02-DEC-1999.
XX
PF 28-MAY-1999; 99WO-US11942.
XX
PR 29-MAY-1998; 98US-0087306.
XX
PA (HESK-) HESKA CORP.
XX
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;
XX
XX WPI; 2000-072623/06.
DR P-PSDB; Y58221.
XX
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,
PT useful for treating or preventing e.g. tumors or autoimmune disease
XX
PS Claim 11; Page 233; 264pp; English.
XX
```

```
CC Sequences Z55552-Z55560 and Z55561-Z55566 represent cDNA
CC sequences encoding canine interleukin-13 (IL-13) clones 80
CC and 78 respectively. The invention relates to canine
CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these
CC immunoregulatory proteins. The proteins, their associated
CC nucleic acids, specific antibodies and inhibitors may be used as
CC vaccines for therapeutic or prophylactic regulation of an immune
CC response in animals (particularly cats, dogs, horses and humans).
CC They may be used to treat autoimmune or infectious diseases including
CC allergies, tumours, inflammation and graft rejection, and to increase
CC the response from a co-administered antigen. The nucleotide sequences
CC can also be used for the recombinant production of a protein, while
CC nucleotide fragments are useful as probes, as amplification primers and
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
CC The proteins may be used to raise antibodies and to screen for
CC modulators of activity, while the antibodies may be used in detection,
CC and in drug targeting.
XX
SQ Sequence 393 BP; 82 A; 100 C; 118 G; 93 T; 0 other;

Query Match          96.1%; Score 317; DB 21; Length 393;
Best Local Similarity 99.1%; Pred. No. 9.7e-85;
Matches 330; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 1 tctgaaattccatggcgataaaactcccttacataggtgagcagggtttttcaccactg 60
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RESULT 11
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ID Z55555 standard; cDNA; 1302 BP.
XX
AC Z55555;
XX
DT 14-MAR-2000 (first entry)
XX
DE Canine interleukin-13 (IL-13) clone 80 cDNA.
XX
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
XX
OS Canis familiaris.
XX
FH Key Location/Qualifiers
FT CDS 52..447
FT /*tag= a
FT /product= "Canine IL-13 clone 80"
XX
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PN WO9961618-A2.  
XX  
PD 02-DEC-1999.  
XX  
PF 28-MAY-1999; 99WO-US11942.  
XX  
PR 29-MAY-1998; 98US-0087306.  
XX  
PA (HESK-) HESKA CORP.  
XX  
PI SIm G, Yang S, Dreitz MJ, Wonderling RS;  
XX  
DR WPI; 2000-072623/06.  
DR P-PSDB; Y58221.  
XX  
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
PT useful for treating or preventing e.g. tumors or autoimmune disease  
XX  
PS Claim 11; Page 229-230; 264pp; English.  
XX  
CC Sequences 255552-255560 and 255561-255566 represent cDNA  
CC sequences encoding canine interleukin-13 (IL-13) clones 80  
CC and 78 respectively. The invention relates to canine  
CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or  
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline  
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage  
CC colony-stimulating factor (GMCSF), and nucleotides which encode these  
CC immunoregulatory proteins. The proteins, their associated  
CC nucleic acids, specific antibodies and inhibitors may be used as  
CC vaccines for therapeutic or prophylactic regulation of an immune  
CC response in animals (particularly cats, dogs, horses and humans).  
CC They may be used to treat autoimmune or infectious diseases including  
CC allergies, tumours, inflammation and graft rejection, and to increase  
CC the response from a co-administered antigen. The nucleotide sequences  
CC can also be used for the recombinant production of a protein, while  
CC nucleotide fragments are useful as probes, as amplification primers and  
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
CC The proteins may be used to raise antibodies and to screen for  
CC modulators of activity, while the antibodies may be used in detection,  
CC and in drug targeting.  
XX  
SQ Sequence 1302 BP; 337 A; 318 C; 340 G; 307 T; 0 other;

Query Match 96.1%; Score 317; DB 21; Length 1302;  
Best Local Similarity 99.1%; Pred. No. 1.5e-84;  
Matches 330; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

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Db 444 TCTGAAATTTCCATGGCGGATAAACTCCCTTACATAGGTGAGCAGGTTTTCACCAACTG 385  
61 gatcacttcaattttggtctcgtcggttcactggaat---ccctgccgcgggctt 117  
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Db 384 GATCACTTCAATTTGGTGCTCGGCTGCGTTCACTGGAATCTGCCCTGCCGCGGCTT 325  
118 ttgagagcacagtgtttcagcatcctctgggtcctttggatggcgtgcagtcggagac 177  
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Db 324 TTGAGAGCACAGTGTCTTACAGCATCCTCTGGGTCTCTTGGATGGCGCTGCAGTCGGAGAC 265  
178 attgatcagagattctagagctgcgcagtagcatccgcggcggtcaggtgacgctccacac 237  
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Db 264 ATTGATCAGAGATTCTAGAGCTGGCGAGTACATGCCGGCGGTTCAGGTTGACGCTCCACAC 205  
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RESULT 12  
Z55556  
ID 255556 standard; cDNA; 1302 BP.  
XX  
AC 255556;  
XX  
DT 14-MAR-2000 (first entry)  
XX  
DE Canine interleukin-13 (IL-13) clone 80 cDNA complement.  
XX  
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;  
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.  
XX  
OS Canis familiaris.  
XX  
FH Key Location/Qualifiers  
FT CDS complement (856..1251)  
FT /tag= a  
FT /product= "Canine IL-13 clone 80"  
XX  
PN WO9961618-A2.  
XX  
PD 02-DEC-1999.  
XX  
PF 28-MAY-1999; 99WO-US11942.  
XX  
PR 29-MAY-1998; 98US-0087306.  
XX  
PA (HESK-) HESKA CORP.  
XX  
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;  
XX  
DR WPI; 2000-072623/06.  
DR P-PSDB; Y58221.  
XX  
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
PT useful for treating or preventing e.g. tumors or autoimmune disease  
XX  
PS Claim 11; Page 231-232; 264pp; English.  
XX  
CC Sequences 255552-255560 and 255561-255566 represent cDNA  
CC sequences encoding canine interleukin-13 (IL-13) clones 80  
CC and 78 respectively. The invention relates to canine  
CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or  
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline  
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage  
CC colony-stimulating factor (GMCSF), and nucleotides which encode these  
CC immunoregulatory proteins. The proteins, their associated  
CC nucleic acids, specific antibodies and inhibitors may be used as  
CC vaccines for therapeutic or prophylactic regulation of an immune  
CC response in animals (particularly cats, dogs, horses and humans).  
CC They may be used to treat autoimmune or infectious diseases including  
CC allergies, tumours, inflammation and graft rejection, and to increase  
CC the response from a co-administered antigen. The nucleotide sequences  
CC can also be used for the recombinant production of a protein, while  
CC nucleotide fragments are useful as probes, as amplification primers and  
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
CC The proteins may be used to raise antibodies and to screen for  
CC modulators of activity, while the antibodies may be used in detection,  
CC and in drug targeting.  
XX  
SQ Sequence 1302 BP; 307 A; 340 C; 318 G; 337 T; 0 other;

Query Match 96.1%; Score 317; DB 21; Length 1302;  
Best Local Similarity 99.1%; Pred. No. 1.5e-84;  
Matches 330; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 1 tctgaaatttccatggcgataaaactcccccttacataggtgagcaggtttttcaccactg 60  
|||  
Db 859 tctgaaatttccatggcgataaaactcccccttacataggtgagcaggtttttcaccactg 918  
61 gatcacttcaattttggtctcgtcggttcactggaat---ccctgccgcgggctt 117

Db 919 gatacattcaatttgggtctcgctgcgttcactgaaatctgcctgcgcgggctt 978  
118 ttgagagcacagtgctttcagcatcctctctggttcctttggatggcgtgcagtcggagac 177  
Db 979 ttgagagcacagtgctttcagcatcctctctggttcctttggatggcgtgcagtcggagac 1038  
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Db 1039 attgatcagagattctagagctgcgcagtagatcccgcggtcaggttgacgtccacac 1098  
Qy 238 catgctgccgttgacaggggatgcctgattctggtgatgttgaccagctcctcaatgag 297  
Db 1099 catgctgccgttgacaggggatgcctgattctggtgatgttgaccagctcctcaatgag 1158  
Qy 298 ctctctgagggttgaggaggaggtcacagggct 330  
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RESULT 13  
255553/c  
ID 255553 standard; cDNA; 272 BP.

XX AC 255553;

XX 14-MAR-2000 (first entry)

DE Canine interleukin-13 (IL-13) cDNA fragment nCaIL13-272.

KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;  
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.

OS Canis familiaris.

PN WO9961618-A2.

XX 02-DEC-1999.

XX 28-MAY-1999; 99WO-US11942.

XX 29-MAY-1998; 98US-0087306.

XX (HESK-) HESKA CORP.

PI Sim G, Yang S, Dreitz MJ, Wonderling RS;

XX WPI; 2000-072623/06.

PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
PT useful for treating or preventing e.g. tumors or autoimmune disease

PS Claim 1i; Page 228; 264pp; English.

CC Sequences 255552-255560 and 255561-255566 represent cDNA  
CC sequences encoding canine interleukin-13 (IL-13) clones 80  
CC and 78 respectively. The invention relates to canine

CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or  
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline  
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage  
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these  
CC immunoregulatory proteins. The proteins, their associated

CC nucleic acids, specific antibodies and inhibitors may be used as  
CC vaccines for therapeutic or prophylactic regulation of an immune  
CC response in animals (particularly cats, dogs, horses and humans).  
CC They may be used to treat autoimmune or infectious diseases including  
CC allergies, tumours, inflammation and graft rejection, and to increase  
CC the response from a co-administered antigen. The nucleotide sequences  
CC can also be used for the recombinant production of a protein, while  
CC nucleotide fragments are useful as probes, as amplification primers and  
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
CC The proteins may be used to raise antibodies and to screen for  
CC modulators of activity, while the antibodies may be used in detection,

CC

XX and in drug targeting.

SQ Sequence 272 BP; 64 A; 91 C; 69 G; 48 T; 0 other;

Query Match 72.7%; Score 240; DB 21; Length 272;  
Best Local Similarity 98.8%; Pred. No. 5.7e-62;  
Matches 253; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

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Qy 195 gagctgcgcagtagatcccgcggtgcaggttgacgtcctcaatgagctccttgagggttggg 254  
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Qy 255 gggatgcctgattctggtgatgttgaccagctcctcaatgagctccttgagggttggg 314  
Db 92 GGGATGCCCTGATTCTGGTGATGTTGACCAGTCTCTCAATGAGCTCCTTGAGGGTTGGGG 33

Qy 315 agggagtcacagggct 330

Db 32 AGGAGTCACAGGGCT 17

RESULT 14  
255554/c

ID 255554 standard; cDNA; 278 BP.

XX AC 255554;

XX 14-MAR-2000 (first entry)

DE Canine interleukin-13 (IL-13) cDNA probe.

KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;  
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.

OS Canis familiaris.

PN WO9961618-A2.

XX 02-DEC-1999.

XX 28-MAY-1999; 99WO-US11942.

XX 29-MAY-1998; 98US-0087306.

XX (HESK-) HESKA CORP.

PI Sim G, Yang S, Dreitz MJ, Wonderling RS;

XX WPI; 2000-072623/06.

PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
PT useful for treating or preventing e.g. tumors or autoimmune disease

PS Claim 1i; Page 229; 264pp; English.

CC Sequences 255552-255560 and 255561-255566 represent cDNA  
CC sequences encoding canine interleukin-13 (IL-13) clones 80  
CC and 78 respectively. The invention relates to canine

CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or  
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline  
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage  
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these  
CC immunoregulatory proteins. The proteins, their associated  
CC nucleic acids, specific antibodies and inhibitors may be used as







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OM nucleic - nucleic search, using sw model

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SUMMARIES

Result No.	Score	Match %	Length	DB ID	Description
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C 5	185.8	56.3	336	1	US-08-371-121-2
C 6	185.8	56.3	1297	1	US-08-371-121-15
C 7	184.2	55.8	384	1	US-08-371-121-17
C 8	182.6	55.3	425	1	US-08-594-469-4
C 9	182.6	55.3	425	2	US-08-906-957-4
C 10	182.6	55.3	4410	1	US-08-594-469-1
C 11	182.6	55.3	4410	2	US-08-906-957-1
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C 13	151.4	45.9	1212	1	US-08-012-543-3
C 14	151.4	45.9	1212	5	PCT-US93-07645A-3
C 15	151.4	45.9	1212	5	PCT-US93-07645-3
C 16	33.4	10.1	1322	4	US-09-128-450-27
C 17	32.4	9.8	720	4	US-09-094-359-3
C 18	32.4	9.8	720	4	US-09-094-359-7
C 19	32.4	9.8	720	4	US-09-172-063-11
C 20	32.4	9.8	720	4	US-09-172-063-13
C 21	32.4	9.8	762	1	US-08-532-390-40
C 22	32.4	9.8	762	4	US-08-717-294-40
C 23	32.4	9.8	768	4	US-09-094-359-11
C 24	32.4	9.8	850	4	US-09-062-102-2
C 25	32.4	9.8	972	4	US-09-172-063-27
C 26	32.4	9.8	972	4	US-09-172-063-29
C 27	32.4	9.8	1095	4	US-09-085-305-5

C 28	32.4	9.8	1929	2	US-08-818-253-1	Sequence 1, Appli
C 29	32.4	9.8	1929	2	US-08-818-253-5	Sequence 5, Appli
C 30	32.4	9.8	1929	4	US-08-818-252-1	Sequence 1, Appli
C 31	32.4	9.8	1929	4	US-08-818-252-5	Sequence 5, Appli
C 32	32.4	9.8	1959	2	US-08-818-253-3	Sequence 3, Appli
C 33	32.4	9.8	1959	4	US-08-818-252-3	Sequence 3, Appli
C 34	32.4	9.8	1971	2	US-08-818-252-7	Sequence 7, Appli
C 35	32.4	9.8	1971	4	US-08-818-252-7	Sequence 7, Appli
C 36	32.4	9.8	7938	4	US-09-331-581-14	Sequence 14, Appl
C 37	32	9.7	1926	2	US-08-978-182-2	Sequence 2, Appli
C 38	32	9.7	1926	2	US-09-205-681-2	Sequence 2, Appli
C 39	31.8	9.6	35081	2	US-08-752-760A-1	Sequence 1, Appli
C 40	31.4	9.5	398	4	US-09-060-756-630	Sequence 630, App
C 41	31.2	9.5	720	4	US-09-094-359-5	Sequence 5, Appli
C 42	31.2	9.5	720	4	US-09-094-359-9	Sequence 9, Appli
C 43	31.2	9.5	720	4	US-09-172-063-12	Sequence 12, Appl
C 44	31.2	9.5	720	4	US-09-172-063-14	Sequence 14, Appl
C 45	31.2	9.5	720	4	US-09-172-063-17	Sequence 17, Appl

ALIGNMENTS

RESULT 1

US-08-371-121-24/c  
; Sequence 24, Application US/08371121  
; Patent No. 5652123

GENERAL INFORMATION:

; APPLICANT: CAPUT, Daniel  
; APPLICANT: FERRARA, Pascual  
; APPLICANT: GUILLEMOT, Jean-Claude  
; APPLICANT: LEPLATOIS, Pascal  
; APPLICANT: MINTY, Adrian  
; APPLICANT: KAGHAD, Mourad  
; APPLICANT: LABIT-LE BOUTEILLER, Christine  
; APPLICANT: MAGAZIN, Marilyn

; TITLE OF INVENTION: Protein having a cytokine type

; TITLE OF INVENTION: activity, recombinant DNA coding for this protein,  
; TITLE OF INVENTION: transformed cells and microorganisms.

; NUMBER OF SEQUENCES: 27

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: FOLEY & LARDNER  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington, D.C.

; COUNTRY: USA

; ZIP: 20007-5109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/371,121

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/938,161

; FILING DATE: 30-NOV-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/FR92/00280

; FILING DATE: 27-MAR-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: FR 91 00137

; FILING DATE: 08-JAN-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: FR 91 03904

; FILING DATE: 29-MAR-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: SAXE, Bernhard D.

; REGISTRATION NUMBER: 28,665

; REFERENCE/DOCKET NUMBER: 16781/383

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 672-5300

```

; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 336 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-371-121-24

Query Match          56.8%; Score 187.4; DB 1; Length 336;
Best Local Similarity 76.9%; Pred. No. 2.1e-50;
Matches 256; Conservative 0; Mismatches 71; Indels 6; Gaps 2;

QY 3 tgaattccatggcgataaaactcccttacataggtgagcaggtttttcaccaactgga 62
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 334 TGAACCGTCCCTCGCGAAAAAGTTTCTTTAAATGTAAGAGCAGGTCCTTTACAAACTGGG 275

QY 63 tcaattcaatttgggtctcggtcggttcactggaaa---tccctgccgcgggctttt 119
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 274 CCACCTCGATTGTGGTGCTCGGACATGCAAGCTGGAAACTGCCAGCTGAGACCTTGT 215

QY 120 gagagcacagtgcctttcagcatcctctgggtccttttgatggcgctgcagtcggagacat 179
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 214 GCGGGCAGAAATCCGCTCAGCATCCTCTGGGTCTTCTCGATGGCACTGCAGCCTGACACGT 155

QY 180 tgatcagagattctagagctgcgagtagatcccgcggtgcaggttgacgctccacacca 239
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 154 TGATCAGGGATTCCAGGGCTGCACAGTACATGCCAGCTGTTCAGGTGATGCTCCATACCA 95

QY 240 tgctgccgttgacagagggatgc---ctgattctgggtgatgttgaccagctcctcaatga 296
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 94 TGCTGCCATTGCAGAGCGGAGCCTTCTGGTTCTGGGTGATGTGACCAGCTCCTCAATGA 35

QY 297 gctccttgagggttgaggagggaggtcacagggc 329
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 34 GCTCCCTGAGGGCTGTAGAGGGAGGCACACAGGCG 2

RESULT 2
US-08-012-543-1/c
; Sequence 1, Application US/08012543
; Patent No. 5596072
; GENERAL INFORMATION:
; APPLICANT: Culpepper, Janice
; APPLICANT: McKenzie, Andrew
; APPLICANT: Dang, Warren
; APPLICANT: de Waal Malefyt, Rene
; APPLICANT: Heath, Andrew
; APPLICANT: Aversa, Gregorio
; APPLICANT: Banchereau, Jacques
; APPLICANT: de Vries, Jan
; APPLICANT: Zurawski, Gerard
; TITLE OF INVENTION: Human Interleukin-13
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/012,543
; FILING DATE: 01-FEB-1993
;
;
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; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/933,416
; FILING DATE: 21-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0302K1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-852-9196
; TELEFAX: 415-496-1200
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1290 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 45..443
US-08-012-543-1

Query Match          56.8%; Score 187.4; DB 1; Length 1290;
Best Local Similarity 76.9%; Pred. No. 3.5e-50;
Matches 256; Conservative 0; Mismatches 71; Indels 6; Gaps 2;

QY 3 tgaatttccatggcgataaaactcccttacataggtgagcaggtttttcaccaactgga 62
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 438 TGAACCGTCCCTCGCGAAAAAGTTTCTTTAAATGTAAGAGCAGGTCCTTTACAAACTGGG 379

QY 63 tcaattcaatttgggtctcggtcggttcactggaaa---tccctgccgcgggctttt 119
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 378 CCACCTCGATTGTGGTGCTCGGACATGCAAGCTGGAAACTGCCAGCTGAGACCTTGT 319

QY 120 gagagcacagtgcctttcagcatcctctgggtccttttgatggcgctgcagtcggagacat 179
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 318 GCGGGCAGAAATCCGCTCAGCATCCTCTGGGTCTTCTCGATGGCACTGCAGCCTGACACGT 259

QY 180 tgatcagagattctagagctgcgagtagatcccgcggtgcaggttgacgctccacacca 239
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 258 TGATCAGGGATTCCAGGGCTGCACAGTACATGCCAGCTGTTCAGGTGATGCTCCATACCA 199

QY 240 tgctgccgttgacagagggatgc---ctgattctgggtgatgttgaccagctcctcaatga 296
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 198 TGCTGCCATTGCAGAGCGGAGCCTTCTGGTTCTGGGTGATGTGACCAGCTCCTCAATGA 139

QY 297 gctccttgagggttgaggagggaggtcacagggc 329
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 138 GCTCCCTGAGGGCTGTAGAGGGAGGCACACAGGCG 106

RESULT 3
PCT-US93-07645A-1/c
; Sequence 1, Application PC/TUS9307645A
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Human Interleukin-13
; NUMBER OF SEQUENCES: 6
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.5
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07645A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/012543
; FILING DATE: 01-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/010977
;
;
```





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; APPLICATION NUMBER: FR 91 03904
; FILING DATE: 29-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 16781/383
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 336 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
;
US-08-371-121-2

Query Match 56.3%; Score 185.8; DB 1; Length 336;
Best Local Similarity 76.6%; Pred. No. 6.7e-50;
Matches 255; Conservative 0; Mismatches 72; Indels 6; Gaps 2;

QY 3 tgaatttccatggcgataaaactcccttacataggtgagcagggtttttcaccactgga 62
Db 334 TGAACCGTCCCTCGCGAAAAAGTTCTTTAAATGTAAGAGCAGGTCCTTTACAAACTGGG 275

QY 63 tcacttcaatttgggtgtctcggttcactgga---tcctgcccgggctttt 119
Db 274 CCACCTCGATTTGGTGTCTCGGACATGCAAGCTGGAAACTGCCAGCTGAGACCTTGT 215

QY 120 gagagcacagtgtcttcagcatcctctgggtccttggatggcgctgcagtcggagacat 179
Db 214 GCGGGCAGAAATCCGCTCAGCATCCTCTGGGTCTTCTCGATGGCACTGCAGCCTGACAGT 155

QY 180 tgatcagagattctagagctgcgagtagatcccggtgcaggttcaggtgacgtccacacca 239
Db 154 TGATCAGGGATTCCAGGGCTGCACAGTACATGTTCAGCTGTTCAGGTTGATGCTCCATACCA 95

QY 240 tgctgccgttgacagaggatgc---ctgattcgtgggtgatgtgaccagctcctcaatga 296
Db 94 TGCTGCCATTGCAGAGCGGAGCCCTTCTGGTTCTGGGTGATGTTGACCAGCTCCTCAATGA 35

QY 297 gctccttgagggttggggaggaggtcacagggc 329
Db 34 GCTCCCTGAGGGCTGTAGAGGGAGGCACAGGGC 2

RESULT 6
US-08-371-121-15/c
; Sequence 15, Application US/08371121
; Patent No. 5652123
; GENERAL INFORMATION:
; APPLICANT: CAPUT, Daniel
; APPLICANT: FERRARA, Pascual
; APPLICANT: GUILLEMOT, Jean-Claude
; APPLICANT: LEPLATOIS, Pascal
; APPLICANT: MINTY, Adrian
; APPLICANT: KAGHAD, Mourad
; APPLICANT: LABIT-LE BOUTEILLER, Christine
; APPLICANT: MAGAZIN, Marilyn
; TITLE OF INVENTION: Protein having a cytokine type
; TITLE OF INVENTION: activity, recombinant DNA coding for this protein,
; TITLE OF INVENTION: transformed cells and microorganisms.
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
;
; COMPUTER READABLE FORM:

```

```

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/371,121
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/938,161
; FILING DATE: 30-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR92/00280
; FILING DATE: 27-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91 00137
; FILING DATE: 08-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91 03904
; FILING DATE: 29-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 16781/383
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1297 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 15..452
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 117..452
;
US-08-371-121-15

Query Match 56.3%; Score 185.8; DB 1; Length 1297;
Best Local Similarity 76.6%; Pred. No. 1.1e-49;
Matches 255; Conservative 0; Mismatches 72; Indels 6; Gaps 2;

QY 3 tgaatttccatggcgataaaactcccttacataggtgagcagggtttttcaccactgga 62
Db 450 TGAACCGTCCCTCGCGAAAAAGTTCTTTAAATGTAAGAGCAGGTCCTTTACAAACTGGG 391

QY 63 tcacttcaatttgggtgtctcggttcactgga---tcctgcccgggctttt 119
Db 390 CCACCTCGATTTGGTGTCTCGGACATGCAAGCTGGAAACTGCCAGCTGAGACCTTGT 331

QY 120 gagagcacagtgtcttcagcatcctctgggtccttggatggcgctgcagtcggagacat 179
Db 330 GCGGGCAGAAATCCGCTCAGCATCCTCTGGGTCTTCTCGATGGCACTGCAGCCTGACAGT 271

QY 180 tgatcagagattctagagctgcgagtagatcccggtgcaggttcaggtgacgtccacacca 239
Db 270 TGATCAGGGATTCCAGGGCTGCACAGTACATGTTCAGCTGTTCAGGTTGATGCTCCATACCA 211

QY 240 tgctgccgttgacagaggatgc---ctgattcgtgggtgatgtgaccagctcctcaatga 296
Db 210 TGCTGCCATTGCAGAGCGGAGCCCTTCTGGTTCTGGGTGATGTTGACCAGCTCCTCAATGA 151

QY 297 gctccttgagggttggggaggaggtcacagggc 329
Db 150 GCTCCCTGAGGGCTGTAGAGGGAGGCACAGGGC 118

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RESULT 7
US-08-371-121-17/c
; Sequence 17, Application US/08371121
; Patent No. 5652123
; GENERAL INFORMATION:
; APPLICANT: CAPUT, Daniel
; APPLICANT: FERRARA, Pascual
; APPLICANT: GUILLEMOT, Jean-Claude
; APPLICANT: LEPLATOIS, Pascal
; APPLICANT: MINTY, Adrian
; APPLICANT: KAGHAD, Mourad
; APPLICANT: LABIT-LE BOUTEILLER, Christine
; APPLICANT: MAGAZIN, Marilyn
; TITLE OF INVENTION: protein having a cytokine type
; TITLE OF INVENTION: activity, recombinant DNA coding for this protein,
; TITLE OF INVENTION: transformed cells and microorganisms.
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/371,121
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/938,161
; FILING DATE: 30-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR92/00280
; FILING DATE: 27-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91 00137
; FILING DATE: 08-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91 03904
; FILING DATE: 29-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 16781/383
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 384 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-371-121-17

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Query Match	55.8%;	Score 184.2;	DB 1;	Length 384;
Best Local Similarity	76.3%;	Pred. No. 2.3e-49;		
Matches 254; Conservative	0;	Mismatches 73;	Indels 6;	Gaps 2;

Qy	3	tgaatattccatggcgataaaactccccttacatagggtgagcaggttttttcaccaactgga	62
Db	355	TGAACCGTCCCTCGGAAAAAGTTCTTAATGTAAAGCAGGTCCTTACAACACTGGG	296
QY	63	tcaattcaatttgggtgtctcggtgcgttcactggaaa---tccctgccgcgggctttt	119
Db	295	CCACCTCGATTGTGGTGCTCGGACATGCAAGCTGGAAAAC TGCCAGCTGAGACCTTGT	236

QY	120	gagagcacagtgtctttcagcatcctgtgggtcccttggatggcgctgcagtcggagacat	179
Db	235	GCGGCAGAATCCGCTCAGCATCCTCTGGGTCTTCTCGATGGCACTGCAGCCTGACACGT	176
QY	180	tgatcagagattctagagctgcgcagttacatgccggcggtcaggttgcagctccacacca	239
Db	175	TGATCAGGGATTCCAGGGCTGCACAGTACATGTTCAGCTGTCAGGTTGATGCTCCATACCA	116
QY	240	tgtgcccgtttgcagaggggatgc---ctgattcttggtgatgttgaccagctcctcaatga	296
Db	115	TGCTGCCATTGCAGAGCGGAGCCCTCTGGTTCTGGGTGATGTTGACCAGGCTCCTCAATGA	56
QY	297	gctccttgagggttgggagggttcacagggc	329
Db	55	GCCTCCTGAGGGCCGTAGAGGGAGGCACAGGGC	23

RESULT 8  
US-08-594-469-4/c  
; Sequence 4, Application US/08594469  
; Patent No. 5700665  
; GENERAL INFORMATION:  
; APPLICANT: LEGOUX, Richard  
; APPLICANT: MALDONADO, Paul  
; APPLICANT: SALOME, Marc  
; TITLE OF INVENTION: Method for the extraction of  
; TITLE OF INVENTION: periplasmic proteins of prokaryotic microorganisms in the  
; TITLE OF INVENTION: presence of arginine  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Bacon & Thomas  
; STREET: 625 Slaters Lane - Fourth Floor  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: USA  
; ZIP: 22314  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/594,469  
; FILING DATE:

FILED DATE: 435  
PRIOR APPLICATION DATA: FR 95 01083  
APPLICATION NUMBER: 31-JAN-1995  
FILING DATE: 26,382  
ATTORNEY/AGENT INFORMATION: REF/LEGOUX  
NAME: FICHTER, Richard E  
REGISTRATION NUMBER: 703) 683-0500  
REFERENCE/DOCKET NUMBER: 703) 683-1080  
TELECOMMUNICATION INFORMATION: TELEPHONE: 703) 683-1080  
TELEFAX: 703) 683-1080  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 425 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-594-469-4

Query Match	55.3%	Score 182.6;	DB 1;	Length 425;
Best Local Similarity	76.0%	Pred. NO. 7.5e-49;		
Matches 253; Conservative	0;	Mismatches 74;	Indels 6;	Gaps 2;

Qy 3 tgaatttccatg gcgataaaactccccttacataggtg agcagggtttttcaccaactgga 62  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 397 TGAACCGTCCCTCGCGAAAAAGTTCTTTAAATGTAAGAGCAGGTCTTTACAAACTGGG 338





US-08-594-469-1

Query Match 55.3%; Score 182.6; DB 1; Length 4410;  
Best Local Similarity 76.0%; Pred. No. 1.8e-48;  
Matches 253; Conservative 0; Mismatches 74; Indels 6; Gaps 2;

QY 3 tgaattccatggtggtctgcgataaaactcccccttacataggtgagcagggtttttccaccaactgga 62  
Db 734 TGAACCGTCCCTCGCGAAAAAGTTTCTTTAAATGTAAGAGCAGGTCCTTTTACAAACTGGG 675  
QY 63 tcacttcaatttgggtctgcggtgcgttcactggaaa---tccctgcccgcgggctttt 119  
Db 674 CCACCTCGATTGTTGGTGTCTCGGACATGCAAGCTGGAAAACTGCCAGCTGAGACCTTGT 615  
QY 120 gagagcacagtgttttcagcatcctctggttcctttggatggcgctgcagtcggagacat 179  
Db 614 GCGGGCAGAAATCCGCTCAGCATCCTCTGGGTCTTCTCGATGGCAGTGCAGCTGACACGT 555  
QY 180 tgatcacagattctagagctgcgcagtcacatgcccggcggttcaggttgacagctcctcaatga 239  
Db 554 TGATCAGGATTCAGGGCTGCACAGTACATGCCAGCTGTCAAGTTGATGCTCCATACCA 495  
QY 240 tgccttgaggttgggagggaggtcagggaggtcagggc 329  
Db 434 GCTCCCTGAGGGCAGTACTGGGAGGCACAGGSC 402

RESULT 11

US-08-906-957-1/c  
; Sequence 1, Application US/08906957  
; Patent No. 5856142  
; GENERAL INFORMATION:  
; APPLICANT: LEGOUX, Richard  
; APPLICANT: MALDONADO, Paul  
; APPLICANT: SALOME, Marc  
; TITLE OF INVENTION: Method for the extraction of  
; TITLE OF INVENTION: periplasmic proteins of prokaryotic microorganisms in the  
; TITLE OF INVENTION: presence of arginine  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Bacon & Thomas  
; STREET: 625 Slaters Lane - Fourth Floor  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: USA  
; ZIP: 22314  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/906,957  
; FILING DATE: 06-AUG-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/594,469  
; FILING DATE:  
; APPLICATION NUMBER: FR 95 01083  
; FILING DATE: 31-JAN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: FICHTER, Richard E  
; REGISTRATION NUMBER: 26,382  
; REFERENCE/DOCKET NUMBER: REF/LEGOUX  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 683-0500  
; TELEFAX: (703) 683-1080  
; INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

; LENGTH: 4410 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-906-957-1

Query Match 55.3%; Score 182.6; DB 2; Length 4410;  
Best Local Similarity 76.0%; Pred. No. 1.8e-48;  
Matches 253; Conservative 0; Mismatches 74; Indels 6; Gaps 2;

QY 3 tgaattccatggtggtctgcgataaaactcccccttacataggtgagcagggtttttccaccaactgga 62  
Db 734 TGAACCGTCCCTCGCGAAAAAGTTTCTTTAAATGTAAGAGCAGGTCCTTTTACAAACTGGG 675  
QY 63 tcacttcaatttgggtctgcggtgcgttcactggaaa---tccctgcccgcgggctttt 119  
Db 674 CCACCTCGATTGTTGGTGTCTCGGACATGCAAGCTGGAAAACTGCCAGCTGAGACCTTGT 615  
QY 120 gagagcacagtgttttcagcatcctctggttcctttggatggcgctgcagtcggagacat 179  
Db 614 GCGGGCAGAAATCCGCTCAGCATCCTCTGGGTCTTCTCGATGGCAGTGCAGCTGACACGT 555  
QY 180 tgatcacagattctagagctgcgcagtcacatgcccggcggttcaggttgacagctcctcaatga 239  
Db 554 TGATCAGGATTCAGGGCTGCACAGTACATGCCAGCTGTCAAGTTGATGCTCCATACCA 495  
QY 240 tgccttgaggttgggagggaggtcagggaggtcagggc 329  
Db 494 TGCTGCCATTGCAGAGCGGAGCCTTCTGGTCTGGGTGATGTTGACCAGCTCCTCAATGA 435  
QY 297 gctccttgaggttgggagggaggtcagggc 329  
Db 434 GCTCCCTGAGGGCAGTACTGGGAGGCACAGGSC 402

RESULT 12

US-08-371-121-26/c  
; Sequence 26, Application US/08371121  
; Patent No. 5652123  
; GENERAL INFORMATION:  
; APPLICANT: CAPUT, Daniel  
; APPLICANT: FERRARA, Pascual  
; APPLICANT: GUILLEMOT, Jean-Claude  
; APPLICANT: LEPLATOIS, Pascal  
; APPLICANT: MINTY, Adrian  
; APPLICANT: KAGHAD, Mourad  
; APPLICANT: LABIT-LE BOUTEILLER, Christine  
; APPLICANT: MAGAZIN, Marilyn  
; TITLE OF INVENTION: Protein having a cytokine type  
; TITLE OF INVENTION: activity, recombinant DNA coding for this protein,  
; TITLE OF INVENTION: transformed cells and microorganisms.  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FOLEY & LARDNER  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington, D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/371,121  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/938,161  
; FILING DATE: 30-NOV-1992



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; TITLE OF INVENTION: Human Interleukin-13
; NUMBER OF SEQUENCES: 6
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.5
; SOFTWARE: Microsoft Word 5.1a
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; APPLICATION NUMBER: PCT/US93/07645A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/012543
; FILING DATE: 01-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/010977
; FILING DATE: 29-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/933416
; FILING DATE: 21-AUG-1992
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1212 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
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PCT-US93-07645A-3

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	Query Match	45.9%;	Score 151.4;	DB 5;	Length 1212;
	Best Local Similarity	68.8%;	Pred. NO. 8.5e-39;		
	Matches 225;	Conservative	0;	Mismatches 96;	Indels 6; Gaps 1;
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Qy	64	cacttcaattttgtgtctcggtcggttcactggaatccctgcccgggcttttgaga	123		
Db	402	TACTTCGATTTGGTATCGGGGAGG-----CTGGAGACCGTAGTGGGGGCCCTTCCGGTT	349		
Qy	124	gcacagtgctttcagcatcctctgggtccttttggatggcgctgcagtcggagacattgat	183		
Db	348	ACAGAGGCCATGCAATATCCTCTGGGTCTGTAGATGGCATTGCAATTGGAGATGTTGGT	289		
Qy	184	cagagattctagagctgcgcagttacatgccggcggttcagggttgacgctccacaccatgct	243		
Db	288	CAGGGAATCCAGGGCTACACAGAACCCGCCAGCGGCCAGGTCCACACTCCATACCATGCT	229		
Qy	244	gccgtttgcagagggtgcctgtattcttgggtgatgttgaccagctcctcaatgagctcctt	303		
Db	228	GCCGTTGCACAGGGGAGTCTGGTCTTGTGTGATGTTGCTCAGTCTCTCAATAAGCTCCTT	169		
Qy	304	gagggttggggaggaggtcacagggct	330		
Db	168	AAGGGTTCAGAGGGGAGACACAGATCT	142		

Search completed: May 13, 2001, 14:21:51  
Job time: 17862 sec

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RESULT 15
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; Sequence 3, Application PC/TUS9307645
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; GENERAL INFORMATION:
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; APPLICANT:
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; TITLE OF INVENTION: Human Interleukin-13
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; NUMBER OF SEQUENCES: 6
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; COMPUTER READABLE FORM:
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; MEDIUM TYPE: Floppy disk
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; COMPUTER: Apple Macintosh
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; OPERATING SYSTEM: Macintosh 6.0.5
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; SOFTWARE: Microsoft Word 5.1a
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; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: PCT/US93/07645
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; FILING DATE: 19930818
;
; PRIOR APPLICATION DATA:
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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 13, 2001, 11:40:59 ; Search time 5997.24 Seconds  
(without alignments)  
480.707 Million cell updates/sec

Title: US-09-451-527-106  
Perfect score: 330  
Sequence: 1 tctgaatttccatggcgat.....ggggaggagtcacagggt 330

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 9623517 seqs, 4368049070 residues  
Total number of hits satisfying chosen parameters: 19247034

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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C 2	39	11.8	521	215	AZ027551	AZ027551 RPCI-23-3
C 3	36.4	11.0	277	137	BE593226	BE593226 WSL_99_B0
C 4	36.4	11.0	537	166	BE357229	BE357229 DGI_147_B
C 5	35.2	10.7	757	174	BG260311	BG260311 602371427
C 6	34.4	10.4	462	143	BF039993	BF039993 BP250023B
C 7	34.4	10.4	507	138	BE705147	BE705147 SC02_08f0
C 8	34.2	10.4	535	161	BE032541	BE032541 131940 MA
C 9	34.2	10.4	546	161	BE032543	BE032543 131942 MA
C 10	34.2	10.4	570	24	AI746678	AI746678 ul06b05.y
C 11	34.2	10.4	965	217	AZ201624	AZ201624 SP_0053_A
C 12	34.2	10.4	2275	14	AF034173	AF034173 AF034173
C 13	34	10.3	370	166	BE363650	BE363650 WSL_64_G1
C 14	34	10.3	562	166	BE361027	BE361027 DGI_69_A0
C 15	33.8	10.2	341	163	BE127683	BE127683 DEPA1432
C 16	33.8	10.2	498	150	BF606532	BF606532 273595 MA
C 17	33.6	10.2	577	166	BE402120	BE402120 CSB004F06
C 18	33.6	10.2	714	166	BE414190	BE414190 SCU007.CO

C 19	33.6	10.2	727	164	BE216356	BE216356 HV_CEB001
C 20	33.4	10.1	177	103	AI909438	AI909438 IL-BT208-
C 21	33.4	10.1	544	13	AA880435	AA880435 vw89f07.r
C 22	33.4	10.1	700	113	AW318852	AW318852 un08d12.y
C 23	33.4	10.1	712	115	AW475303	AW475303 un64b04.y
C 24	33.4	10.1	1056	144	BF143984	BF143984 601791238
C 25	33.2	10.1	462	164	BE228410	BE228410 98AS2556
C 26	33.2	10.1	616	15	AI062250	AI062250 GH01393.5
C 27	33.2	10.1	621	175	C97983	C97983 C97983 Rice
C 28	33.2	10.1	683	15	AI064071	AI064071 GH04331.5
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C 30	33.2	10.1	1100	140	BE871785	BE871785 601448347
C 31	33	10.0	600	146	BF312933	BF312933 601896391
C 32	33	10.0	779	231	CNS03LV7	AL249964 Tetraodon
C 33	32.6	9.9	285	6	AA360834	AA360834 EST70082
C 34	32.6	9.9	335	6	AA361196	AA361196 EST70439
C 35	32.6	9.9	452	158	W80370	W80370 zh50f02.s1
C 36	32.6	9.9	468	107	AU129052	AU129052 AU129052
C 37	32.6	9.9	484	121	AW862698	AW862698 945006D06
C 38	32.6	9.9	531	121	AW927591	AW927591 945006D06
C 39	32.6	9.9	662	107	AU162975	AU162975 AU162975
C 40	32.6	9.9	805	15	AI068702	AI068702 mgae0003d
C 41	32.6	9.9	891	151	BF685554	BF685554 602140603
C 42	32.4	9.8	448	166	BE380347	BE380347 601270411
C 43	32.4	9.8	546	120	AW786287	AW786287 119229 MA
C 44	32.4	9.8	576	141	BE907816	BE907816 601501924
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  RPCI-23-123P23.TV RPCI-23 Mus musculus genomic clone RPCI-23-123P23
  , DNA sequence.
ACCESSION
  AZ261971
VERSION
  AZ261971.1 GI:9470858
KEYWORDS
  GSS.
SOURCE
  house mouse.
ORGANISM
  Mus musculus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
  1 (bases 1 to 477)
  Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S., Akinret
  ,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P.
  and Fraser,C.M.
  Mouse BAC End Sequences from Library RPCI-23
  Unpublished (1999)
  Other_GSSs: RPCI-23-123P23.TJ
  Contact: Shaying Zhao
  Department of Eukaryotic Genomics
  The Institute for Genomic Research
  9712 Medical Center Dr., Rockville, MD 20850, USA
  Tel: 301 838 0200
  Fax: 301 838 0208
  Email: szhao@tigr.org
  Clones are derived from the mouse BAC library RPCI-23. For BAC
  library availability, please contact Pieter de Jong
  (pieter@dejong.med.buffalo.edu). Clones may be purchased from
  BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
  or from Resea ch Genetics (info@resgen.com). BAC end page:
  http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
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FEATURES
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/sex="Female"
/lab_host="DH10B"
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
EcoRI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies)."
BASE COUNT 129 a 121 c 113 g 114 t
ORIGIN
Query Match 11.8%; Score 39; DB 218; Length 477;
Best Local Similarity 52.1%; Pred. No. 0.66;
Matches 87; Conservative 0; Mismatches 80; Indels 0; Gaps 0;
QY 70 aattttgtgtctcggtcggttcactggaatccctgcggcgttttgagagcacag 129
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QY 130 tgccttcagcatcctctggttcctttggatggcgtcgcagtcggagacattgatcagaga 189
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Db 379 TGTTCTCAGTTGTCCCACTGTCTATCCCACTACGCTCCAGCTGCCATATTTATTTCAGAAAT 320
QY 190 ttctagagctgcgcagtcacatgcgcggcgtcaggttgacgtccaca 236
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Db 319 GATCCAATCACCTCAGTCCAGTCTGACCATGTGACTGAAGCTAGCCA 273
RESULT 2
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DEFINITION
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ACCESSION
  AZ027551
VERSION
  AZ027551.1 GI:7102935
KEYWORDS
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SOURCE
  house mouse.
ORGANISM
  Mus musculus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
  1 (bases 1 to 521)
  Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S., Akinret
  ,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P.
  and Fraser,C.M.
  Mouse BAC End Sequences from Library RPCI-23
  Unpublished (1999)
  Contact: Shaying Zhao
  Department of Eukaryotic Genomics
  The Institute for Genomic Research
  9712 Medical Center Dr., Rockville, MD 20850, USA
  Tel: 301 838 0200
  Fax: 301 838 0208
  Email: szhao@tigr.org
  Clones are derived from the mouse BAC library RPCI-23. For BAC
  library availability, please contact Pieter de Jong
  (pieter@dejong.med.buffalo.edu). Clones may be purchased from
  BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
  or from Resea ch Genetics (info@resgen.com). BAC end page:
  http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
  Plate: 343 row: M column: 24
  Seq primer: SP6
  Class: BAC ends.
  Location/Qualifiers
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      /db_xref="taxon:10090"
      /clone="RPCI-23-343M24"
      /clone_lib="RPCI-23"
      /sex="Female"
FEATURES
  source
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Db 330 GTTGACCCACTCGCGGCGTGGTGCAGAGGAACCGACCACCGCGCGGATGTCGCGGG 271

QY 286 ctccctcaatgagctccttgagg 307

Db 270 CTCCCCGAGCCTCTCCATGGGG 249

RESULT 5

BG260311 757 bp mRNA EST 13-FEB-2001

LOCUS 602371427F1 NIH\_MGC\_93 Homo sapiens cDNA clone IMAGE:4479367 5', mRNA sequence.

ACCESSION BG260311

VERSION BG260311.1 GI:12770127

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS 1 (bases 1 to 757)

TITLE NIH-MGC <http://mgc.nci.nih.gov/>.

JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert\_Strausberg@nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Plate: LLAM10311 row: f column: 08

High quality sequence stop: 736.

Location/Qualifiers

1. 757

source

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:4479367"

/clone\_lib="NIH\_MGC\_93"

/tissue\_type="transitional cell papilloma, cell line"

/lab\_host="DH10B (phage-resistant)"

/note="Organ: bladder; Vector: pCMV-SPORT6; Site\_1: NotI; Site\_2: Sali; Cloned unidirectionally; oligo-dT primed. Average insert size 1.7 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH\_MGC Library."

BASE COUNT 186 a 200 c 201 g 170 t

ORIGIN

Query Match 10.7%; Score 35.2; DB 174; Length 757;

Best Local Similarity 49.0%; Pred. No. 9.5;

Matches 94; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

QY 3 tgaatttcctgcatgataaaactcccttaccataggtgagcaggtttttccaccaactgga 62

Db 497 TCAAGTTCTTGGCCGCCAGAGATCCACATCTCAAGAAGTGGGGCTTCAACCAAGTTCA 556

QY 63 tcacttcaatttttggtgtctcggtcggttcaactggaaatccctgcgcgggcttttgag 122

Db 557 ATGCTGATGAATTTGAAGACATGGTGGCTGAAAGCGGCTCATCCCAGATGGCTTGTGGG 616

QY 123 agcacagtgttttcagcatcctctggttcctttggatggtgcgtgcagtcggagacattga 182

Db 617 GTCAAAGTACATAACCCAGTGGTGGCCCTCTGGACAAAGTGGCGGCCCTTGGCACTCA 676

QY 183 tcagagattcta 194

Db 677 TGAGGGCTTCCA 688

RESULT 6

BF039993/c 462 bp mRNA EST 10-OCT-2000

LOCUS BP250023B10D12 Soares normalized bovine placenta Bos taurus cDNA clone BP250023B10D12 5', mRNA sequence.

DEFINITION

ACCESSION BF039993

VERSION BF039993.1 GI:10757048

KEYWORDS EST.

SOURCE COW.

ORGANISM Bos taurus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.

AUTHORS 1 (bases 1 to 462)

Lewin,H.A., Soares,M.B., Rebeiz,M., Pardinas,J., Liu,L. and Larson ,J.H.

TITLE Bovine ESTs

JOURNAL Unpublished (2000)

COMMENT Contact: Lewin, H. A.

W. M. Keck Center for Comparative and Functional Genomics

University of Illinois at Urbana-Champaign

340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL 61801, USA

Tel: 217 333 5998

Fax: 217 244 5617

Email: h-lewin@uiuc.edu

Funding for cattle EST sequencing was provided by the USDA National Research Initiative, Animal Genome Resource Grant AG 99-3205-8534 to H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED from Washington University Genome Center. Vector Trimmi g: Cross\_match from Washington University Genome Center PHRAP suite. This sequence is vector free and at least 200 bp in length.

PCR Primers

FORWARD: TAATACGACTCACTATAGGG

BACKWARD: ATTAACCCCTCACTAAAG

Insert Length: 462 Std Error: 0.00

Plate: BP250023B10 row: D column: 12

Seq primer: AGCGGATAACAAATTTCACACAGGA

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Location/Qualifiers

1. 462

source

/organism="Bos taurus"

/db\_xref="taxon:9913"

/clone="BP250023B10D12"

/clone\_lib="Soares normalized bovine placenta"

/sex="female"

/lab\_host="DH10B"

/note="Organ: placenta; Vector: pT7T3Pac; Site\_1: EcoRI; Site\_2: NotI; The cDNA library was contributed by the Soares laboratory and it was constructed and normalized as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806."

BASE COUNT 110 a 153 c 123 g 73 t

ORIGIN

Query Match 10.4%; Score 34.4; DB 143; Length 462;

Best Local Similarity 49.2%; Pred. No. 14;

Matches 89; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

QY 134 ttccagcatcctctggttcctttggatggcgctgcagtcggagacattgatcagattct 193

Db 285 TTCTGCTTCAGCTTGGCCTTGTAGANCTCGCGGAAGCGCCCTTGCCCCACAGGGTGTCC 226

QY 194 agagctgcgcatcatgccggcggtcaggttgacgtccacaccatgctgccgttgag 253

Db 225 AGCTCGATGGGCAGCAGCTCCCGTGTGTGTTGATGTTGTTGGCGCAGGTGGAGCTGATG 166

QY 254 agggatgcctgattcttggtgatgttgaccagctcctcaatgagctccttgaggggtggg 313

Db 165 TCGGAGCGGTCGTCCTCCAGGATGATGGCCAGGTGCTCACTGAACCTCATCATCTTGGC 106



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Db 330 GTTACCCACTCGCGCGCGTTCGGTGCAGAGGACCCGACCACCGCGCGATGTCGCGGG 271
QY 286 ctctcctcaatgagctccttgagg 307
Db 270 CTCCCCGAGCCTCTCCATGGG 249

RESULT 5
BG260311 757 bp mRNA EST 13-FEB-2001
LOCUS 602371427F1 NIH_MGC_93 Homo sapiens cDNA clone IMAGE:4479367 5',
DEFINITION mRNA sequence.
ACCESSION BG260311
VERSION BG260311.1 GI:12770127
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 757)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10311 row: f column: 08
High quality sequence stop: 736.
Location/Qualifiers
1. .757
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4479367"
/clone_lib="NIH_MGC_93"
/tissue_type="transitional cell papilloma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: bladder; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sali; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
BASE COUNT 186 a 200 c 201 g 170 t
ORIGIN
Query Match 10.7%; Score 35.2; DB 174; Length 757;
Best Local Similarity 49.0%; Pred. No. 9.5;
Matches 94; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

QY 3 tgaatttcctatggcgataaactcccccttacataggtgagcaggtttttccaccaactgga 62
Db 497 TCAAGTTCTCTGGCCGCCAGAGATCCACATCTCAAGAAGTGGGGCTTACCACAGTTCA 556

QY 63 tcaactcaatttttggtgtctcggctcggttcaactggaaatccctgcgcggcgttttgag 122
Db 557 ATGCTGATGAATTGAAGACATGGTGGCTGAAAGCGGCTCATCCAGATGGCTTGTGGG 616

QY 123 agcacagtgtttcagcatcctctgggtcctcttgatggcgctgcagtcggagacattga 182
Db 617 GTCAAAGTACATACCCAGTCGTTGGGCCCTCTCTGGACAAAGTGGCGGCCCTGGCACTCA 676

QY 183 tcagagattcta 194
Db 677 TGAGGGCTTCCA 688
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```

RESULT 6
BF039993/c 462 bp mRNA EST 10-OCT-2000
LOCUS BP250023B10D12 Soares normalized bovine placenta Bos taurus cDNA
DEFINITION clone BP250023B10D12 5', mRNA sequence.
ACCESSION BF039993
VERSION BF039993.1 GI:10757048
KEYWORDS EST.
SOURCE cow.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 462)
AUTHORS Lewin,H.A., Soares,M.B., Rebeiz,M., Pardinas,J., Liu,L. and Larson
,J.H.
TITLE Bovine ESTs
JOURNAL Unpublished (2000)
COMMENT Contact: Lewin, H. A.
W. M. Keck Center for Comparative and Functional Genomics
University of Illinois at Urbana-Champaign
340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL
61801, USA
Tel: 217 333 5998
Fax: 217 244 5617
Email: h-lewin@uiuc.edu
Funding for cattle EST sequencing was provided by the USDA National
Research Initiative, Animal Genome Resource Grant AG 99-3205-8534
to H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED
from Washington University Genome Center. Vector Trimmig:
Cross_match from Washington University Genome Center PHRAP suite.
This sequence is vector free and at least 200 bp in length.
PCR Primers
FORWARD: TAATACGACTCACTATAGG
BACKWARD: ATTAACCTCTACTAAAG
Insert Length: 462 Std Error: 0.00
Plate: BP250023B10 row: D column: 12
Seq primer: AGCGGATAACAATTTCACACAGGA
High quality sequence stop: 462.
Location/Qualifiers
1. .462
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone="BP250023B10D12"
/clone_lib="Soares normalized bovine placenta"
/sex="female"
/lab_host="DH10B"
/note="Organ: placenta; Vector: pF7T3Pac; Site_1: EcoRI;
Site_2: NotI; The cDNA library was contributed by the
Soares laboratory and it was constructed and normalized
as described by Bonaldo, M.F., Lennon, G. and Soares,
M.B. (1996), Genome Research 6(9): 791-806."
BASE COUNT 110 a 153 c 123 g 73 t 3 others
ORIGIN
Query Match 10.4%; Score 34.4; DB 143; Length 462;
Best Local Similarity 49.2%; Pred. No. 14;
Matches 89; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

QY 134 ttccagcatcctctgggtccctttggatggcgctgcagtcggagacattgatcagagattct 193
Db 285 TTCTGCTTCAGCTTGGCCTTGAGANCTCGGCGAAGCGCCCTTGCCCCACCGGTTGTCC 226

QY 194 agagctgcgcatcacatgccggcggtcaggttgacgtccacacacatgctgccgttgag 253
Db 225 AGCTCGATGGCGCAGCAGCTCCCGTGTGTGGTTGATGTTGTTGGCGCAGGTGGAGCTGATG 166

QY 254 agggatgcctgattcttggtgatgttgaccagctcctcaatgagctccttgaggggttggg 313
Db 165 TCGGAGCGGTCGTCCTCCAGGATGATGGCCAGGTGCTCACTGAACCTCCATCCATCGCTTGGCG 106
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JOURNAL  
COMMENT

---



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 13, 2001, 14:22:00 ; Search time 79.9 Seconds  
(without alignments)  
93.722 Million cell updates/sec

Title: US-09-451-527-92  
Perfect score: 663  
Sequence: 1 MALWLTVVIALTCIGGLASP.....QLVKNLLTYRGVYRHGNER 131

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 390729 seqs, 57163235 residues

Total number of hits satisfying chosen parameters: 390729

Minimum DB seq length: 0  
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_0401:\*  
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3: /cgnl\_8/gcgdata/geneseq/geneseqp/AA1982.DAT:\*  
4: /cgnl\_8/gcgdata/geneseq/geneseqp/AA1983.DAT:\*  
5: /cgnl\_8/gcgdata/geneseq/geneseqp/AA1984.DAT:\*  
6: /cgnl\_8/gcgdata/geneseq/geneseqp/AA1985.DAT:\*  
7: /cgnl\_8/gcgdata/geneseq/geneseqp/AA1986.DAT:\*  
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22: /cgnl\_8/gcgdata/geneseq/geneseqp/AA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	663	100.0	131	21 Y58221	Canine interleukin
2	647.5	97.7	130	21 Y58223	Canine interleukin
3	561	84.6	111	21 Y58222	Canine mature inte
4	545.5	82.3	110	21 Y58224	Canine mature inte
5	463.5	69.9	132	15 R48624	Sequence of human
6	456.5	68.9	146	13 R27348	Cytokine NC30. R
7	382.5	57.7	112	13 R27347	Protein with cytot
8	382.5	57.7	112	17 R92793	Human interleukin-
9	378.5	57.1	131	15 R48625	Sequence of mouse
10	375.5	56.6	112	13 R27346	Protein with cytot
11	367	55.4	111	17 R92794	Human interleukin-

12	295.5	44.6	111	17	R92795	Murine P600. Mus
13	81	12.2	20	13	R27345	Cytokine signal pe
14	81	12.2	34	13	R27344	Cytokine signal pe
15	78.5	11.8	665	21	B38312	Human secreted pro
16	78.5	11.8	667	21	B38311	Gene 38 human secr
17	78.5	11.8	1230	18	W15764	TIP120. Rattus ra
18	78.5	11.8	1230	21	B42180	Human ORFX ORF1944
19	78	11.8	21	20	Y49702	Human interleukin
20	77.5	11.7	482	19	W62025	Recombinantly prod
21	75.5	11.4	482	13	R20641	Placental-derived
22	75.5	11.4	482	17	R77531	Human platelet der
23	75.5	11.4	482	19	W62026	Recombinantly prod
24	72	10.9	356	21	Y81649	Streptococcus pneu
25	71.5	10.8	141	21	G35063	Arabidopsis thalia
26	71.5	10.8	382	21	Y84919	Amino acid sequenc
27	71	10.7	279	21	B44998	Human secreted pro
28	71	10.7	718	20	W84067	Drosophila mitofus
29	70	10.6	513	11	R04585	Aquaricine I. The
30	70	10.6	513	12	R13181	T.aquaticus Aquari
31	70	10.6	513	16	R67653	Aqualysin I. Ther
32	69.5	10.5	237	21	Y84892	A human proliferat
33	69.5	10.5	715	20	Y30341	Amino acid sequenc
34	69.5	10.5	2404	20	W30640	HIV-1-NC7 envelope
35	69	10.4	286	21	Y58998	Wheat sulfite redu
36	68	10.3	221	21	Y91434	Human secreted pro
37	67	10.1	634	20	Y21548	Human heparin-bind
38	66	10.0	101	21	B53687	Human colon cancer
39	66	10.0	283	21	G45469	Arabidopsis thalia
40	66	10.0	299	21	G30635	Arabidopsis thalia
41	66	10.0	299	21	G45468	Arabidopsis thalia
42	66	10.0	312	21	G30634	Arabidopsis thalia
43	66	10.0	357	21	G30633	Arabidopsis thalia
44	66	10.0	1032	21	G45673	Arabidopsis thalia
45	66	10.0	1045	21	G45672	Arabidopsis thalia

ALIGNMENTS

RESULT	1
Y58221	
ID	Y58221 standard; Protein; 131 AA.
XX	
AC	Y58221;
XX	
DT	14-MAR-2000 (first entry)
XX	
DE	Canine interleukin-13 (IL-13) clone 80.
XX	
KW	Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;
KW	immunoregulation; tumour; cancer; autoimmune disease; vaccine.
XX	
OS	Canis familiaris.
XX	
PN	WO9961618-A2.
XX	
PD	02-DEC-1999.
XX	
PF	28-MAY-1999; 99WO-US11942.
XX	
PR	29-MAY-1998; 98US-0087306.
XX	
PA	(HESK-) HESKA CORP.
XX	
PI	Sim G, Yang S, Dreitz MJ, Wonderling RS;
XX	
DR	WPI; 2000-072623/06.
DR	N-PSDB; Z55555, Z55556, Z55557, Z55558.
XX	
PT	Nucleic acids encoding immunoregulatory proteins from cats or dogs,
PT	useful for treating or preventing e.g. tumors or autoimmune disease
XX	
PS	Claim 3i; Page 231; 264pp; English.

XX Sequences Y58221-Y58222 and Y58223-Y58224 represent encoded and mature  
CC canine interleukin-13 (IL-13) clones 80 and 78. The invention relates to  
CC canine IL-4, canine or feline Flt-3 ligand, canine IL-5, canine IL-13, feline  
CC canine or feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline  
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage  
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these  
CC immunoregulatory proteins. The proteins, their associated  
CC nucleic acids, specific antibodies and inhibitors may be used as  
CC vaccines for therapeutic or prophylactic regulation of an immune  
CC response in animals (particularly cats, dogs, horses and humans).  
CC They may be used to treat autoimmune or infectious diseases including  
CC allergies, tumours, inflammation and graft rejection, and to increase  
CC the response from a co-administered antigen. The nucleotide sequences  
CC can also be used for the recombinant production of a protein, while  
CC nucleotide fragments are useful as probes, as amplification primers and  
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
CC The proteins may be used to raise antibodies and to screen for  
CC modulators of activity, while the antibodies may be used in detection,  
CC and in drug targeting.  
XX  
SQ Sequence 131 AA;

Query Match 100.0%; Score 663; DB 21; Length 131;  
Best Local Similarity 100.0%; Pred. No. 5.6e-68;  
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MALWLTVVVIALTCLGGLASPSVPTSPPTLKELIEELVNITQNASLCSGSMVSVNLTAG 60  
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QY 61 MYCAALESLINVSDCSAIQRTQRMKALCSQKPAAGQISSERSRDTKIEVQLVKNLLTY 120  
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QY 121 VRGVYRHGNFR 131  
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Db 121 vrgvyrhgnfr 131

RESULT 2  
Y58223  
ID Y58223 standard; Protein; 130 AA.  
XX  
AC Y58223;  
XX  
DT 14-MAR-2000 (first entry)  
XX  
DE Canine interleukin-13 (IL-13) clone 78.  
XX  
DE Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;  
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine.  
XX  
OS Canis familiaris.  
XX  
PN WO9961618-A2.  
XX  
PD 02-DEC-1999.  
XX  
PF 28-MAY-1999; 99WO-US11942.  
XX  
PR 29-MAY-1998; 98US-0087306.  
XX  
PA (HESK-) HESKA CORP.  
XX  
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;  
XX  
XX WPI; 2000-072623/06.  
DR N-PSDB; 255561, 255562, 255563, 255564.  
XX  
XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
PT useful for treating or preventing e.g. tumors or autoimmune disease

XX Claim 3i; Page 237; 264pp; English.  
PS  
XX  
CC Sequences Y58221-Y58222 and Y58223-Y58224 represent encoded and mature  
CC canine interleukin-13 (IL-13) clones 80 and 78. The invention relates to  
CC canine IL-4, canine or feline Flt-3 ligand, canine IL-5, canine IL-13, feline  
CC canine or feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline  
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage  
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these  
CC immunoregulatory proteins. The proteins, their associated  
CC nucleic acids, specific antibodies and inhibitors may be used as  
CC vaccines for therapeutic or prophylactic regulation of an immune  
CC response in animals (particularly cats, dogs, horses and humans).  
CC They may be used to treat autoimmune or infectious diseases including  
CC allergies, tumours, inflammation and graft rejection, and to increase  
CC the response from a co-administered antigen. The nucleotide sequences  
CC can also be used for the recombinant production of a protein, while  
CC nucleotide fragments are useful as probes, as amplification primers and  
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
CC The proteins may be used to raise antibodies and to screen for  
CC modulators of activity, while the antibodies may be used in detection,  
CC and in drug targeting.  
XX  
SQ Sequence 130 AA;

Query Match 97.7%; Score 647.5; DB 21; Length 130;  
Best Local Similarity 99.2%; Pred. No. 3.3e-66;  
Matches 130; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
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Db 1 malwltvvvialtclgglaspsvptspptlkelielvnitqnaslcsngsmvsvnltag 60  
QY 61 MYCAALESLINVSDCSAIQRTQRMKALCSQKPAAGQISSERSRDTKIEVQLVKNLLTY 120  
|||||  
Db 61 mycaaleslinvsdc Saiqr tgr mklalcsqkpaag-issersrdtkievlvknllty 119  
QY 121 VRGVYRHGNFR 131  
|||||  
Db 120 vrgvyrhgnfr 130

RESULT 3  
Y58222  
ID Y58222 standard; Protein; 111 AA.  
XX  
AC Y58222;  
XX  
DT 14-MAR-2000 (first entry)  
XX  
DE Canine mature interleukin-13 (IL-13) clone 80.  
XX  
DE Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;  
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine.  
XX  
OS Canis familiaris.  
XX  
PN WO9961618-A2.  
XX  
PD 02-DEC-1999.  
XX  
PF 28-MAY-1999; 99WO-US11942.  
XX  
PR 29-MAY-1998; 98US-0087306.  
XX  
PA (HESK-) HESKA CORP.  
XX  
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;  
XX  
XX WPI; 2000-072623/06.  
DR N-PSDB; 255559, 255560.  
XX

PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
PT useful for treating or preventing e.g. tumors or autoimmune disease  
XX  
PS Claim 3i; Page 234; 264pp; English.  
XX  
CC Sequences Y58221-Y58222 and Y58223-Y58224 represent encoded and mature  
CC canine interleukin-13 (IL-13) clones 80 and 78. The invention relates to  
CC canine IL-4, canine or feline Flt-3 ligand, canine or feline CD40,  
CC canine or feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline  
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage  
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these  
CC immunoregulatory proteins. The proteins, their associated  
CC nucleic acids, specific antibodies and inhibitors may be used as  
CC vaccines for therapeutic or prophylactic regulation of an immune  
CC response in animals (particularly cats, dogs, horses and humans).  
CC They may be used to treat autoimmune or infectious diseases including  
CC allergies, tumours, inflammation and graft rejection, and to increase  
CC the response from a co-administered antigen. The nucleotide sequences  
CC can also be used for the recombinant production of a protein, while  
CC nucleotide fragments are useful as probes, as amplification primers and  
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
CC The proteins may be used to raise antibodies and to screen for  
CC modulators of activity, while the antibodies may be used in detection,  
CC and in drug targeting.  
XX  
SQ Sequence 111 AA;

Query Match 84.6%; Score 561; DB 21; Length 111;  
Best Local Similarity 100.0%; Pred. No. 2e-56;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 21 SPVTPSPTLKEELVNITQNASLCSMGWSVNLTAGMYCAALESLINVSDCSAIQR 80  
Db 1 spvtspptlkelieelvnitqnaslcsmgwsvnltagmycaaleslinvsdcsaiqr 60  
QY 81 TQRLKALCSQKPAAGQISSERSRDTKIEVIQLVKNLITYVRGVYRHGNFR 131  
Db 61 tqrlmkalcsqkpaagqissersrdtkieviqlvknllityvrgvyrhgnfr 111

RESULT 4  
Y58224  
ID Y58224 standard; Protein; 110 AA.  
XX  
AC Y58224;  
XX  
DT 14-MAR-2000 (first entry)  
XX  
DE Canine mature interleukin-13 (IL-13) clone 78.  
XX  
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;  
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine.  
XX  
OS Canis familiaris.  
XX  
PN WO9961618-A2.  
XX  
PD 02-DEC-1999.  
XX  
PF 28-MAY-1999; 99WO-US11942.  
XX  
PR 29-MAY-1998; 98US-0087306.  
XX  
PA (HESK-) HESKA CORP.  
XX  
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;  
XX  
DR WPI; 2000-072623/06.  
DR N-PSDB; Z55565, Z55566.  
XX  
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
PT useful for treating or preventing e.g. tumors or autoimmune disease

XX  
PS Claim 3i; Page 240; 264pp; English.  
XX  
CC Sequences Y58221-Y58222 and Y58223-Y58224 represent encoded and mature  
CC canine interleukin-13 (IL-13) clones 80 and 78. The invention relates to  
CC canine IL-4, canine or feline Flt-3 ligand, canine or feline CD40,  
CC canine or feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline  
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage  
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these  
CC immunoregulatory proteins. The proteins, their associated  
CC nucleic acids, specific antibodies and inhibitors may be used as  
CC vaccines for therapeutic or prophylactic regulation of an immune  
CC response in animals (particularly cats, dogs, horses and humans).  
CC They may be used to treat autoimmune or infectious diseases including  
CC allergies, tumours, inflammation and graft rejection, and to increase  
CC the response from a co-administered antigen. The nucleotide sequences  
CC can also be used for the recombinant production of a protein, while  
CC nucleotide fragments are useful as probes, as amplification primers and  
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
CC The proteins may be used to raise antibodies and to screen for  
CC modulators of activity, while the antibodies may be used in detection,  
CC and in drug targeting.  
XX  
SQ Sequence 110 AA;

Query Match 82.3%; Score 545.5; DB 21; Length 110;  
Best Local Similarity 99.1%; Pred. No. 1.1e-54;  
Matches 110; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
QY 21 SPVTPSPTLKEELVNITQNASLCSMGWSVNLTAGMYCAALESLINVSDCSAIQR 80  
Db 1 spvtspptlkelieelvnitqnaslcsmgwsvnltagmycaaleslinvsdcsaiqr 60  
QY 81 TQRLKALCSQKPAAGQISSERSRDTKIEVIQLVKNLITYVRGVYRHGNFR 131  
Db 61 tqrlmkalcsqkpaag-issersrdtkieviqlvknllityvrgvyrhgnfr 110

RESULT 5  
R48624  
ID R48624 standard; Protein; 132 AA.  
XX  
AC R48624;  
XX  
DT 14-SEP-1994 (first entry)  
XX  
DE Sequence of human interleukin-13 (IL-13).  
XX  
KW Interleukin-13; lymphokine; immunological disorder; therapy;  
KW diagnostic.  
XX  
OS Homo sapiens.  
XX  
PN WO9404680-A.  
XX  
PD 03-MAR-1994.  
XX  
PF 18-AUG-1993; 93WO-US07645.  
XX  
PR 21-AUG-1992; 92US-0933416.  
PR 29-JAN-1993; 93US-0010977.  
PR 01-FEB-1993; 93US-0012543.  
XX  
PA (SCHE ) SCHERING CORP.  
XX  
PI Aversa G, Banchereau J, Briere F, Coffman RL, Cooks BG;  
PI Culpepper, Dang W, De Vries J, De Waal Malefyt R;  
PI Doherty TM, Heath A, Mckenzie A, Punnonen J, Zurawski G;  
XX  
DR WPI; 1994-083197/10.  
DR N-PSDB; Q56692.  
XX

PT Purified interleukin-13 proteins and antibodies - obt'd. using  
PT mouse gene encoding related protein P600  
XX  
PS Claim 1; Page 126-127; 135pp; English.  
XX  
CC An approx. 400 bp DNA fragment derived from a Pst/PvuII restriction  
CC digest of the mouse P600 cDNA clone was isolated. This fragment,  
CC which encompasses most of the coding region of the mouse P600 cDNA,  
CC was radioactively labelled and hybridised with filter lifts prepd.  
CC from a cDNA library made from a clone of an A10 T cell line. One  
CC clone, designated PA 10.66, was subcloned into M13 and sequenced.  
CC This sequence encodes human IL-13.  
XX  
SQ Sequence 132 AA;  
  
Query Match 69.9%; Score 463.5; DB 15; Length 132;  
Best Local Similarity 71.8%; Pred. NO. 3.4e-45;  
Matches 94; Conservative 11; Mismatches 25; Indels 1; Gaps 1;  
  
QY 1 MALWLTVVIALTCLGLASPSVPTSPPTLKELIEELVNITQNO-ASLCNGSMVWSVNLTA 59  
Db 1 malllttvialtclgfgfaspvpstaltrelieelvnitqngkaplcnsgmvwsinlta 60  
  
QY 60 GMYCAALESLINVSDCSAIQRTQRLKALCSQKPAAGQISSERSRDTKIEVIQLVKNLLT 119  
Db 61 gmycaaleslinvsgcsaiektqrmlsgfcphkvsagqfsslhvrdtkievafvkdlll 120  
  
QY 120 YVRGVYRHGNF 130  
Db 121 hlklfregrf 131  
  
RESULT 6  
R27348  
ID R27348 standard; Protein; 146 AA.  
XX  
AC R27348;  
XX  
DT 24-FEB-1993 (first entry)  
XX  
DE Cytokine NC30.  
XX  
KW Interleukin; chemotaxis; immunomodulation; inflammation.  
XX  
FH Location/Qualifiers  
FT cleavage\_site 20..21 "putative signal peptide cleavage site"  
FT /note= 24..25  
FT cleavage\_site "putative signal peptide cleavage site"  
FT /note= 32..33  
FT cleavage\_site "putative signal peptide cleavage site"  
FT /note= 34..35  
FT cleavage\_site "putative signal peptide cleavage site"  
FT /note= 35..146  
FT protein /label= NC30  
XX  
PN EP506574-A.  
XX  
XX 30-SEP-1992.  
PD  
XX  
PF 27-MAR-1992; 92EP-0400858.  
XX  
PR 29-MAR-1991; 91FR-0003904.  
PR 08-JAN-1992; 92FR-0000137.  
XX  
PA (SNFI ) ELF SANOFI.  
XX  
PI Caput D, Ferrara P, Guillemot J, Kaghad M, Labit-le Bouteiller C;  
PI Leplatols P, Magazin M, Minty A;  
XX  
XX WPI; 1992-325841/40.  
DR  
DR N-PSDB; Q28947.

XX New cytokine having immunomodulatory activity - useful for  
PT treating tumours and infectious or inflammatory conditions  
XX  
PS Claim 1; Page 52-53; 78pp; French.  
XX  
CC A novel cytokine produced by T lymphocytes induced by phorbol-2-  
CC myristate-3-acetate and phytohaemagglutinin was coded for by the  
CC sequence in clone pSE1-NC30. A second clone was also identified  
CC (pSE1-NC30bis) which differed only in the identity of codon 41.  
CC The corresponding proteins differ in the amino acid at position 41  
CC which is either Asp (in NC30) or Gly (in NC30bis). The cytokine  
CC acts on monocytes and B lymphocytes and is useful in treatment of  
CC tumours and some infections and inflammatory conditions.  
CC See Q28941-Q28947.  
XX  
SQ Sequence 146 AA;  
  
Query Match 68.9%; Score 456.5; DB 13; Length 146;  
Best Local Similarity 71.0%; Pred. NO. 2.4e-44;  
Matches 93; Conservative 11; Mismatches 26; Indels 1; Gaps 1;  
  
QY 1 MALWLTVVIALTCLGLASPSVPTSPPTLKELIEELVNITQNO-ASLCNGSMVWSVNLTA 59  
Db 15 malllttvialtclgfgfaspvpstaltrelieelvnitqngkaplcnsgmvwsinlta 74  
  
QY 60 GMYCAALESLINVSDCSAIQRTQRLKALCSQKPAAGQISSERSRDTKIEVIQLVKNLLT 119  
Db 75 dmycaaleslinvsgcsaiektqrmlsgfcphkvsagqfsslhvrdtkievafvkdlll 134  
  
QY 120 YVRGVYRHGNF 130  
Db 135 hlklfregrf 145  
  
RESULT 7  
R27347  
ID R27347 standard; Protein; 112 AA.  
XX  
AC R27347;  
XX  
DT 24-FEB-1993 (first entry)  
XX  
DE Protein with cytokine activity encoded by Nal'.  
XX  
KW Interleukin; chemotaxis; immunomodulation; inflammation.  
XX  
PN EP506574-A.  
XX  
PD 30-SEP-1992.  
XX  
PF 27-MAR-1992; 92EP-0400858.  
XX  
PR 29-MAR-1991; 91FR-0003904.  
PR 08-JAN-1992; 92FR-0000137.  
XX  
PA (SNFI ) ELF SANOFI.  
XX  
PI Caput D, Ferrara P, Guillemot J, Kaghad M, Labit-le Bouteiller C;  
PI Leplatols P, Magazin M, Minty A;  
XX  
XX WPI; 1992-325841/40.  
DR  
DR N-PSDB; Q28944.  
XX  
PT New cytokine having immunomodulatory activity - useful for  
PT treating tumours and infectious or inflammatory conditions  
XX  
PS Claim 1; Page 60; 78pp; French.  
XX  
CC This protein is one of two possible forms of a new cytokine  
CC produced by T lymphocytes induced by phorbol-2-myristate-3-acetate  
CC and phytohaemagglutinin. The proteins differ only in the amino acid



CC at position 41 which is either Asp or Gly. The cytokine acts on  
CC monocytes and B lymphocytes and is useful in treatment of tumours  
CC and some infections and inflammatory conditions.  
CC See Q28941-Q28947.  
XX  
SQ Sequence 112 AA;

Query Match 57.7%; Score 382.5; DB 13; Length 112;  
Best Local Similarity 70.0%; Pred. No. 4.7e-36;  
Matches 77; Conservative 11; Mismatches 21; Indels 1; Gaps 1;

QY 22 PVTPTSPTLKEELVNTQNO-ASLCNGSMVWSVNLTAGMYCAALESINVSDCSAIQR 80  
II II I:IIIIIIIIII I IIIIIIIII:IIIIIIIIIIIIIIIIII IIII::  
Db 2 pvpbstalrelieelvnitqkplcngsmvwsinltagmycaaleslinvsgcsaiek 61  
IIII I:IIIIIIIIII I IIIIIIIII:IIIIIIIIIIIIIIIIII IIII::

QY 81 TQRLMKALCSQKPAAGQISSERSRDTKIEVIQLVKNLLTYVRGVYRHGNF 130  
IIII I:IIIIIIIIII I IIIIIIIII:IIIIIIIIIIIIIIIIII IIII I  
Db 62 tqrmisgfcphkvsagqfsslhvrdtkievafvkdllhlkklfregrf 111  
IIII I:IIIIIIIIII I IIIIIIIII:IIIIIIIIIIIIIIIIII IIII I

RESULT 8  
R92793  
ID R92793 standard; Protein; 112 AA.  
XX  
AC R92793;  
XX  
DT 24-MAY-1996 (first entry)  
XX  
DE Human interleukin-13 mutein 1.  
XX  
KW Cytokine; mutein; interleukin-13; IL-13; agonist; antagonist;  
KW diagnosis; therapy; cancer; inflammation; degenerative disease.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 11 /note= "Glu at position 11 may be replaced by an  
FT amidated amino acid, including Lys"  
FT  
FT Misc-difference 64 /note= "Arg at position 64 may be replaced by an  
FT acidic amino acid, including Asp"  
XX  
PN WO9604306-A2.  
XX  
PD 15-FEB-1996.  
XX  
PF 31-JUL-1995; 95WO-US08950.  
XX  
PR 01-AUG-1994; 94US-0284393.  
XX  
PA (SCHE ) SCHERING CORP.  
XX  
PI Zurawski G, Zurawski SM;  
XX  
DR WPI; 1996-129335/13.  
XX  
PT Mutein(s) of human and murine cytokine(s), esp. interleukin(s) and  
PT murine P600 contg. amino acid substitutions. - useful for the  
PT diagnosis and treatment of cancer, inflammation, etc.  
XX  
PS Claim 12; Page 46; 52pp; English.  
XX  
CC Muteins 1 and 2 (R92793-94) of human interleukin-13 (IL-13) contain  
CC amino acid substitutions at amino acid position 11 in helix A and/or  
CC at position 64 in helix C. They are obtd. by site-directed  
CC mutagenesis of natural IL-13 sequences. The muteins antagonise the  
CC activity of IL-13 or IL-4. They have partial cytokine agonist  
CC activity, exhibit less than 80% maximal agonist activity of natural  
CC IL-2, and/or antagonize cytokine activity by least about 50% when  
CC present at a 100-fold excess. They and other cytokine muteins  
CC (see also R92790-92, R92795-802) are useful in the screening of

CC cytokine and cytokine receptor levels, and in the diagnosis or  
CC treatment of e.g. inflammation, cancer, and degenerative disorders.  
XX  
SQ Sequence 112 AA;

Query Match 57.7%; Score 382.5; DB 17; Length 112;  
Best Local Similarity 70.0%; Pred. No. 4.7e-36;  
Matches 77; Conservative 11; Mismatches 21; Indels 1; Gaps 1;

QY 22 PVTPTSPTLKEELVNTQNO-ASLCNGSMVWSVNLTAGMYCAALESINVSDCSAIQR 80  
II II I:IIIIIIIIII I IIIIIIIII:IIIIIIIIIIIIIIIIII IIII::  
Db 2 pvpbstalrelieelvnitqkplcngsmvwsinltagmycaaleslinvsgcsaiek 61  
IIII I:IIIIIIIIII I IIIIIIIII:IIIIIIIIIIIIIIIIII IIII::

QY 81 TQRLMKALCSQKPAAGQISSERSRDTKIEVIQLVKNLLTYVRGVYRHGNF 130  
IIII I:IIIIIIIIII I IIIIIIIII:IIIIIIIIIIIIIIIIII IIII I  
Db 62 tqrmisgfcphkvsagqfsslhvrdtkievafvkdllhlkklfregrf 111  
IIII I:IIIIIIIIII I IIIIIIIII:IIIIIIIIIIIIIIIIII IIII I

RESULT 9  
R48625  
ID R48625 standard; Protein; 131 AA.  
XX  
AC R48625;  
XX  
DT 14-SEP-1994 (first entry)  
XX  
DE Sequence of mouse P600.  
XX  
KW Interleukin-13; lymphokine; P600; immunological disorder; therapy;  
KW diagnostic.  
XX  
OS Mus musculus.  
XX  
PN WO9404680-A.  
XX  
PD 03-MAR-1994.  
XX  
PF 18-AUG-1993; 93WO-US07645.  
XX  
PR 21-AUG-1992; 92US-0933416.  
PR 29-JAN-1993; 93US-0010977.  
PR 01-FEB-1993; 93US-0012543.  
XX  
PA (SCHE ) SCHERING CORP.  
XX  
PI Aversa G, Banchereau J, Briere F, Coffman RL, Cooks BG;  
PI Culpepper, Dang W, De Vries J, De Waal Malefyt R,  
PI Doherty TM, Heath A, Mckenzie A, Punnonen J, Zurawski G;  
XX  
DR WPI; 1994-083197/10.  
DR N-PSDB; Q56693.  
XX  
PT Purified interleukin-13 proteins and antibodies - obtd. using  
PT mouse gene encoding related protein P600  
XX  
PS Disclosure; Page 128-129; 135pp; English.  
XX  
CC An approx. 400 bp DNA fragment derived from a Pst/PvuII restriction  
CC digest of the mouse P600 cDNA clone was isolated. This fragment,  
CC which encompasses most of the coding region of the mouse P600 cDNA,  
CC was radioactively labelled and hybridised with filter lifts prepd.  
CC from a cDNA library made from a clone of an A10 T cell line. One  
CC clone, designated PA 10.66, was subcloned into M13 and sequenced.  
CC This sequence encodes human IL-13.  
XX  
SQ Sequence 131 AA;

Query Match 57.1%; Score 378.5; DB 15; Length 131;  
Best Local Similarity 59.0%; Pred. No. 1.7e-35;  
Matches 79; Conservative 19; Mismatches 29; Indels 7; Gaps 3;



AC R92795;  
XX  
DT 24-MAY-1996 (first entry)  
XX  
DE Murine P600.  
XX  
KW Cytokine; mutein; P600; interleukin-13; IL-13; agonist; antagonist;  
KW diagnosis; therapy; cancer; inflammation; degenerative disease.  
XX  
OS Mus musculus.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 67  
FT /note= "Arg at position 67 may be replaced by an  
FT acid amino acid, including Asp"  
XX  
PN WO9604306-A2.  
XX  
PD 15-FEB-1996.  
XX  
PF 31-JUL-1995; 95WO-US08950.  
XX  
PR 01-AUG-1994; 94US-0284393.  
XX  
PA (SCHE ) SCHERING CORP.  
XX  
PI Zurawski G, Zurawski SM;  
XX  
DR WPI; 1996-129335/13.  
XX  
PT Mutein(s) of human and murine cytokine(s), esp. interleukin(s) and  
PT murine P600 contg. amino acid substitutions. - useful for the  
PT diagnosis and treatment of cancer, inflammation, etc.  
XX  
PS Claim 12; Page 46; 52pp; English.  
XX  
CC Muteins of mouse P600 (R92795) contain amino acid substitutions at  
CC amino acid position 67 in helix C. They are obtd. by site-directed  
CC mutagenesis of natural P600 sequences. The muteins antagonise the  
CC activity of IL-13 or IL-4. They have partial cytokine agonist  
CC activity, exhibit less than 80% maximal agonist activity of natural  
CC IL-2, and/or antagonize cytokine activity by least about 50% when  
CC present at a 100-fold excess. They and other cytokine muteins  
CC (see also R92790-94, R92796-802) are useful in the screening of  
CC cytokine and cytokine receptor levels, and in the diagnosis or  
CC treatment of e.g. inflammation, cancer, and degenerative disorders.  
XX  
SQ Sequence 111 AA;

Query Match 44.6%; Score 295.5; DB 17; Length 111;  
Best Local Similarity 55.9%; Pred. No. 4e-26;  
Matches 62; Conservative 18; Mismatches 28; Indels 3; Gaps 2;

QY 20 PSPVTPSPTLKELIEELVNITQNASLCNGSMVWSVNLTAGMYCAALESLINVSDCSAIQ 79  
Db | | : ||||| ||||: ||||| ||||: || : |||| | : ||||  
4 prsvslpltlkelieelsnltqdetplcngsmvwsvdlaagffcvaldslnisncnaiy 63

QY 80 RTQRMKALCSQKPAAGQISSERSRDTKIEVLIQLVKNLLTYVRGVYRHGNF 130  
Db ||||: | ||: | || : || |||| : |||| : |||| : ||||  
64 rtqrihlhglcnrk-apttvss--lptdkievahfktllsytkqlfchgpf 111

RESULT 13  
R27345  
ID R27345 standard; peptide; 20 AA.  
XX  
AC R27345;  
XX  
DT 24-FEB-1993 (first entry)  
XX  
DE Cytokine signal peptide b4.  
XX

KW Interleukin; chemotaxis; immunomodulation; inflammation.  
XX  
PN EP506574-A.  
XX  
PD 30-SEP-1992.  
XX  
PF 27-MAR-1992; 92EP-0400858.  
XX  
PR 29-MAR-1991; 91FR-0003904.  
PR 08-JAN-1992; 92FR-0000137.  
XX  
PA (SNFI ) ELF SANOFI.  
XX  
PI Caput D, Ferrara P, Guillemot J, Kaghad M, Labit-le Bouteiller C;  
PI Lepiatols P, Magazin M, Minty A;  
XX  
DR WPI; 1992-325841/40.  
DR N-PSDB; Q28941.  
XX  
PT New cytokine having immunomodulatory activity - useful for  
PT treating tumours and infectious or inflammatory conditions  
XX  
PS Claim 12; Page 61; 78pp; French.  
XX  
CC The b4 peptide is a preferred signal peptide to be fused to the  
CC N-terminus of the new cytokine. The last two amino acids (Ser-Pro)  
CC are opt. absent; when absent the signal peptide is designated b3.  
CC See Q28942-Q28947.  
XX  
SQ Sequence 20 AA;

Query Match 12.2%; Score 81; DB 13; Length 20;  
Best Local Similarity 85.0%; Pred. No. 0.012;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MALWLTVVVIALTCLGGLASP 20  
Db ||| || ||||| |||| ||||  
1 malllttvialtclggfasp 20

RESULT 14  
R27344  
ID R27344 standard; peptide; 34 AA.  
XX  
AC R27344;  
XX  
DT 21-MAY-1998 (first entry)  
XX  
DE Cytokine signal peptide b2.  
XX  
KW Interleukin; chemotaxis; immunomodulation; inflammation.  
XX  
OS Homo sapiens.  
XX  
PN EP506574-A.  
XX  
PD 30-SEP-1992.  
XX  
PF 27-MAR-1992; 92EP-0400858.  
XX  
PR 29-MAR-1991; 91FR-0003904.  
PR 08-JAN-1992; 92FR-0000137.  
XX  
PA (SNFI ) ELF SANOFI.  
XX  
PI Caput D, Ferrara P, Guillemot J, Kaghad M, Labit-le Bouteiller C;  
PI Lepiatols P, Magazin M, Minty A;  
XX  
DR WPI; 1992-325841/40.  
DR N-PSDB; Q28941.  
XX  
PT New cytokine having immunomodulatory activity - useful for

PT treating tumours and infectious or inflammatory conditions  
XX Claim 12; Page 61; 78pp; French.  
PS  
XX The b2 peptide is a preferred signal peptide to be fused to the  
CC N-terminus of the new cytokine. The last two amino acids (Ser-Pro)  
CC are opt. absent; when absent the signal peptide is designated b1.  
CC See Q28942-Q28947.  
XX  
SQ Sequence 34 AA;  
  
Query Match 12.2%; Score 81; DB 13; Length 34;  
Best Local Similarity 85.0%; Pred. No. 0.025;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 MALWLTVVIALTCLGLASP 20  
Db 15 mallttvtialtciggfasp 34  
  
RESULT 15  
B38312  
ID B38312 standard; Protein; 665 AA.  
XX B38312;  
XX  
DT 30-JAN-2001 (first entry)  
XX Human secreted protein sequence encoded by gene 38 SEQ ID NO:168.  
DE  
XX Human; secreted protein; diagnosis; immunosuppressive; antiarthritic;  
KW antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic;  
KW cerebroprotective; nootropic; neuroprotective; antibacterial; virucide;  
KW fungicide; ophthalmological; gene therapy; autoimmune disease; infection;  
KW hyperproliferative disorder; cardiovascular disorder; angiogenesis;  
KW cerebrovascular disorder; nervous system disorder; ocular disorder;  
KW wound healing; skin aging; food additive; preservative.  
XX  
OS Homo sapiens.  
XX  
XX WO200058469-A1.  
XX  
XX 05-OCT-2000.  
XX  
XX 23-MAR-2000; 2000WO-US07579.  
XX  
XX 26-MAR-1999; 99US-0126509.  
PR 07-JAN-2000; 2000US-0174853.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Rosen CA, Ruben SM, Komatsoulis G;  
PI  
XX WPI; 2000-594642/56.  
DR  
XX Isolated nucleic acid molecule encoding a human secreted protein is  
PT used in preventing, treating or ameliorating a medical condition -  
XX  
XX Disclosure; Page 407-409; 416pp; English.  
XX  
CC The polynucleotide sequences given in C69455 to C69502 encode the human  
CC secreted proteins given in B38203 to B38250. B38251 to B38320 represent  
CC human secreted polypeptide sequences and proteins homologous to them,  
CC which are given in the exemplification of the present invention. Human  
CC secreted proteins have activities based on the tissues and cells the  
CC genes are expressed in. Example of activities include: immunosuppressive;  
CC antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiant;  
CC vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial;  
CC virucide; fungicide; and ophthalmological. The polynucleotides and  
CC polypeptides can be used to prevent, treat or ameliorate a medical  
CC condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs,  
CC chickens or sheep. They are also used in diagnosing a pathological

CC condition or susceptibility to a pathological condition. Disorders which  
CC are diagnosed or treated include autoimmune diseases, hyperproliferative  
CC disorders, cardiovascular disorders, cerebrovascular disorders,  
CC angiogenesis, nervous system disorders, infections caused by bacteria,  
CC viruses and fungi and ocular disorders. The polypeptides can also be used  
CC to aid wound healing and epithelial cell proliferation, to prevent skin  
CC aging due to sunburn, to maintain organs before transplantation, for  
CC supporting cell culture of primary tissues, to regenerate tissues and in  
CC chemotaxis. The polypeptides can also be used as a food additive or  
CC preservative to increase or decrease storage capabilities. C69446 to  
CC C69454 and B38202 represent sequences used in the exemplification of the  
CC present invention.  
XX  
SQ Sequence 665 AA;  
  
Query Match 11.8%; Score 78.5; DB 21; Length 665;  
Best Local Similarity 31.0%; Pred. No. 2.7;  
Matches 39; Conservative 19; Mismatches 51; Indels 17; Gaps 5;  
  
QY 5 LTVVIALTCLGLASPVTPPTLKELEELVN-ITQNASLNCNSMV-----WSV 55  
Db 479 lttvkaltliag--splkidlrpvlgegvpilasflrknqralkigtlsaldliknysd 536  
QY 56 NLTAGMYCAALES---LINVSDCSAIQRTQRMKALCSQKPAAGQISSERSRDTKIEVIO 112  
Db 537 sltaamidavidelpplisesdmhvsqmaislfttlakvypss---lskisgsilnelig 593  
QY 113 LVKNLL 118  
Db 594 lvrsp1 599  
  
Search completed: May 13, 2001, 17:47:33  
Job time: 12333 sec



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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 13, 2001, 14:26:17 ; Search time 42.06 Seconds  
(without alignments)  
59.834 Million cell updates/sec

Title: US-09-451-527-92  
Perfect score: 663  
Sequence: 1 MALWLTVVIALTCLGLASP.....QLVKNLLTYVRGVYRHGNER 131

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 185757 seqs, 19210857 residues

Total number of hits satisfying chosen parameters: 185757

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
1: /cgnl\_7/ptodata/1/iaa/5A\_COMB.pep:\*  
2: /cgnl\_7/ptodata/1/iaa/5B\_COMB.pep:\*  
3: /cgnl\_7/ptodata/1/iaa/6A\_COMB.pep:\*  
4: /cgnl\_7/ptodata/1/iaa/6B\_COMB.pep:\*  
5: /cgnl\_7/ptodata/1/iaa/PCTUS\_COMB.pep:\*  
6: /cgnl\_7/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	463.5	69.9	132	1 US-08-012-543-2	Sequence 2, Appli
2	463.5	69.9	132	5 PCT-US93-07645A-2	Sequence 2, Appli
3	463.5	69.9	132	5 PCT-US93-07645-2	Sequence 2, Appli
4	456.5	68.9	146	1 US-08-371-121-16	Sequence 16, Appli
5	382.5	57.7	112	1 US-08-284-393B-4	Sequence 4, Appli
6	382.5	57.7	112	5 PCT-US95-08950-4	Sequence 4, Appli
7	378.5	57.1	131	1 US-08-012-543-4	Sequence 4, Appli
8	378.5	57.1	131	1 US-08-371-121-25	Sequence 25, Appli
9	378.5	57.1	131	5 PCT-US93-07645A-4	Sequence 4, Appli
10	378.5	57.1	131	5 PCT-US93-07645-4	Sequence 4, Appli
11	375.5	56.6	112	1 US-08-371-121-1	Sequence 1, Appli
12	371.5	56.0	112	1 US-08-284-393B-14	Sequence 14, Appli
13	367	55.4	111	1 US-08-284-393B-5	Sequence 5, Appli
14	367	55.4	111	5 PCT-US95-08950-5	Sequence 5, Appli
15	356	53.7	111	1 US-08-284-393B-15	Sequence 15, Appli
16	295.5	44.6	111	1 US-08-284-393B-6	Sequence 6, Appli
17	295.5	44.6	111	5 PCT-US95-08950-6	Sequence 6, Appli
18	288.5	43.5	111	1 US-08-284-393B-16	Sequence 16, Appli
19	81	12.2	20	1 US-08-371-121-8	Sequence 8, Appli
20	81	12.2	34	1 US-08-371-121-6	Sequence 6, Appli
21	71	10.7	718	4 US-09-090-808-2	Sequence 2, Appli
22	70	10.6	18	1 US-08-371-121-7	Sequence 7, Appli
23	70	10.6	32	1 US-08-371-121-5	Sequence 5, Appli
24	70	10.6	1754	1 US-07-745-206A-13	Sequence 13, Appli
25	70	10.6	1754	2 US-08-311-363-13	Sequence 13, Appli
26	65.5	9.9	477	2 US-08-770-544-16	Sequence 16, Appli
27	64.5	9.7	268	2 US-08-176-414B-2	Sequence 2, Appli

28	64.5	9.7	268	2 US-08-687-559-25	Sequence 25, Appli
29	64	9.7	168	3 US-09-188-579-85	Sequence 85, Appli
30	64	9.7	206	3 US-09-041-889-6	Sequence 6, Appli
31	64	9.7	206	3 US-08-837-058-6	Sequence 6, Appli
32	64	9.7	228	4 US-08-569-221A-2	Sequence 2, Appli
33	63.5	9.6	338	1 US-07-809-457A-16	Sequence 16, Appli
34	63.5	9.6	338	1 US-08-553-943-16	Sequence 16, Appli
35	63.5	9.6	338	5 PCT-US91-09437-16	Sequence 16, Appli
36	63.5	9.6	1461	2 US-08-993-228-10	Sequence 10, Appli
37	63	9.5	599	1 US-08-222-619-2	Sequence 2, Appli
38	63	9.5	599	5 PCT-US95-04075-2	Sequence 2, Appli
39	63	9.5	731	1 US-08-731-716-2	Sequence 2, Appli
40	63	9.5	848	4 US-08-976-255-10	Sequence 10, Appli
41	63	9.5	871	2 US-08-775-009-35	Sequence 35, Appli
42	62	9.4	496	2 US-08-696-349-2	Sequence 2, Appli
43	62	9.4	496	5 PCT-US96-13156-2	Sequence 2, Appli
44	62	9.4	1117	2 US-08-841-483-6	Sequence 6, Appli
45	61.5	9.3	338	3 US-08-722-184-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1  
US-08-012-543-2  
; Sequence 2, Application US/08012543  
; Patent No. 5596072  
; GENERAL INFORMATION:  
; APPLICANT: Culpepper, Janice  
; APPLICANT: McKenzie, Andrew  
; APPLICANT: Dang, Warren  
; APPLICANT: de Waal Malefyt, Rene  
; APPLICANT: Heath, Andrew  
; APPLICANT: Aversa, Gregorio  
; APPLICANT: Briere, Francine  
; APPLICANT: Bancheureau, Jacques  
; APPLICANT: de Vries, Jan  
; APPLICANT: Zurawski, Gerard  
; TITLE OF INVENTION: Human Interleukin-13  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/012,543  
; FILING DATE: 01-FEB-1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/933,416  
; FILING DATE: 21-AUG-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0302K1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-852-9196  
; TELEFAX: 415-496-1200  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 132 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-012-543-2



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Query Match      68.9%; Score 456.5; DB 1; Length 146;
Best Local Similarity 71.0%; Pred. No. 8.1e-48;
Matches 93; Conservative 11; Mismatches 26; Indels 1; Gaps 1;

QY 1 MALWLTVVIALTCGLGASPSVPTPSPTLKELIEELVNITNQ-ASLCNGSMVWSVNLT 59
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Db 15 MALLTTVIALTCGLGFASPGVPVPPSTALRELIEELVNITNQKAPLCNGSMVWSINLT 74
   ||| || ||||| ||| ||| ||| ||||| ||||| ||| ||||| |||||
QY 60 GMYCAALESLINVSDCSATQRTQRMALKALCSQKPAAGQISSERSRDTKIEVIQLVKNLLT 119
   ||||| ||||| ||||| ||||| ||| ||| ||| ||||| ||||| |||
Db 75 DMYCAALESLINVSGSAIEKTQRMLSGFCPHKVSAGQFSSLHVRDTKIEVAQFVKDLLL 134
   ||||| ||||| ||||| ||||| ||| ||| ||| ||||| ||||| |||
QY 120 YVRGVYRHGNE 130
   ::: :|| | |
Db 135 HLKKLFGREF 145

RESULT 5
US-08-284-393B-4
; Sequence 4, Application US/08284393B
; Patent No. 5696234
; GENERAL INFORMATION:
; APPLICANT: Zurawski, Sandra M.
; APPLICANT: Zurawski, Gerard
; TITLE OF INVENTION: MUTAINS OF MAMMALIAN CYTOKINES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, version #1.30
; CURRENT APPLICATION DATA:

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RESULT 6
PCT-US95-08950-4
; Sequence 4, Application PC/TUS9508950
; GENERAL INFORMATION:
; APPLICANT: Zurawski, Sandra M.
; APPLICANT: Zurawski, Gerard
; TITLE OF INVENTION: MUTEINS OF MAMMALIAN CYTOKINES
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/08950
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/284,393
; FILING DATE: 01-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0389
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-852-9196
; TELEFAX: 415-496-1200
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 13, 2001, 14:31:11 ; Search time 64.5 Seconds  
(without alignments)  
139.577 Million cell updates/sec

Title: US-09-451-527-92  
Perfect score: 663  
Sequence: 1 MALWLTVVIALTCLGLASP.....QLVKNLLTYVRGVYRHGNER 131

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 198801 seqs, 68722935 residues

Total number of hits satisfying chosen parameters: 198801

Minimum DB seq length: 0  
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_67:\*  
1: Pirl:\*  
2: Pirl2:\*  
3: Pirl3:\*  
4: Pirl4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	463.5	69.9	146	1 A47481	interleukin-13 pre
2	378.5	57.1	131	2 E30552	T-cell activation
3	378	57.0	131	2 I52290	interleukin-13 - r
4	78.5	11.8	1230	2 T42735	TBP-interacting pr
5	75.5	11.4	482	1 S03904	platelet-derived e
6	75.5	11.4	505	2 E83551	conserved hypothet
7	75	11.3	430	2 S77393	cell division prot
8	74	11.2	261	2 S52110	sepiapterin reduct
9	74	11.2	262	2 A36024	sepiapterin reduct
10	73.5	11.1	586	2 T51211	hypothetical prote
11	73	11.0	701	2 S17196	transcription fact
12	73	11.0	1806	2 T23298	hypothetical prote
13	72.5	10.9	425	2 T50355	hypothetical prote
14	72	10.9	211	1 HSPG1T	histone H1t - pig
15	72	10.9	431	2 S47538	acrosin (EC 3.4.21
16	71.5	10.8	382	1 A60112	42K membrane antig
17	71	10.7	261	2 JQ1176	sepiapterin reduct
18	70	10.6	382	2 S15578	ipac protein - Shi
19	70	10.6	513	1 A35742	aqualysin (EC 3.4.
20	70	10.6	677	2 S15667	transcription fact
21	70	10.6	2195	2 T34264	hypothetical prote
22	69.5	10.5	267	2 JC1339	movement protein -
23	69.5	10.5	1057	2 T38694	probable translati
24	69	10.4	208	2 I70195	histone H1t - rhes
25	69	10.4	323	1 GHRB	Ig gamma chain C r
26	69	10.4	1026	2 T05882	hypothetical prote
27	68.5	10.3	494	2 F82660	penicillin binding
28	68.5	10.3	559	2 T00714	hypothetical prote
29	68.5	10.3	2606	2 T03159	large tegument pro

30 68.5 10.3 2761 2 T21064 hypothetical prote  
31 68 10.3 1004 2 S53939 probable membrane  
32 67 10.1 408 2 C82178 conserved hypothet  
33 67 10.1 481 2 S62423 ATP-dependent RNA  
34 67 10.1 516 2 H72427 DNA mismatch repai  
35 66.5 10.0 459 2 T04808 hypothetical prote  
36 66.5 10.0 585 2 S44851 K12H4.7 protein -  
37 66 10.0 242 2 T12513 hypothetical prote  
38 66 10.0 1037 2 E65022 acriflavin resista  
39 66 10.0 1234 2 G70622 probable transcrip  
40 65.5 9.9 283 2 T25523 hypothetical prote  
41 65.5 9.9 325 2 T16995 probable cinnamyl-  
42 65.5 9.9 326 2 S49937 hypothetical prote  
43 65.5 9.9 540 2 A71610 HSP60 fold T-compl  
44 65.5 9.9 1681 2 S42369 Clathrin heavy cha  
45 65 9.8 99 2 S40012 fill protein - gar

ALIGNMENTS

RESULT 1  
A47481  
interleukin-13 precursor - human  
N;Contains: interleukin 13, short form  
C;Species: Homo sapiens (man)  
C;Date: 21-Jan-1994 #sequence\_revision 06-Dec-1996 #text\_change 22-Jun-1999  
C;Accession: I38060; I38061; A47481  
R;Minty, A.J.; Chalon, P.; Derocq, J.M.; Dumont, X.; Guillemot, J.C.; Kaghad, M.; Lab  
a, P.; Caput, D.  
Nature 362, 248-250, 1993  
A;Title: Interleukin-13 is a new human lymphokine regulating inflammatory and immune  
A;Reference number: I38060; MUID:93211479  
A;Accession: I38060  
A;Status: translated from GB/EMBL/DDBJ  
A;Molecule type: mRNA  
A;Residues: 1-146 <RES>  
A;Cross-references: EMBL:X69079; NID:g297787; PIDN:CAA48823.1; PID:g580330  
A;Accession: I38061  
A;Status: translated from GB/EMBL/DDBJ  
A;Molecule type: mRNA  
A;Residues: 15-146 <RE2>  
A;Cross-references: EMBL:X69079; NID:g297787; PIDN:CAA48824.1; PID:g673420  
R;McKenzie, A.N.; Culpepper, J.A.; de Waal Malefyt, R.; Briere, F.; Punnonen, J.; Ave  
Proc. Natl. Acad. Sci. U.S.A. 90, 3735-3739, 1993  
A;Title: Interleukin 13, a T-cell-derived cytokine that regulates human monocyte and  
A;Reference number: A47481; MUID:93234572  
A;Accession: A47481  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 15-146 <MCK>  
A;Cross-references: GB:L06801; NID:gl86275; PIDN:AAA36107.1; PID:gl86276  
A;Experimental source: Con A-activated CD8+ T-cell clone, A10  
A;Note: sequence extracted from NCBI backbone (NCBIP:129773)  
C;Genetics:  
A;Gene: GDB:IL13; P600; NC30  
A;Cross-references: GDB:138171; OMIM:147683  
A;Map position: 5q31-5q31  
C;Superfamily: interleukin-13  
C;Keywords: alternative initiators; cytokine; glycoprotein  
F;1-146/Product: interleukin-13 precursor, long splice form #status predicted <SIG>  
F;15-146/Product: signal sequence #status predicted <SIG>  
F;25-146/Product: interleukin-13 precursor, short splice form #status predicted <PRS>  
F;52,63,71,86/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 69.9%; Score 463.5; DB 1; Length 146;  
Best Local Similarity 71.8%; Pred. No. 1e-38;  
Matches 94; Conservative 11; Mismatches 25; Indels 1; Gaps 1;  
QY 1 MALWLTVVIALTCLGLASPSVTPPTLKEELVNITQNQ-ASLCNGSMVWSVNLTA 59  
||||| ||||||||| ||||| ||| | :||||||||||||| | |||||||:||||











C;Keywords: glycoprotein; hydrolase; serine proteinase  
F;40-283/Domain: trypsin homology <TRY>

Query Match 10.9%; Score 72; DB 2; Length 431;  
Best Local Similarity 32.3%; Pred. No. 18;  
Matches 20; Conservative 8; Mismatches 26; Indels 8; Gaps 2;

QY 10 ALTCL---GGLASPSVTPSPTLKEELVNITQNASLCSMWWSVNLTAGMYCAAL 66  
| | | | : | | | | : | | : | | : | |  
Db 172 AQTCTVAGWGYVKENAPRPSPTLMEARVDLINL-----ELCNSTQWYNGRITASNLCAGY 226

QY 67 ES 68  
|  
Db 227 PS 228

Search completed: May 13, 2001, 21:48:37  
Job time: 26246 sec







```
GN IL13 OR IL-13.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89093958; PubMed=2521353;
RA Brown K.D., Zurawski S.M., Mosmann T.R., Zurawski G.;
RT "A family of small inducible proteins secreted by leukocytes are
RT members of a new superfamily that includes leukocyte and
RT fibroblast-derived inflammatory agents, growth factors, and
RT indicators of various activation processes.";
RL J. Immunol. 142:679-687(1989).
CC -!- FUNCTION: CYTOKINE. INHIBITS INFLAMMATORY CYTOKINE PRODUCTION.
CC SYNERGIZES WITH IL2 IN REGULATING INTERFERON-GAMMA SYNTHESIS.
CC MAY BE CRITICAL IN REGULATING INFLAMMATORY AND IMMUNE RESPONSES
CC (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: SECRETED.
CC -!- SIMILARITY: BELONGS TO THE IL-4 / IL-13 FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M23504; AAA40149.1; -.
DR PIR; E30552; E30552.
DR HSSP; P35225; 3ITR.
DR MGD; MGI:96541; IL13.
DR InterPro; IPR001325; -.
DR PROSITE; PS00838; INTERLEUKIN_4_13; 1.
KW Cytokine; Glycoprotein; Signal.
FT SIGNAL 1 21 BY SIMILARITY.
FT CHAIN 22 131 INTERLEUKIN-13.
FT DISULFID 51 79 BY SIMILARITY.
FT DISULFID 67 93 BY SIMILARITY.
FT CARBOHYD 42 42 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 52 52 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 75 75 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 131 AA; 14107 MW; 954F93F105713FED CRC64;

Query Match 57.1%; Score 378.5; DB 1; Length 131;
Best Local Similarity 59.0%; Pred. No. 2.8e-31;
Matches 79; Conservative 19; Mismatches 29; Indels 7; Gaps 3;

QY 1 MALWLTWVIALTCGLGSPVTPSP- - - - - TLKELIEELVNITQNQASLCNGSMVWSVN 56
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Db 1 MALWVTAVLALACLGGLAAGVPRSVSLPLTLKELIEELSNTIQDQTPLCNGSMVWSVD 60
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :

QY 57 LTAGMYCAALESLINVDCSAIQRTQRMKALCSQKPAAGQISSERSRDTKIEVIQLVKN 116
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 61 LAAGGFCVALDSLNTISNCNIAIYRTQRIHLHGLCNRK-APTIVSS--LPDTKIEVAHFITK 117
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QY 117 LLTYVRGVYRHGNE 130
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 118 LLSYTKQLFRHGPF 131
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :

RESULT 4
IL13_RAT
ID IL13_RAT STANDARD; PRT; 131 AA.
AC P42203;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE INTERLEUKIN-13 PRECURSOR (IL-13) (T-CELL ACTIVATION PROTEIN P600).
GN IL13 OR IL-13.
OS Rattus norvegicus (Rat).
```

```
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=SPRAGUE-DAWLEY; TISSUE=Kidney cortex;
RX MEDLINE=94092138; PubMed=7916615;
RA Lakkis F.G., Cruet E.N.;
RT "Cloning of rat interleukin-13 (IL-13) cDNA and analysis of IL-13
RT gene expression in experimental glomerulonephritis.";
RL Biochem. Biophys. Res. Commun. 197:612-618(1993).
CC -!- FUNCTION: CYTOKINE. INHIBITS INFLAMMATORY CYTOKINE PRODUCTION.
CC SYNERGIZES WITH IL2 IN REGULATING INTERFERON-GAMMA SYNTHESIS.
CC MAY BE CRITICAL IN REGULATING INFLAMMATORY AND IMMUNE RESPONSES
CC (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: SECRETED.
CC -!- SIMILARITY: BELONGS TO THE IL-4 / IL-13 FAMILY.
CC -----
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CC -----
DR EMBL; L26913; AAA16478.1; -.
DR HSSP; P35225; 3ITR.
DR InterPro; IPR001325; -.
DR PROSITE; PS00838; INTERLEUKIN_4_13; 1.
KW Cytokine; Glycoprotein; Signal.
FT SIGNAL 1 21 BY SIMILARITY.
FT CHAIN 22 131 INTERLEUKIN-13.
FT DISULFID 52 80 BY SIMILARITY.
FT DISULFID 68 94 BY SIMILARITY.
FT CARBOHYD 42 42 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 76 76 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 121 121 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 131 AA; 14093 MW; E5008CAB8DE8C201 CRC64;

Query Match 57.0%; Score 378; DB 1; Length 131;
Best Local Similarity 59.0%; Pred. No. 3.1e-31;
Matches 79; Conservative 20; Mismatches 27; Indels 8; Gaps 4;

QY 1 MALWLTWVIALTCGLGSPSPV- - - - - TPSPTLKELIEELVNITQNQ-ASLCNGSMVWSV 55
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 1 MALWVTAVLALACLGGLATPGVRRSTSPVALRELIEELSNTIQDQKTSLCNSSMVWSV 60
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :

QY 56 NLTAGMYCAALESLINVDCSAIQRTQRMKALCSQKPAAGQISSERSRDTKIEVIQLVK 115
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 61 DLTAGGFCFAALESLTNISCNAIHRQIRILNGLCNQK--ASDVASS-PPDTKIEVAQFIS 117
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :

QY 116 LLTYVRGVYRHGN 129
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 118 KLLNYSKQLFRYGH 131
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :

RESULT 5
TYPH_HUMAN
ID TYPH_HUMAN STANDARD; PRT; 482 AA.
AC P19971; Q13390;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE THYMIDINE PHOSPHORYLASE PRECURSOR (EC 2.4.2.4) (TDRPASE) (TP)
DE (PLATELET-DERIVED ENDOTHELIAL CELL GROWTH FACTOR) (PD-ECGF)
DE (GLIOSTATIN).
GN ECGF1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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FT CONFLICT 669 669 D -> E (IN REF. 2).
SQ SEQUENCE 701 AA; 82014 MW; 7795B29BFE8545E2 CRC64;

Query Match
Best Local Similarity 11.0%; Score 73; DB 1; Length 701;
Matches 21; Conservative 15; Mismatches 14; Indels 16; Gaps 4;

QY 61 MYCAALESLINVSDCSAIQRTQRMKALCSQ-----KPAAGQISSERSRDTKIEVI 111
   |||| I : I : I : ||| ||| I : I : I : I : I : I :
Db 307 MYCA--ELMANMKD---VPSTERMV--LCSQRWKLLSQEKDAYHKKEQKQKDYVELM 359
   : : : : :

QY 112 QLVKNL 117
   : : |||
Db 360 RFLENL 365

RESULT 10
FHOS_HUMAN STANDARD; PRT; 1164 AA.
AC Q9Y613;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE FH1/FH2 DOMAINS-CONTAINING PROTEIN (FORMIN HOMOLOGUE OVEREXPRESSED IN
DE SPLEEN) (PHOS).
GN PHOS.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9228222; PubMed=10352228;
RA Westendorf J.J., Mernaugh R., Hiebert S.W.;
RT "Identification and characterization of a protein containing formin
RT homology (FH1/FH2) domains.";
RL Gene 232:173-182(1999).
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC; PREDOMINANTLY.
CC -!- TISSUE SPECIFICITY: UBIQUITOUS. HIGHLY EXPRESSED IN SPLEEN.
CC -!- SIMILARITY: CONTAINS 1 FORMIN HOMOLOGY 1 (FH1) DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 FORMIN HOMOLOGY 2 (FH2) DOMAIN.
CC -!- SIMILARITY: BELONGS TO THE FORMIN HOMOLOGY FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF113615; AAD39906.1; -.
DR InterPro; IPR003104; -.
DR Pfam; PF02181; FH2; 1.
KW Coiled coil.
FT DOMAIN 487 621 FH1 (PRO-RICH).
FT DOMAIN 594 1069 FH2.
FT DOMAIN 884 921 COILED COIL (POTENTIAL).
FT DOMAIN 583 593 POLY-PRO.
FT DOMAIN 597 605 POLY-PRO.
FT DOMAIN 996 1001 POLY-GLN.
SQ SEQUENCE 1164 AA; 126496 MW; 1BC6ABE3E2E70CB2 CRC64;

Query Match
Best Local Similarity 11.0%; Score 73; DB 1; Length 1164;
Matches 38; Conservative 18; Mismatches 42; Indels 46; Gaps 7;

QY 8 VIALTCLUGGLASPSV-----TPSPTLKEIIEELVNITQNASLC----- 47
   : : | : ||| : | | : ||| | |
Db 768 LMTLASIGGLAARLQLWAFKLDYDSMERETAEPLFDLKVGMQLV---QNATFCILATL 824
```

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QY 48 -----NGSMVWSVNLTAGMYCAALESLINVSDCSAIQRTQRMKALCS-----QKPAAG 96
   ||| : : | : ||| | | : | : ||| : | :
Db 825 LAVGNFLNGSQ-----SSGFELSYLE---KVSDVKDVTVRRQSLHLHLCSLVLQTRPSS 875
   : || : | : ||| | | : |||

QY 97 QISSE--RSRDTKIEVIQLVKNL 117
   : || : | : ||| | | : |||
Db 876 DLYSEIPALTRCAKVDFEQLTENL 899

RESULT 11
H1T_PIG STANDARD; PRT; 211 AA.
ID H1T_PIG
AC P06348;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE HISTONE H1T.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE.
RX MEDLINE=85054795; PubMed=6389534;
RA Cole K.D., York R.G., Kistler W.S.;
RT "The amino acid sequence of boar H1t, a testis-specific H1 histone
RT variant.";
RL J. Biol. Chem. 259:13695-13702(1984).
CC -!- FUNCTION: HISTONES H1 ARE NECESSARY FOR THE CONDENSATION OF
CC NUCLEOSOME CHAINS INTO HIGHER ORDER STRUCTURES.
CC -!- SUBCELLULAR LOCATION: NUCLEAR.
CC -!- DEVELOPMENTAL STAGE: THIS HISTONE IS A TESTIS-SPECIFIC H1 VARIANT
CC THAT APPEARS DURING MEIOSIS IN SPERMATOGENESIS.
CC -!- SIMILARITY: BELONGS TO THE HISTONE H1/H5 FAMILY.
DR PIR; A02581; HSPG1T.
DR HSSP; P08287; IGHC.
DR InterPro; IPR001386; -.
DR Pfam; PF00538; linker_histone; 1.
KW Chromosomal protein; Nuclear protein; DNA-binding; Multigene family;
KW Acetylation; Spermatogenesis; Testis.
FT MOD_RES 1 ACETYLATION.
FT DOMAIN 39 112 GLOBULAR.
SQ SEQUENCE 211 AA; 22059 MW; EACA47C51A8F5364 CRC64;

Query Match
Best Local Similarity 10.9%; Score 72; DB 1; Length 211;
Matches 30; Conservative 16; Mismatches 33; Indels 38; Gaps 4;

QY 16 GLASPSVTPSPTLKEIIEELVNITQNASLCNGSMVWSVNLTAGMYCAALESLINVSDC 75
   || | || : ||| : ||| : |||
Db 30 GLGTSRKAPSASVSKLITEALSVSQER-----AGMSLAALK----- 66

QY 76 SAIQRTQRMKALCSQKPAAGQISSERSRDTKIEVIQLV-KNLLTYVRGVYRHGNFR 131
   ||| ||| : : | : ||| | | : ||| | : | :
Db 67 -----KALA---AAGYDVEKNNSRIKLGKSLVKGKILVQTRGTGASGSFK 109

RESULT 12
ACRO_RABIT STANDARD; PRT; 431 AA.
ID ACRO_RABIT
AC P48038;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE ACROSIN PRECURSOR (EC 3.4.21.10).
GN ACR.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
```









GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: May 13, 2001, 17:48:37 ; Search time 133.94 Seconds  
(without alignments)  
114.635 Million cell updates/sec

Title: US-09-451-527-92  
Perfect score: 663  
Sequence: 1 MALWLTVVIALTCLGGLASP.....QLVKNLITYVRGVYRHGNFR 131

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_15:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_unclassified:\*
- 13: sp\_vertebrate:\*
- 14: sp\_virus:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	663	100.0	131	6	Q9N0W9	Q9n0w9 canis famil
2	398.5	60.1	114	6	Q9TV84	Q9tv84 bos taurus
3	157.5	23.8	49	4	Q9UDC7	Q9udc7 homo sapien
4	82.5	12.4	275	6	Q28609	Q28609 oryctolagus
5	78.5	11.8	1183	4	Q94918	Q94918 homo sapien
6	78.5	11.8	1230	4	Q9P0H7	Q9p0h7 homo sapien
7	78.5	11.8	1230	11	P97536	P97536 rattus norv
8	76	11.5	1448	5	Q9N946	Q9n946 trypanosoma
9	75	11.3	1448	5	Q9N949	Q9n949 trypanosoma
10	74	11.2	415	8	Q9MUM4	Q9mum4 mesostigma
11	73.5	11.1	336	10	Q9SMD4	Q9smd4 lycopersico
12	73.5	11.1	586	3	Q9P3A1	Q9p3a1 neurospora
13	73	11.0	150	14	Q98779	Q98779 vesicular s
14	73	11.0	350	14	Q9Q8P4	Q9q8p4 myxoma viru
15	73	11.0	1164	4	Q9Y613	Q9y613 homo sapien
16	73	11.0	1806	5	O45657	O45657 caenorhabdi
17	72.5	10.9	425	3	Q9P7L2	Q9p7l2 schizosacch
18	72.5	10.9	670	5	Q9N9C4	Q9n9c4 leishmania
19	72	10.9	150	14	Q98791	Q98791 vesicular s

20	72	10.9	438	10	Q9M3H8	Q9m3h8 cicer ariet
21	71	10.7	150	14	Q98780	Q98780 vesicular s
22	71	10.7	150	14	Q98787	Q98787 vesicular s
23	71	10.7	150	14	Q98789	Q98789 vesicular s
24	71	10.7	718	5	O18412	O18412 drosophila
25	71	10.7	1596	13	Q9I8E1	Q9i8e1 fugu rubrip
26	70.5	10.6	156	14	Q9IWI4	Q9iwi4 crimean-con
27	70.5	10.6	1510	5	Q9VX92	Q9vx92 drosophila
28	70	10.6	274	14	Q89048	Q89048 vesicular s
29	70	10.6	925	10	Q9SIX4	Q9six4 arabidopsi
30	70	10.6	1449	5	Q9N937	Q9n937 trypanosoma
31	69.5	10.5	424	5	Q9NEI5	Q9nei5 caenorhabdi
32	69.5	10.5	425	4	Q95810	Q95810 homo sapien
33	69.5	10.5	1057	3	O14134	O14134 schizosacch
34	69	10.4	209	2	Q9X561	Q9x561 enterococcu
35	69	10.4	431	4	Q9NV02	Q9nv02 homo sapien
36	69	10.4	665	11	O61003	O61003 mus musculu
37	69	10.4	1026	10	O49529	O49529 arabidopsi
38	68.5	10.3	475	2	Q9RAB9	Q9rab9 rickettsia
39	68.5	10.3	494	2	Q9PCZ0	Q9pcz0 xylella fas
40	68.5	10.3	2606	14	O36414	O36414 alcelaphine
41	68.5	10.3	2761	5	Q19522	Q19522 caenorhabdi
42	68	10.3	150	14	Q98778	Q98778 vesicular s
43	68	10.3	1063	5	Q9VWL7	Q9vwl7 drosophila
44	68	10.3	1790	5	Q9VUH6	Q9vuh6 drosophila
45	67.5	10.2	198	4	Q9UBB1	Q9ubb1 homo sapien

ALIGNMENTS

RESULT 1

Q9NOW9

ID Q9NOW9 PRELIMINARY; PRT; 131 AA.

AC Q9NOW9;

DT 01-OCT-2000 (TremBLrel. 15, Created)

DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)

DT 01-OCT-2000 (TremBLrel. 15, Last annotation update)

DE INTERLEUKIN-13.

OS Canis familiaris (Dog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

OX NCBI\_TaxID=9615;

RN [1]

RP SEQUENCE FROM N.A.

RA Yang S., Boroughs K.L., McDermott M.J.;

RT "Canine Interleukin-13: Molecular Cloning of Full-Length cDNA and Expression of Biologically Active Recombinant Protein.";

RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF244915; AAF63204.1; -

SQ SEQUENCE 131 AA; 14268 MW; 9A142B4D0F80370F CRC64;

Query Match 100.0%; Score 663; DB 6; Length 131;  
Best Local Similarity 100.0%; Pred. No. 1.3e-61;  
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MALWLTVVIALTCLGGLASPSVPTLKEI	ELVNITQNQASLCNGSMW	SVNLTAG 60
Db	1	MALWLTVVIALTCLGGLASPSVPTLKEI	ELVNITQNQASLCNGSMW	SVNLTAG 60
QY	61	MYCAALES	LINVSDCSAIQRTQRMKALCSQKPAAGQISSERSRDTKIEVIQLVKNLLTY	120
Db	61	MYCAALES	LINVSDCSAIQRTQRMKALCSQKPAAGQISSERSRDTKIEVIQLVKNLLTY	120
QY	121	VRGVYRHGNFR	131	
Db	121	VRGVYRHGNFR	131	

RESULT 2

Q9TV84

ID Q9TV84 PRELIMINARY; PRT; 114 AA.

```
AC Q9TV84;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE INTERLEUKIN-13 PRECURSOR (FRAGMENT).
CN IL-13.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Trigon W.T., Hirano A., Brown W.;
RT "Biological activities of interleukin-13 (IL-13) on bovine lymphocytes: implications for signaling through IL-13R1.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF072807; AAD22748.1; -.
DR HSSP; P35225; 3ITR.
DR INTERPRO; IPR001325; -.
DR PROSITE; PS00838; INTERLEUKIN_4_13; UNKNOWN_1.
FT NON_TER 114 114
SQ SEQUENCE 114 AA; 12355 MW; D8CC56E5627D030A CRC64;

Query Match 60.1%; Score 398.5; DB 6; Length 114;
Best Local Similarity 71.7%; Pred. No. 4e-34;
Matches 81; Conservative 10; Mismatches 21; Indels 1; Gaps 1;

QY 1 MALWLTVVIALTCGLGLASPSVPTSPPTLKELIEELVNITQ-NQ-ASLCNGSMVWSVNLTA 59
Db 1 MALLLTAVIVLCFGGLTSPSPVPSATALKELIEELVNITQNKVPLCNGSMVWSNLITS 60

QY 60 GMYCAALESLINVSDCSAIQRTQRLKALCSQKPAAGQISSERSRDTKIEVIQ 112
Db 61 SMYCAALDSLISNCSVQRTKRLNALCPHPSAKQVSSEYVRDTKIEVAQ 113

RESULT 3
Q9UDC7 PRELIMINARY; PRT; 49 AA.
AC Q9UDC7;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE P600 HOMOLOG.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93027259; PubMed=1408833;
RA Morgan J.G., Dolganov G.M., Robbins S.E., Hinton L.M., Lovett M.;
RT "The selective isolation of novel cDNAs encoded by the regions surrounding the human interleukin 4 and 5 genes.";
RL Nucleic Acids Res. 20:5173-5179(1992).
DR HSSP; P35225; 3ITR.
SQ SEQUENCE 49 AA; 5109 MW; 679CD23A190C778E CRC64;

Query Match 23.8%; Score 157.5; DB 4; Length 49;
Best Local Similarity 71.4%; Pred. No. 2e-09;
Matches 35; Conservative 1; Mismatches 12; Indels 1; Gaps 1;

QY 1 MALWLTVVIALTCGLGLASPSVPTSPPTLKELIEELVNITQ-NQ-ASLCN 48
Db 1 MALLLTVIALACLGFDSPGPVPPSTALRELIEELSNITQTQKAPLCN 49

RESULT 4
Q28609 PRELIMINARY; PRT; 275 AA.
ID Q28609
```

```
AC Q28609;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE PUTATIVE PREPROSPERMINOGEN PRECURSOR.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NEW ZEALAND WHITE; TISSUE=TESTIS;
RX MEDLINE=94368861; PubMed=8086468;
RA Richardson R.T., O'Rand M.G.;
RT "Cloning and sequencing of cDNAs for rabbit preproacrosin and a novel preproacrosin-related cDNA.";
RL Biochim. Biophys. Acta 1219:215-218(1994).
DR EMBL; U05203; AAA61629.1; -.
DR HSSP; P00734; 2HNT.
DR INTERPRO; IPR001254; -.
DR PFAM; PF00089; trypsin; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
KW Signal.
FT SIGNAL 1 16 POTENTIAL.
FT CHAIN 17 275 PROSPERMINOGEN.
SQ SEQUENCE 275 AA; 29965 MW; 8FC2467414069C61 CRC64;

Query Match 12.4%; Score 82.5; DB 6; Length 275;
Best Local Similarity 30.0%; Pred. No. 0.91;
Matches 24; Conservative 12; Mismatches 35; Indels 9; Gaps 3;

QY 10 ALTCL---GGLASPSVPTSPPTLKELIEELVNITQNASLCNGSMVWSVNLTAGMYCAAL 66
Db 172 AQTCYVAGWGYVKENAPRPSPTLMEARVDLINL-----ELCNSTQWYNGRITASNLCAGY 226

QY 67 ESLINVSDCSAIQRTQRLK 86
Db 227 PS-GKIDTCQRLQQLVEVLK 245

RESULT 5
O94918 PRELIMINARY; PRT; 1183 AA.
ID O94918
AC O94918;
DT 01-MAY-1999 (TReMBLrel. 10, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
DE KIAA0829 PROTEIN (FRAGMENT).
GN KIAA0829.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=99156230; PubMed=10048485;
RA Nagase T., Ishikawa K., Suyama M., Kikuno R., Hirose M.,
RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XII. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";
RL DNA Res. 5:355-364(1998).
DR EMBL; AB020636; BAA74852.1; -.
FT NON_TER 1 1
SQ SEQUENCE 1183 AA; 130962 MW; 1FE0EE56C0DFFE3A CRC64;

Query Match 11.8%; Score 78.5; DB 4; Length 1183;
Best Local Similarity 31.0%; Pred. No. 12;
Matches 39; Conservative 19; Mismatches 51; Indels 17; Gaps 5;
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QY 5 LTVVIALTCGLGLASPSVTPSPPTLKEIEELVN-ITQNASLNGSMV-----WSV 55  
||| ||| : | || : | || : | : : ||| : | ||| : |  
Db 579 LTTVKALTLIAG--SPLKIDLRPVLGEGVPILASFLRKNQRAKLGTLKSALDILIKNYS 636  
QY 56 NLTAGMYCAALES---LINVSDCSAIQRTQRMKALCSQKPAAGQISSERSRDTKIEVIQ 112  
: ||| | | | : ||| : | | | : ||| : | | : | | : | |  
Db 637 SLTAAMIDAVLDELPLPPLISESDMHVSQMAISFLTTLAKVYPSS---LSKISGSILNELIG 693  
QY 113 LVKNLL 118  
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Db 694 LVRSP 699  
RESULT 6  
Q9P0H7 PRELIMINARY; PRT; 1230 AA.  
ID Q9P0H7  
AC Q9P0H7;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)  
DE TIP120 PROTEIN.  
GN TIP120.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=ADRENAL GLAND;  
RA Fu S., Li Y., Wu T., Peng Y., Gu Y., Zhang L., Jiang C., Huang C.,  
RA Han Z., Fu G., Chen Z., Wang Y.;  
RT "A novel gene expressed in the human adrenal gland.";  
RL Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=ADRENAL GLAND;  
RA Ren S., Shi J., Huang C., Jiang C., Li Y., Zhou J., Yu Y., Xu S.,  
RA Wang Y., Fu G., Chen Z., Han Z.;  
RL Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AF157326; AAF67492.1; -  
SQ SEQUENCE 1230 AA; 136360 MW; A3ACF0E99B99A1D7 CRC64;

Query Match 11.8%; Score 78.5; DB 4; Length 1230;  
Best Local Similarity 31.0%; Pred. No. 13;  
Matches 39; Conservative 19; Mismatches 51; Indels 17; Gaps 5;

QY 5 LTVVIALTCGLGLASPSVTPSPPTLKEIEELVN-ITQNASLNGSMV-----WSV 55  
||| ||| : | || : | || : | : : ||| : | ||| : |  
Db 626 LTTVKALTLIAG--SPLKIDLRPVLGEGVPILASFLRKNQRAKLGTLKSALDILIKNYS 683  
QY 56 NLTAGMYCAALES---LINVSDCSAIQRTQRMKALCSQKPAAGQISSERSRDTKIEVIQ 112  
: ||| | | | : ||| : | | | : ||| : | | : | | : | |  
Db 684 SLTAAMIDAVLDELPLPPLISESDMHVSQMAISFLTTLAKVYPSS---LSKISGSILNELIG 740  
QY 113 LVKNLL 118  
||| : |  
Db 741 LVRSP 746  
RESULT 7  
P97536 PRELIMINARY; PRT; 1230 AA.  
ID P97536  
AC P97536;  
DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
DE TIP120.  
GN TIP120.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;

RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97127450; PubMed=8954946;  
RA Yogosawa S., Makino Y., Yoshida T., Kishimoto T., Muramatsu M.,  
RA Tamura T.;  
RT "Molecular cloning of a novel 120-kDa TBP-interacting protein.";  
RL Biochem. Biophys. Res. Commun. 229:612-617(1996).  
DR EMBL; D87671; BAA13432.1; -  
SQ SEQUENCE 1230 AA; 136360 MW; A3ACF0E99B99A1D7 CRC64;

Query Match 11.8%; Score 78.5; DB 11; Length 1230;  
Best Local Similarity 31.0%; Pred. No. 13;  
Matches 39; Conservative 19; Mismatches 51; Indels 17; Gaps 5;

QY 5 LTVVIALTCGLGLASPSVTPSPPTLKEIEELVN-ITQNASLNGSMV-----WSV 55  
||| ||| : | || : | || : | : : ||| : | ||| : |  
Db 626 LTTVKALTLIAG--SPLKIDLRPVLGEGVPILASFLRKNQRAKLGTLKSALDILIKNYS 683  
QY 56 NLTAGMYCAALES---LINVSDCSAIQRTQRMKALCSQKPAAGQISSERSRDTKIEVIQ 112  
: ||| | | | : ||| : | | | : ||| : | | : | | : | |  
Db 684 SLTAAMIDAVLDELPLPPLISESDMHVSQMAISFLTTLAKVYPSS---LSKISGSILNELIG 740  
QY 113 LVKNLL 118  
||| : |  
Db 741 LVRSP 746  
RESULT 8  
Q9N946 PRELIMINARY; PRT; 1448 AA.  
ID Q9N946  
AC Q9N946;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)  
DE POSSIBLE PUTATIVE ADENYLATE CYCLASE REGULATORY PROTEIN.  
GN CHR1.19.  
OS Trypanosoma brucei.  
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.  
OX NCBI\_TaxID=5691;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=TREU927;  
RA Hall N., Bowman S., Quail M., Ivens A.C., Kay M.P., Bray-Allen S.,  
RA Lennard N.J., Clark L.N., Harris B.R., Melville S., Lawson D.,  
RA Gerrard C., Rajandream M.A., Barrell B.G.;  
RL Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AL359782; CAB95333.1; -  
SQ SEQUENCE 1448 AA; 160479 MW; 688B26228AD2046B CRC64;

Query Match 11.5%; Score 76; DB 5; Length 1448;  
Best Local Similarity 29.0%; Pred. No. 28;  
Matches 36; Conservative 18; Mismatches 34; Indels 36; Gaps 7;

QY 13 CLGGLASPSVTPSPPTLKEIEELVNITQNA--SLCNGSMVWSVNL-----TAGMYCA 64  
||| | | | : ||| : | | | : ||| : | | : | | : | |  
Db 557 CLGNL-----POLKMLDLSGTN-TDNESLRSCLSLQTVVSLNLSHCWKMTNVSHIS 606  
QY 65 ALES--INVSDC-----SAIQRTQRMKALCSQKPAAGQISSERSRDTKIEVIQ 115  
: ||| : | : | : | | | : ||| : | : | : | : | : | : | : |  
Db 607 SLEALNELNSCIRINAGWEAIEKIQQLHVAI-----LSNTHITDRDISHFSKCK 657  
QY 116 NLLT 119  
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Db 658 NLVT 661  
RESULT 9  
Q9N949 PRELIMINARY; PRT; 1448 AA.  
ID Q9N949  
AC Q9N949;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)







Job time: 43951 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 13, 2001, 17:47:33 ; Search time 79.9 Seconds  
(without alignments)  
79.413.Million cell updates/sec

Title: US-09-451-527-97  
Perfect score: 561  
Sequence: 1 SPVTPSPTLKELIELVNIT.....QLVKNLLTYVRGVYRHGNFR 111

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 390729 seqs, 57163235 residues

Total number of hits satisfying chosen parameters: 390729

Minimum DB seq length: 0  
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_0401.\*  
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2: /cgnl\_8/gcgdata/geneseq/geneseqp/AA1981.DAT:\*  
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4: /cgnl\_8/gcgdata/geneseq/geneseqp/AA1983.DAT:\*  
5: /cgnl\_8/gcgdata/geneseq/geneseqp/AA1984.DAT:\*  
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10: /cgnl\_8/gcgdata/geneseq/geneseqp/AA1989.DAT:\*  
11: /cgnl\_8/gcgdata/geneseq/geneseqp/AA1990.DAT:\*  
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22: /cgnl\_8/gcgdata/geneseq/geneseqp/AA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	561	100.0	111	21 Y58222	Canine mature inte
2	561	100.0	131	21 Y58221	Canine interleukin
3	545.5	97.2	110	21 Y58224	Canine mature inte
4	545.5	97.2	130	21 Y58223	Canine interleukin
5	382.5	68.2	112	13 R27347	Protein with cytot
6	382.5	68.2	112	17 R92793	Human interleukin-
7	382.5	68.2	132	15 R48624	Sequence of human
8	375.5	66.9	112	13 R27346	Protein with cytot
9	375.5	66.9	146	13 R27348	Cytokine NC30. R
10	367	65.4	111	17 R92794	Human interleukin-
11	295.5	52.7	131	15 R48625	Sequence of mouse

12	292.5	52.1	111	17	R92795	Murine P600. Mus
13	71.5	12.7	382	21	Y84919	Amino acid sequenc
14	67	11.9	21	20	Y49702	Human interleukin
15	65.5	11.7	279	21	B44998	Human secreted pro
16	65.5	11.7	286	21	Y58998	Wheat sulfite redu
17	65.5	11.7	330	21	G06262	Arabidopsis thalia
18	65.5	11.7	407	21	G06261	Arabidopsis thalia
19	65	11.6	482	19	W62025	Recombinantly prod
20	65	11.6	2404	20	W30640	HIV-1-NC7 envelope
21	64.5	11.5	267	22	Y71919	Alternative versio
22	64.5	11.5	268	16	R78388	Tobacco mosaic vir
23	64.5	11.5	268	19	W71250	Protein sequence o
24	64.5	11.5	268	22	Y71917	Wild type viral mo
25	64.5	11.5	268	22	Y71920	Alternative versio
26	64.5	11.5	472	15	R56447	TMV replicon-encod
27	64.5	11.5	485	19	W71249	Protein encoded by
28	64.5	11.5	634	20	Y21548	Human heparin-bind
29	63.5	11.3	229	22	B63822	Human prostate can
30	63.5	11.3	299	21	G30635	Arabidopsis thalia
31	63.5	11.3	299	21	G45468	Arabidopsis thalia
32	63.5	11.3	312	21	G30634	Arabidopsis thalia
33	63.5	11.3	357	21	G30633	Arabidopsis thalia
34	63.5	11.3	514	21	G55503	Arabidopsis thalia
35	63.5	11.3	602	21	G55502	Arabidopsis thalia
36	63.5	11.3	620	21	G55501	Arabidopsis thalia
37	63.5	11.3	673	21	Y58996	Rice sulfite reduc
38	63.5	11.3	889	21	Y95988	Moraxella catarrha
39	63.5	11.3	919	21	Y95987	Moraxella catarrha
40	63.5	11.3	1032	21	G45673	Arabidopsis thalia
41	63.5	11.3	1045	21	G45672	Arabidopsis thalia
42	63.5	11.3	1090	21	G45671	Arabidopsis thalia
43	63.5	11.3	1461	19	W64468	Human secreted pro
44	63	11.2	101	21	B53687	Human colon cancer
45	63	11.2	168	21	B35513	Baculovirus RNA ba

ALIGNMENTS

RESULT	1
Y58222	
ID	Y58222 standard; Protein; 111 AA.
XX	
AC	Y58222;
XX	
DT	14-MAR-2000 (first entry)
XX	
DE	Canine mature interleukin-13 (IL-13) clone 80.
XX	
KW	Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;
KW	immunoregulation; tumour; cancer; autoimmune disease; vaccine.
XX	
OS	Canis familiaris.
XX	
PN	WO9961618-A2.
XX	
PD	02-DEC-1999.
XX	
PF	28-MAY-1999; 99WO-US11942.
XX	
PR	29-MAY-1998; 98US-0087306.
XX	
PA	(HESK-) HESKA CORP.
XX	
PI	Sim G, Yang S, Dreitz MJ, Wonderling RS;
XX	
DR	WPI; 2000-072623/06.
DR	N-PSDB; Z55559, Z55560.
XX	
PT	Nucleic acids encoding immunoregulatory proteins from cats or dogs,
PT	useful for treating or preventing e.g. tumors or autoimmune disease
XX	
PS	Claim 31; Page 234; 264pp; English.



XX Sequences Y58221-Y58222 and Y58223-Y58224 represent encoded and mature  
CC canine interleukin-13 (IL-13) clones 80 and 78. The invention relates to  
CC canine IL-4, canine or feline Flt-3 ligand, canine or feline CD40,  
CC canine IL-4, canine or feline Flt-3 ligand, canine or feline CD40,  
CC canine or feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline  
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage  
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these  
CC immunoregulatory proteins. The proteins, their associated  
CC nucleic acids, specific antibodies and inhibitors may be used as  
CC vaccines for therapeutic or prophylactic regulation of an immune  
CC response in animals (particularly cats, dogs, horses and humans).  
CC They may be used to treat autoimmune or infectious diseases including  
CC allergies, tumours, inflammation and graft rejection, and to increase  
CC the response from a co-administered antigen. The nucleotide sequences  
CC can also be used for the recombinant production of a protein, while  
CC nucleotide fragments are useful as probes, as amplification primers and  
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
CC The proteins may be used to raise antibodies and to screen for  
CC modulators of activity, while the antibodies may be used in detection,  
CC and in drug targeting.  
XX  
SQ Sequence 111 AA;

Query Match 100.0%; Score 561; DB 21; Length 111;  
Best Local Similarity 100.0%; Pred. No. 1.1e-60;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SPVTPSPTLKELIEELVNITQNQASLCNGSMVWSVNLTAGMYCAALESLINVSDCSAIQR 60  
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Db 1 spvtpspptlkelieelvnitqnqaslcngsmvwsvnltagmycaaleslinvsdcsaigr 60  
QY 61 TQRLKALCSQKPAAGQISSERSRDTKIEVIQLVKNLLTYVYRGVYRHGNFR 111  
|||||  
Db 61 tqrlmkalcsqkpaagqissersrdrtdkievqlvknlltyvrgvyrhgnfr 111

RESULT 2  
Y58221  
ID Y58221 standard; Protein; 131 AA.  
XX  
AC Y58221;  
XX  
DT 14-MAR-2000 (first entry)  
XX  
DE Canine interleukin-13 (IL-13) clone 80.  
XX Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;  
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine.  
KW  
XX Canis familiaris.  
OS  
XX WO9961618-A2.  
PN  
XX 02-DEC-1999;  
XX  
PD 28-MAY-1999; 99WO-US11942.  
XX  
PF 29-MAY-1998; 98US-0087306.  
XX  
PR (HESK-) HESKA CORP.  
XX  
PA Sim G, Yang S, Dreitz MJ, Wonderling RS;  
XX  
PI WPI; 2000-072623/06.  
XX  
DR N-PSDB; 255555, 255557, 255558.  
DR  
XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
PT useful for treating or preventing e.g. tumors or autoimmune disease  
PT  
XX Claim 3i; Page 231; 264pp; English.  
PS  
XX Sequences Y58221-Y58222 and Y58223-Y58224 represent encoded and mature

CC canine interleukin-13 (IL-13) clones 80 and 78. The invention relates to  
CC canine IL-4, canine or feline Flt-3 ligand, canine or feline CD40,  
CC canine or feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline  
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage  
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these  
CC immunoregulatory proteins. The proteins, their associated  
CC nucleic acids, specific antibodies and inhibitors may be used as  
CC vaccines for therapeutic or prophylactic regulation of an immune  
CC response in animals (particularly cats, dogs, horses and humans).  
CC They may be used to treat autoimmune or infectious diseases including  
CC allergies, tumours, inflammation and graft rejection, and to increase  
CC the response from a co-administered antigen. The nucleotide sequences  
CC can also be used for the recombinant production of a protein, while  
CC nucleotide fragments are useful as probes, as amplification primers and  
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
CC The proteins may be used to raise antibodies and to screen for  
CC modulators of activity, while the antibodies may be used in detection,  
CC and in drug targeting.  
XX  
SQ Sequence 131 AA;

Query Match 100.0%; Score 561; DB 21; Length 131;  
Best Local Similarity 100.0%; Pred. No. 1.4e-60;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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|||||  
Db 21 spvtpspptlkelieelvnitqnqaslcngsmvwsvnltagmycaaleslinvsdcsaigr 80  
QY 61 TQRLKALCSQKPAAGQISSERSRDTKIEVIQLVKNLLTYVYRGVYRHGNFR 111  
|||||  
Db 81 tqrlmkalcsqkpaagqissersrdrtdkievqlvknlltyvrgvyrhgnfr 131

RESULT 3  
Y58224  
ID Y58224 standard; Protein; 110 AA.  
XX  
AC Y58224;  
XX  
DT 14-MAR-2000 (first entry)  
XX  
DE Canine mature interleukin-13 (IL-13) clone 78.  
XX  
DE Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;  
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine.  
KW  
XX Canis familiaris.  
OS  
XX WO9961618-A2.  
PN  
XX 02-DEC-1999.  
XX  
PD 28-MAY-1999; 99WO-US11942.  
XX  
PF 29-MAY-1998; 98US-0087306.  
XX  
PR (HESK-) HESKA CORP.  
XX  
PA Sim G, Yang S, Dreitz MJ, Wonderling RS;  
XX  
PI WPI; 2000-072623/06.  
XX  
DR N-PSDB; 255565, 255566.  
DR  
XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
PT useful for treating or preventing e.g. tumors or autoimmune disease  
PT  
XX Claim 3i; Page 240; 264pp; English.  
PS  
XX Sequences Y58221-Y58222 and Y58223-Y58224 represent encoded and mature  
CC canine interleukin-13 (IL-13) clones 80 and 78. The invention relates to  
CC canine IL-4, canine or feline Flt-3 ligand, canine or feline CD40,

CC canine or feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline  
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage  
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these  
CC immunoregulatory proteins. The proteins, their associated  
CC nucleic acids, specific antibodies and inhibitors may be used as  
CC vaccines for therapeutic or prophylactic regulation of an immune  
CC response in animals (particularly cats, dogs, horses and humans).  
CC They may be used to treat autoimmune or infectious diseases including  
CC allergies, tumours, inflammation and graft rejection, and to increase  
CC the response from a co-administered antigen. The nucleotide sequences  
CC can also be used for the recombinant production of a protein, while  
CC nucleotide fragments are useful as probes, as amplification primers and  
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
CC The proteins may be used to raise antibodies and to screen for  
CC modulators of activity, while the antibodies may be used in detection,  
CC and in drug targeting.  
XX  
SQ Sequence 110 AA;  
  
Query Match 97.2%; Score 545.5; DB 21; Length 110;  
Best Local Similarity 99.1%; Pred. No. 8.6e-59;  
Matches 110; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
  
QY 1 SPVTPSPTLKEELVNITQNQASLCNGSMVSVNLTAGMYCAALESLINVSDCSAIQR 60  
Db 1 spvtspptlkelieelvnitqngaslcngsmvsvnltagmycaaleslinvdsaiqr 60  
  
QY 61 TQRLKALCSQKPAAGQISSERSRDTKIEVIQLVKNLLTYVRGVYRHGNFR 111  
Db 61 tqrlmkalcsqkpaag-issersrdtkieviqlvknlltyvrgvyrhgnfr 110  
  
RESULT 4  
Y58223  
ID Y58223 standard; Protein; 130 AA.  
XX  
AC Y58223;  
XX  
DT 14-MAR-2000 (first entry)  
XX  
DE Canine interleukin-13 (IL-13) clone 78.  
XX  
DE Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;  
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine.  
XX  
OS Canis familiaris.  
XX  
PN WO9961618-A2.  
XX  
PD 02-DEC-1999.  
XX  
PF 28-MAY-1999; 99WO-US11942.  
XX  
PR 29-MAY-1998; 98US-0087306.  
XX  
PA (HESK-) HESKA CORP.  
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;  
XX  
DR WPI; 2000-072623/06.  
DR N-PSDB; 255561, 255562, 255563, 255564.  
XX  
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
PT useful for treating or preventing e.g. tumors or autoimmune disease -  
XX  
PS Claim 3i; Page 237; 264pp; English.  
XX  
CC Sequences Y58221-Y58222 and Y58223-Y58224 represent encoded and mature  
CC canine interleukin-13 (IL-13) clones 80 and 78. The invention relates to  
CC canine IL-4, canine or feline Flt-3 ligand, canine or feline CD40,  
CC canine or feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline  
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage

CC colony-stimulating factor (GM-CSF), and nucleotides which encode these  
CC immunoregulatory proteins. The proteins, their associated  
CC nucleic acids, specific antibodies and inhibitors may be used as  
CC vaccines for therapeutic or prophylactic regulation of an immune  
CC response in animals (particularly cats, dogs, horses and humans).  
CC They may be used to treat autoimmune or infectious diseases including  
CC allergies, tumours, inflammation and graft rejection, and to increase  
CC the response from a co-administered antigen. The nucleotide sequences  
CC can also be used for the recombinant production of a protein, while  
CC nucleotide fragments are useful as probes, as amplification primers and  
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
CC The proteins may be used to raise antibodies and to screen for  
CC modulators of activity, while the antibodies may be used in detection,  
CC and in drug targeting.  
XX  
SQ Sequence 130 AA;  
  
Query Match 97.2%; Score 545.5; DB 21; Length 130;  
Best Local Similarity 99.1%; Pred. No. 1.1e-58;  
Matches 110; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
  
QY 1 SPVTPSPTLKEELVNITQNQASLCNGSMVSVNLTAGMYCAALESLINVSDCSAIQR 60  
Db 21 spvtspptlkelieelvnitqngaslcngsmvsvnltagmycaaleslinvdsaiqr 80  
  
QY 61 TQRLKALCSQKPAAGQISSERSRDTKIEVIQLVKNLLTYVRGVYRHGNFR 111  
Db 81 tqrlmkalcsqkpaag-issersrdtkieviqlvknlltyvrgvyrhgnfr 130  
  
RESULT 5  
R27347  
ID R27347 standard; Protein; 112 AA.  
XX  
AC R27347;  
XX  
DT 24-FEB-1993 (first entry)  
XX  
DE Protein with cytokine activity encoded by Nal'.  
XX  
KW Interleukin; chemotaxis; immunomodulation; inflammation.  
XX  
PN EP506574-A.  
XX  
PD 30-SEP-1992.  
XX  
PF 27-MAR-1992; 92EP-0400858.  
XX  
PR 29-MAR-1991; 91FR-0003904.  
PR 08-JAN-1992; 92FR-0000137.  
XX  
PA (SNFI ) ELF SANOFI.  
XX  
PI Caput D, Ferrara P, Guillemot J, Kaghad M, Labit-le Bouteiller C;  
PI Leplatois P, Magazin M, Minty A;  
XX  
DR WPI; 1992-325841/40.  
DR N-PSDB; Q28944.  
XX  
PT New cytokine having immunomodulatory activity - useful for  
PT treating tumours and infectious or inflammatory conditions  
XX  
PS Claim 1; Page 60; 78pp; French.  
XX  
CC This protein is one of two possible forms of a new cytokine  
CC produced by T lymphocytes induced by phorbol-2-myristate-3-acetate  
CC and phytohaemagglutinin. The proteins differ only in the amino acid  
CC at position 41 which is either Asp or Gly. The cytokine acts on  
CC monocytes and B lymphocytes and is useful in treatment of tumours  
CC and some infections and inflammatory conditions.  
CC See Q28941-Q28947.  
XX

SQ Sequence 112 AA;

Query Match 68.2%; Score 382.5; DB 13; Length 112;  
Best Local Similarity 70.0%; Pred. No. 6.4e-39;  
Matches 77; Conservative 11; Mismatches 21; Indels 1; Gaps 1;

QY 2 PVTPSPTLKELIEELVNITQNO-ASLCNGSMVWSVNLTAGMYCAALESINVSDCSAIQR 60  
|| || :||||| ||||| | ||||| :||||| ||||| ||||| ||||| :||| :  
Db 2 pvpstalrelieelvnitgnqkaplcngsmvwsinltagmycaaleslinvsgcsaiek 61

QY 61 TQRLKALCSQKPAAGQISSERSRDTKIEVIQLVKNLLTYVRGVYRHGNF 110  
|||| | :||| || ||||| | ||||| :||| :||| | |  
Db 62 tqrlsgfcphkvsagqfsslhvrdtkievagfvkdlllhkklfregrf 111

RESULT 6  
R92793  
ID R92793 standard; Protein; 112 AA.  
XX  
AC  
XX  
XX  
DT 24-MAY-1996 (first entry)  
XX  
DE Human interleukin-13 mutein 1.  
XX  
DE Cytokine; mutein; interleukin-13; IL-13; agonist; antagonist;  
KW diagnosis; therapy; cancer; inflammation; degenerative disease.  
KW  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 11 /note= "Glu at position 11 may be replaced by an  
FT amidated amino acid, including Lys"  
FT  
FT Misc-difference 64 /note= "Arg at position 64 may be replaced by an  
FT acidic amino acid, including Asp"  
FT  
XX  
PN WO9604306-A2.  
XX  
PD 15-FEB-1996.  
XX  
PF 31-JUL-1995; 95WO-US08950.  
XX  
PR 01-AUG-1994; 94US-0284393.  
XX  
PA (SCHE ) SCHERING CORP.  
XX  
PI Zurawski G, Zurawski SM;  
XX  
DR WPI; 1996-129335/13.  
XX  
PT Mutein(s) of human and murine cytokine(s), esp. interleukin(s) and  
PT murine P600 contg. amino acid substitutions. - useful for the  
PT diagnosis and treatment of cancer, inflammation, etc.  
XX  
PS Claim 12; Page 46; 52pp; English.  
XX  
CC Muteins 1 and 2 (R92793-94) of human interleukin-13 (IL-13) contain  
CC amino acid substitutions at amino acid position 11 in helix A and/or  
CC at position 64 in helix C. They are obtd. by site-directed  
CC mutagenesis of natural IL-13 sequences. The muteins antagonise the  
CC activity of IL-13 or IL-4. They have partial cytokine agonist  
CC activity, exhibit less than 80% maximal agonist activity of natural  
CC IL-2, and/or antagonize cytokine activity by least about 50% when  
CC present at a 100-fold excess. They and other cytokine muteins  
CC (see also R92790-92, R92795-802) are useful in the screening of  
CC cytokine and cytokine receptor levels, and in the diagnosis or  
CC treatment of e.g. inflammation, cancer, and degenerative disorders.  
XX  
SQ Sequence-- 112 AA;

Query Match 68.2%; Score 382.5; DB 17; Length 112;  
Best Local Similarity 70.0%; Pred. No. 6.4e-39;  
Matches 77; Conservative 11; Mismatches 21; Indels 1; Gaps 1;

QY 2 PVTPSPTLKELIEELVNITQNO-ASLCNGSMVWSVNLTAGMYCAALESINVSDCSAIQR 60  
|| || :||||| ||||| | ||||| :||||| ||||| ||||| ||||| :||| :  
Db 2 pvpstalrelieelvnitgnqkaplcngsmvwsinltagmycaaleslinvsgcsaiek 61

QY 61 TQRLKALCSQKPAAGQISSERSRDTKIEVIQLVKNLLTYVRGVYRHGNF 110  
|||| | :||| || ||||| | ||||| :||| :||| | |  
Db 62 tqrlsgfcphkvsagqfsslhvrdtkievagfvkdlllhkklfregrf 111

RESULT 7  
R48624  
ID R48624 standard; Protein; 132 AA.  
XX  
AC R48624;  
XX  
XX  
DT 14-SEP-1994 (first entry)  
XX  
DE Sequence of human interleukin-13 (IL-13).  
XX  
KW Interleukin-13; lymphokine; immunological disorder; therapy;  
KW diagnostic.  
XX  
OS Homo sapiens.  
XX  
PN WO9404680-A.  
XX  
PD 03-MAR-1994.  
XX  
PF 18-AUG-1993; 93WO-US07645.  
XX  
PR 21-AUG-1992; 92US-0933416.  
PR 29-JAN-1993; 93US-0010977.  
PR 01-FEB-1993; 93US-0012543.  
XX  
PA (SCHE ) SCHERING CORP.  
XX  
PI Aversa G, Banchereau J, Briere F, Coffman RL, Cooks BG;  
PI Culpepper, Dang W, De Vries J, De Waal Malefyt R;  
PI Doherty TM, Heath A, Mckenzie A, Punnonen J, Zurawski G;  
XX  
DR WPI; 1994-083197/10.  
DR N-PSDB; Q56692.  
XX  
PT Purified interleukin-13 proteins and antibodies - obtd. using  
PT mouse gene encoding related protein P600  
XX  
PS Claime 1; Page 126-127; 135pp; English.  
XX  
CC An approx. 400 bp DNA fragment derived from a Pst/PvuII restriction  
CC digest of the mouse P600 cDNA clone was isolated. This fragment,  
CC which encompasses most of the coding region of the mouse P600 cDNA,  
CC was radioactively labelled and hybridised with filter lifts prepd.  
CC from a cDNA library made from a clone of an A10 T cell line. One  
CC clone, designated PA 10.66, was subcloned into M13 and sequenced.  
CC This sequence encodes human IL-13.  
XX  
SQ Sequence 132 AA;

Query Match 68.2%; Score 382.5; DB 15; Length 132;  
Best Local Similarity 70.0%; Pred. No. 7.9e-39;  
Matches 77; Conservative 11; Mismatches 21; Indels 1; Gaps 1;

QY 2 PVTPSPTLKELIEELVNITQNO-ASLCNGSMVWSVNLTAGMYCAALESINVSDCSAIQR 60  
|| || :||||| ||||| | ||||| :||||| ||||| ||||| ||||| :||| :  
Db 22 pvpstalrelieelvnitgnqkaplcngsmvwsinltagmycaaleslinvsgcsaiek 81

QY 61 TQRLKALCSQKPAAGQISSERSRDTKIEVIQLVKNLLTYVRGVYRHGNF 110

Db 82 tqrmisgfcphkvsagqfsslhvrdtkievafvkdllhlhklkifregf 131

RESULT 8  
R27346  
ID R27346 standard; Protein; 112 AA.  
XX AC R27346;  
XX DT 24-FEB-1993 (first entry)  
XX DE Protein with cytokine activity encoded by Nal.  
XX KW Interleukin; chemotaxis; immunomodulation; inflammation.

PN EP506574-A.  
XX 30-SEP-1992.  
XX PF 27-MAR-1992; 92EP-0400858.  
XX PR 29-MAR-1991; 91FR-0003904.  
XX PR 08-JAN-1992; 92FR-0000137.

XX PA (SNFI ) ELF SANOFI.  
XX PI Caput D, Ferrara P, Guillemot J, Kaghad M, Labit-le Bouteiller C;  
XX PI Lepiatols P, Magazin M, Minty A;

DR WPI; 1992-325841/40.  
DR N-PSDB; Q28943.

XX PT New cytokine having immunomodulatory activity - useful for  
XX PT treating tumours and infectious or inflammatory conditions

XX PS Claim 1; Page 60; 78pp; French.  
XX CC This protein is one of two possible forms of a new cytokine  
XX CC produced by T lymphocytes induced by phorbol-2-myristate-3-acetate  
XX CC and phytohaemagglutinin. The proteins differ only in the amino acid  
XX CC at position 41 which is either Asp or Gly. The cytokine acts on  
XX CC monocytes and B lymphocytes and is useful in treatment of tumours  
XX CC and some infections and inflammatory conditions.  
XX CC See Q28941-Q28947.

XX SQ Sequence 112 AA;

Query Match 66.9%; Score 375.5; DB 13; Length 112;  
Best Local Similarity 69.1%; Pred. No. 4.5e-38;  
Matches 76; Conservative 11; Mismatches 22; Indels 1; Gaps 1;

QY 2 PVTPSPTLKEELVNIQTNQ-ASLCNGSMVSVNLTAGMYCAALESINVSDCSAIQR 60  
Db 2 pvpptalrelieelvntqkqplcngsmvwsinltadmycaaleslinvsgcsaiek 61  
QY 61 TQRLMKALCSQKPAAGQISSERSRDTKIEVIQLVKNLLTYVVRGVYRHGNF 110  
Db 62 tqrmisgfcphkvsagqfsslhvrdtkievafvkdllhlhklkifregf 111

RESULT 9  
R27348  
ID R27348 standard; Protein; 146 AA.  
XX AC R27348;  
XX DT 24-FEB-1993 (first entry)  
XX DE Cytokine NC30.  
XX KW Interleukin; chemotaxis; immunomodulation; inflammation.

XX FH cleavage\_site Location/Qualifiers  
FT 20..21 /note= "putative signal peptide cleavage site"  
FT 24..25 /note= "putative signal peptide cleavage site"  
FT 32..33 /note= "putative signal peptide cleavage site"  
FT 34..35 /note= "putative signal peptide cleavage site"  
FT 35..146 /note= "putative signal peptide cleavage site"  
FT /label= NC30

XX PN EP506574-A.  
XX PD 30-SEP-1992.  
XX PF 27-MAR-1992; 92EP-0400858.  
XX PR 29-MAR-1991; 91FR-0003904.  
XX PR 08-JAN-1992; 92FR-0000137.

XX PA (SNFI ) ELF SANOFI.  
XX PI Caput D, Ferrara P, Guillemot J, Kaghad M, Labit-le Bouteiller C;  
XX PI Lepiatols P, Magazin M, Minty A;

DR WPI; 1992-325841/40.  
DR N-PSDB; Q28947.

XX PT New cytokine having immunomodulatory activity - useful for  
XX PT treating tumours and infectious or inflammatory conditions

XX PS Claim 1; Page 52-53; 78pp; French.  
XX CC A novel cytokine produced by T lymphocytes induced by phorbol-2-  
XX CC myristate-3-acetate and phytohaemagglutinin was coded for by the  
XX CC sequence in clone pSEI-NC30. A second clone was also identified  
XX CC (pSEI-NC30bis) which differed only in the identity of codon 41.  
XX CC The corresponding proteins differ in the amino acid at position 41  
XX CC which is either Asp (in NC30) or Gly (in NC30bis). The cytokine  
XX CC acts on monocytes and B lymphocytes and is useful in treatment of  
XX CC tumours and some infections and inflammatory conditions.  
XX CC See Q28941-Q28947.

XX SQ Sequence 146 AA;

Query Match 66.9%; Score 375.5; DB 13; Length 146;  
Best Local Similarity 69.1%; Pred. No. 6.5e-38;  
Matches 76; Conservative 11; Mismatches 22; Indels 1; Gaps 1;

QY 2 PVTPSPTLKEELVNIQTNQ-ASLCNGSMVSVNLTAGMYCAALESINVSDCSAIQR 60  
Db 36 pvpptalrelieelvntqkqplcngsmvwsinltadmycaaleslinvsgcsaiek 95  
QY 61 TQRLMKALCSQKPAAGQISSERSRDTKIEVIQLVKNLLTYVVRGVYRHGNF 110  
Db 96 tqrmisgfcphkvsagqfsslhvrdtkievafvkdllhlhklkifregf 145

RESULT 10  
R92794  
ID R92794 standard; Protein; 111 AA.  
XX AC R92794;  
XX DT 24-MAY-1996 (first entry)  
XX DE Human interleukin-13 mutein 2.  
XX KW Cytokine; mutein; interleukin-13; IL-13; agonist; antagonist;  
KW diagnosis; therapy; cancer; inflammation; degenerative disease.



XX OS Synthetic.

XX XX

XX Key Location/Qualifiers

XX FT Misc-difference 11

XX FT /note= "Glu at position 11 may be replaced by an

XX FT amidated amino acid, including Lys"

XX FT Misc-difference 64

XX FT /note= "Arg at position 64 may be replaced by an

XX FT acidic amino acid, including Asp"

XX XX

XX PN WO9604306-A2.

XX XX

XX PD 15-FEB-1996.

XX XX

XX PF 31-JUL-1995; 95WO-US08950.

XX XX

XX PR 01-AUG-1994; 94US-0284393.

XX XX

XX PA (SCHE ) SCHERING CORP.

XX XX

XX PI Zurawski G, Zurawski SM;

XX XX

XX DR WPI; 1996-129335/13.

XX XX

XX PT Mutein(s) of human and murine cytokine(s), esp. interleukin(s) and

XX PT murine P600 contg. amino acid substitutions. - useful for the

XX PT diagnosis and treatment of cancer, inflammation, etc.

XX PS Claim 12; Page 46; 52pp; English.

XX XX

XX CC Muteins 1 and 2 (R92793-94) of human interleukin-13 (IL-13) contain

XX CC amino acid substitutions at amino acid position 11 in helix A and/or

XX CC at position 64 in helix C. They are obtd. by site-directed

XX CC mutagenesis of natural IL-13 sequences. The muteins antagonise the

XX CC activity of IL-13 or IL-4. They have partial cytokine agonist

XX CC activity, exhibit less than 80% maximal agonist activity of natural

XX CC IL-2, and/or antagonize cytokine activity by least about 50% when

XX CC present at a 100-fold excess. They and other cytokine muteins

XX CC (see also R92790-92, R92795-802) are useful in the screening of

XX CC cytokine and cytokine receptor levels, and in the diagnosis or

XX CC treatment of e.g. inflammation, cancer, and degenerative disorders.

XX XX

XX SQ Sequence 111 AA;

Query Match 65.4%; Score 367; DB 17; Length 111;

Best Local Similarity 69.1%; Pred. NO. 4.9e-37;

Matches 76; Conservative 11; Mismatches 21; Indels 2; Gaps 2;

QY 2 PVTSPSTLKELIEELVNITQNQ-ASLCNGSMVWSVNLTAGMYCAALESINVSDCSAIQR 60

Db 2 pvpptalrelielvnitqngkaplcnsgmvslnltagmycaaleslinvsgcsaiek 61

QY 61 TQRLKALCSQKPAAGQISSERSRDTKIEVIQLVKNLLTYVRGVYRHGNF 110

Db 62 tqrmisgfcphkvsag-fsslhvrtdkievaqfvdllhlklfregrf 110

RESULT 11

R48625

ID R48625 standard; Protein; 131 AA.

XX

AC R48625;

XX XX

XX DT 14-SEP-1994 (first entry)

XX DE Sequence of mouse P600.

XX XX

XX KW Interleukin-13; lymphokine; P600; immunological disorder; therapy;

XX KW diagnostic.

XX XX

XX OS Mus musculus.

XX XX WO9404680-A.

XX XX

XX PD 03-MAR-1994.

XX XX

XX PF 18-AUG-1993; 93WO-US07645.

XX XX

XX PR 21-AUG-1992; 92US-0933416.

XX PR 29-JAN-1993; 93US-0010977.

XX PR 01-FEB-1993; 93US-0012543.

XX XX

XX PA (SCHE ) SCHERING CORP.

XX XX

XX PI Aversa G, Banchereau J, Briere F, Coffman RL, Cooks BG;

XX PI Culpepper, Dang W, De Vries J, De Waal Malefyt R;

XX PI Doherty TM, Heath A, Mckenzie A, Punnonen J, Zurawski G;

XX XX

XX DR WPI; 1994-083197/10.

XX DR N-PSDB; Q56693.

XX XX

XX PT Purified interleukin-13 proteins and antibodies - obtd. using

XX PT mouse gene encoding related protein P600

XX XX

XX PS Disclosure; Page 128-129; 135pp; English.

XX XX

XX CC An approx. 400 bp DNA fragment derived from a Pst/PvuII restriction

XX CC digest of the mouse P600 cDNA clone was isolated. This fragment,

XX CC which encompasses most of the coding region of the mouse P600 cDNA,

XX CC was radioactively labelled and hybridised with filter lifts prepd.

XX CC from a cDNA library made from a clone of an A10 T cell line. One

XX CC clone, designated PA 10.66, was subcloned into M13 and sequenced.

XX CC This sequence encodes human IL-13.

XX XX

XX SQ Sequence 131 AA;

Query Match 52.7%; Score 295.5; DB 15; Length 131;

Best Local Similarity 59.2%; Pred. No. 3.1e-28;

Matches 61; Conservative 16; Mismatches 23; Indels 3; Gaps 2;

QY 8 TLKELIEELVNITQNASLCNGSMVWSVNLTAGMYCAALESINVSDCSAIQRTQRLKA 67

Db 32 tlkelieelsnitqdtqplcnsgmvsdlaaggfcvaldslnsncaiyrtqrilhg 91

QY 68 LCSQKPAAGQISSERSRDTKIEVIQLVKNLLTYVRGVYRHGNF 110

Db 92 lcnrk-apttvss--lpdtkievahfitkllsytkqlfrhgp 131

RESULT 12

R92795

ID R92795 standard; Protein; 111 AA.

XX

AC R92795;

XX XX

XX DT 24-MAY-1996 (first entry)

XX XX

XX DE Murine P600.

XX XX

XX KW Cytokine; mutein; P600; interleukin-13; IL-13; agonist; antagonist;

XX KW diagnosis; therapy; cancer; inflammation; degenerative disease.

XX OS Mus musculus.

XX XX

XX FH Key Location/Qualifiers

XX FT Misc-difference 67

XX FT /note= "Arg at position 67 may be replaced by an

XX FT acid amino acid, including Asp"

XX XX

XX PN WO9604306-A2.

XX XX

XX PD 15-FEB-1996.

XX XX











QY 61 TQRLKALCSQKPAAGQISSERSRDTKIEVIQLVKNLLTYVRGVYRHGNF 110  
||||| | | :||| || ||||| | | :||| :|| | |  
Db 62 TQRLSGFCPHKVSAGQFSSLHVRDTKIEVAQFVKDLLHLKLLFREGRE 111

RESULT 2  
PCT-US95-08950-4  
; Sequence 4, Application PC/TUS9508950  
; GENERAL INFORMATION:  
; APPLICANT: Zurawski, Sandra M.  
; APPLICANT: Zurawski, Gerard  
; TITLE OF INVENTION: MUTEINS OF MAMMALIAN CYTOKINES  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/08950  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/284,393  
; FILING DATE: 01-AUG-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0389  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-852-9196  
; TELEFAX: 415-496-1200  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 112 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; PCT-US95-08950-4

Query Match 68.2%; Score 382.5; DB 5; Length 112;  
Best Local Similarity 70.0%; Pred. No. 3.2e-41;  
Matches 77; Conservative 11; Mismatches 21; Indels 1; Gaps 1;  
  
QY 2 PVTPTSPTLKEELVNITQNK-ASLCNGSMVWSVNLTAGMYCAALESINVSDCSAIQR 60  
|| || | :||| || ||||| | | :||| :|| | |  
Db 2 PVPSTALRELIEELVNITQNKAPLCNGSMVWSINLTAGMYCAALESINVSGCSAIEK 61  
  
QY 61 TQRLKALCSQKPAAGQISSERSRDTKIEVIQLVKNLLTYVRGVYRHGNF 110  
||||| | | :||| || ||||| | | :||| :|| | |  
Db 62 TQRLSGFCPHKVSAGQFSSLHVRDTKIEVAQFVKDLLHLKLLFREGRE 111

RESULT 3  
US-08-012-543-2  
; Sequence 2, Application US/08012543  
; Patent No. 5596072  
; GENERAL INFORMATION:  
; APPLICANT: Culpepper, Janice  
; APPLICANT: McKenzie, Andrew  
; APPLICANT: Dang, Warren  
; APPLICANT: de Waal Malefyt, Rene  
; APPLICANT: Heath, Andrew  
; APPLICANT: Aversa, Gregorio

; APPLICANT: Briere, Francine  
; APPLICANT: Banchereau, Jacques  
; APPLICANT: de Vries, Jan  
; APPLICANT: Zurawski, Gerard  
; TITLE OF INVENTION: Human Interleukin-13  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/012,543  
; FILING DATE: 01-FEB-1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/933,416  
; FILING DATE: 21-AUG-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0302K1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-852-9196  
; TELEFAX: 415-496-1200  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 132 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-012-543-2

Query Match 68.2%; Score 382.5; DB 1; Length 132;  
Best Local Similarity 70.0%; Pred. No. 4.1e-41;  
Matches 77; Conservative 11; Mismatches 21; Indels 1; Gaps 1;  
  
QY 2 PVTPTSPTLKEELVNITQNK-ASLCNGSMVWSVNLTAGMYCAALESINVSDCSAIQR 60  
|| || | :||| || ||||| | | :||| :|| | |  
Db 22 PVPSTALRELIEELVNITQNKAPLCNGSMVWSINLTAGMYCAALESINVSGCSAIEK 81

QY 61 TQRLKALCSQKPAAGQISSERSRDTKIEVIQLVKNLLTYVRGVYRHGNF 110  
||||| | | :||| || ||||| | | :||| :|| | |  
Db 82 TQRLSGFCPHKVSAGQFSSLHVRDTKIEVAQFVKDLLHLKLLFREGRE 131

RESULT 4  
PCT-US93-07645A-2  
; Sequence 2, Application PC/TUS9307645A  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: Human Interleukin-13  
; NUMBER OF SEQUENCES: 6  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Macintosh 6.0.5  
; SOFTWARE: Microsoft Word 5.1a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US93/07645A  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/012543  
; FILING DATE: 01-FEB-1993  
; PRIOR APPLICATION DATA:

[illegible]

```

Query Match      66.9%; Score 375.5; DB 1; Length 112;
Best Local Similarity 69.1%; Pred. No. 2.5e-40;
Matches 76; Conservative 11; Mismatches 22; Indels 1; Gaps 1;

QY  2  PVTPTS TLKELIEELVNITQNQ-ASLCNGSMVWSVNLTAGMYCAALES LINVSDCSAIQR 60
      || || |:||||| ||||| | ||||| ||||| ||||| ||||| ||||| ||||| :
Db   2  PVPSTALRELIEELVNITQNQKAPLCNGSMVWSINLTAXMYCAALES LINVSGCSAIEK 61

```

Qy	61	TQRLKALCSQKPAAGQISSERSRDTKIEIVQLVKNLLTYVRGVYRHGNF	110
		-   :                                : :    -	
Db	62	TQRLMSGFCPHKVSAGQFSSLHVHVDTKIEVAQFVKDLLHLKKLFREGRE	111

## RESULTS

US-08-371-121-16  
; Sequence 16, Application US/083711121  
; Patent No. 5652123  
; GENERAL INFORMATION:  
; APPLICANT: CAPUT, Daniel  
; APPLICANT: FERRARA, Pascual  
; APPLICANT: GUILLEMOT, Jean-Claude  
; APPLICANT: LEPLATOIS, Pascal  
; APPLICANT: MINTY, Adrian  
; APPLICANT: KAGHAD, Mourad  
; APPLICANT: LABIT-LE BOUTEILLER, Christine  
; APPLICANT: MAGAZIN, Marilyn  
; TITLE OF INVENTION: Protein having a cytokine type  
; TITLE OF INVENTION: activity, recombinant DNA coding for this protein,  
; TITLE OF INVENTION: transformed cells and microorganisms.  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FOLEY & LARDNER  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington, D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/371,121  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/938,161  
; FILING DATE: 30-NOV-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/FR92/00280  
; FILING DATE: 27-MAR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 91 00137  
; FILING DATE: 08-JAN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 91 03904  
; FILING DATE: 29-MAR-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SAXE, Bernhard D.  
; REGISTRATION NUMBER: 28,665  
; REFERENCE/DOCKET NUMBER: 16781/383  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 672-5300  
; TELEFAX: (202) 672-5399  
; TELEX: 904136  
; INFORMATION FOR SEQ ID NO: 16:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 146 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-371-121-16

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QY      61  TQRLMKALCSQKPAAGQISSERSRDTKIEVIQLVKNLITYVRGVYRHGNE 110
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Db      96  TQRLMSGFCPHKVSAGQFSSLHVRDTKIEVAQFVKDLLHLKKLFREGRE 145

RESULT      8
US-08-284-393B-14
; Sequence 14, Application US/08284393B
; Patent No. 5696234
; GENERAL INFORMATION:
; APPLICANT: Zurawski, Sandra M.
; APPLICANT: Zurawski, Gerard
; TITLE OF INVENTION: MUTINS OF MAMMALIAN CYTOKINES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/284,393B
; FILING DATE: 01-AUG-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0389
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-852-9196
; TELEFAX: 415-496-1200
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-284-393B-14

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## RESULT

US-08-284-393B-5  
; Sequence 5, Application US/08284393B.  
; Patent No. 5696234  
; GENERAL INFORMATION:  
; APPLICANT: Zurawski, Sandra M.  
; APPLICANT: Zurawski, Gerard  
; TITLE OF INVENTION: MUTEINS OF MAMMALIAN CYTOKINES  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute





[illegible]

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RESULT      12
US-08-012-543-4
; Sequence 4, Application US/08012543
; Patent No. 5596072
; GENERAL INFORMATION:
; APPLICANT: Culpepper, Janice
; APPLICANT: McKenzie, Andrew
; APPLICANT: Dang, Warren
; APPLICANT: de Waal Malefyt, Rene
; APPLICANT: Heath, Andrew
; APPLICANT: Aversa, Gregorio
; APPLICANT: Briere, Francine
; APPLICANT: Banchereau, Jacques
; APPLICANT: de Vries, Jan
; APPLICANT: Zurawski, Gerard
; TITLE OF INVENTION: Human Interleukin-13
; NUMBER OF SEQUENCES: 27

```

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CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/08/012,543
; FILING DATE: 01-FEB-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/933,416
; FILING DATE: 21-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0302K1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-852-9196
; TELEFAX: 415-496-1200
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 131 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-012-543-4

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Dd	32	TLKELIEELSNTIQDTPLCNGSMVWSVDLAAGFCVALDSLTNISNCNAIYRTQILHG	91
Qy	68	LCSQKPAAGQISSERSRDTKIEVIQLVKNLITYRGVYRHGNF	110
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RESULT 13
US-08-371-121-25
; Sequence 25, Application US/08371121
; Patent No. 5652123
; GENERAL INFORMATION:
; APPLICANT: CAPUT, Daniel
; APPLICANT: FERRARA, Pascual
; APPLICANT: GUILLEMOT, Jean-Claude
; APPLICANT: LEPLATOIS, Pascal
; APPLICANT: MINTY, Adrian
; APPLICANT: KAGHAD, Mourad
; APPLICANT: LABIT-LE BOUTEILLER, Christine
; APPLICANT: MAGAZIN, Marilyn
; TITLE OF INVENTION: Protein having a cytokine type
; TITLE OF INVENTION: activity, recombinant DNA coding for this protein,
; TITLE OF INVENTION: transformed cells and microorganisms.
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/371,121
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/938,161
; FILING DATE: 30-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR92/00280
; FILING DATE: 27-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91 00137
; FILING DATE: 08-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91 03904
; FILING DATE: 29-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 16781/383
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 131 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-371-121-25

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	Query Match	52.7%;	Score 295.5;	DB 1;	Length 131;
	Best Local Similarity	59.2%;	Pred. No. 4.7e-30;		
	Matches 61;	Conservative 16;	Mismatches 23;	Indels 3;	Gaps 2;
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Db	32	TLKELIEELSNIQTQPLCNGSMWVSDLAAGGFCVALDSLTNISCNAIYRTQRIILHG	91		
Qy	68	LCSQKPAAGQISSERSRDTKIEVIQLVKNLLTYVRGVYRHGNF	110		

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Query Match 12.2%; Score 68.5; DB 2; Length 559;  
Best Local Similarity 28.2%; Pred. No. 23;  
Matches 31; Conservative 19; Mismatches 37; Indels 23; Gaps 6;

QY 13 IEELVNITQNASLNCNMGWWSVNLTAGMYCAALESLINVSDCSAIQRTQRLKALC---- 69  
Db 333 VEEILNI-MYQTSYCPVTITYNI-LINGLCKARLLS-----RAIDFFYQMLEQKCLPD 383

QY 70 --SQKPAAGQISSERSRDTKIEVIQLVKN-----LLTY---VRGVYRHG 108  
Db 384 IVTYNTVLGAMSKEGMVDDAIELLGLLKNTCCPPGLITYNSVIDGLAKKG 433

Search completed: May 13, 2001, 21:48:39  
Job time: 26248 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 14, 2001, 06:02:04 ; Search time 44.64 Seconds  
(without alignments)  
85.178 Million cell updates/sec

Title: US-09-451-527-97  
Perfect score: 561  
Sequence: 1 SPVTPSPTLKELIELVNIT.....QLVKNLLTYVRGVYRHGNER 111

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a  
.score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match	Length	DB	ID	Description
1	382.5	68.2	132	1	IL13_HUMAN	P35225 homo sapien
2	360.5	64.3	132	1	IL13_BOVIN	Q9xsv9 bos taurus
3	295.5	52.7	131	1	IL13_MOUSE	P20109 mus musculus
4	294	52.4	131	1	IL13_RAT	P42203 rattus norv
5	73	13.0	701	1	UBF2_XENLA	P25980 xenopus lae
6	71.5	12.7	382	1	IPAC_SHIFL	P18012 shigella fl
7	71	12.7	261	1	SPRE_HUMAN	P35270 homo sapien
8	70.5	12.6	192	1	FLHC_SALTY	O52222 salmonella
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11	70	12.5	430	1	FTSZ_SYNY3	P73456 synechocyst
12	70	12.5	677	1	UBF1_XENLA	P25979 xenopus lae
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14	68.5	12.2	261	1	SPRE_MOUSE	Q64105 mus musculus
15	68	12.1	1004	1	YG21_YEAST	P53067 saccharomyc
16	67.5	12.0	1164	1	PHOS_HUMAN	Q9y613 homo sapien
17	67	11.9	481	1	YA88_SCHPO	Q09775 schizosacch
18	67	11.9	510	1	MUTL_THEMEA	P74925 thermotoga
19	66.5	11.9	323	1	GC_RABIT	P01870 oryctolagus
20	66	11.8	1234	1	MFJ_MYCTU	P96380 mycobacteri
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22	65.5	11.7	1681	1	CLH_CAEEL	P34574 caenorhabdi
23	65	11.6	268	1	MOVPT_TMKVR	P30737 tobacco mos
24	64.5	11.5	268	1	MOVPT_TMV	P03583 tobacco mos
25	64.5	11.5	268	1	MOVPT_TMVVB	O91275 tobacco mos
26	64.5	11.5	268	1	MOVPT_TMVRA	Q98746 tobacco mos
27	64	11.4	1164	1	KEL1_YEAST	P38853 saccharomyc
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29	63.5	11.3	725	1	VR2A_BPT4	P03690 bacterioph
30	63.5	11.3	1477	1	ALI3_RAT	P14046 rattus norv
31	63.5	11.3	1539	1	Y373_HUMAN	O15078 homo sapien
32	63	11.2	168	1	PTP_NPVAC	P24656 autographa
33	63	11.2	211	1	HIT_PIG	P06348 sus scrofa

RESULT 1	IL13_HUMAN	63	11.2	482	1	TYPH_HUMAN	P19971 homo sapien
34	AC	63	11.2	599	1	AFAM_HUMAN	P43652 homo sapien
35	ID	63	11.2	764	1	UBF1_HUMAN	P17480 homo sapien
36	DT	63	11.2	764	1	UBF1_RAT	P25977 rattus norv
37	DT	63	11.2	765	1	UBF1_MOUSE	P25976 mus musculus
38	DT	63	11.2	1675	1	CLH1_HUMAN	Q00610 homo sapien
39	DT	63	11.2	1675	1	CLH1_BOVIN	P49951 bos taurus
40	DT	63	11.2	1675	1	CLH1_RAT	P11442 rattus norv
41	DT	63	11.2	1934	1	MYSB_MESAU	P13540 mesocricetu
42	DT	63	11.2	1935	1	MYSB_HUMAN	P12883 homo sapien
43	DT	63	11.2	1935	1	MYSB_PIG	P79293 sus scrofa
44	DT	63	11.2	2875	1	RRPL_TSWV1	P28976 tomato spot
45	DT	63	11.2	2875	1	RRPL_TSWV1	P28976 tomato spot

ALIGNMENTS

SEQUENCE FROM N.A.	SEQUENCE FROM N.A.
MEDLINE=93211479; PubMed=8096327;	MEDLINE=93234572; PubMed=8097324;
Minty A.J., Chalon P., Derocq J.M., Dumont X., Guillemot J.C.,	McKenzie A.N., Culpepper J.A., Waal Malefyt R., Briere F.,
Kaghad M., Labit C., Leplatois P., Liauzun P., Miloux B.,	Punnonen J., Aversa G., Sato A., Dang W., Cocks B.G., Menon S.,
Minty C., Casellas P., Loison G., Lupker J., Shire D., Ferrara P.,	de Vries J.E., Banchereau J., Zurawski G.R.;
Caput D.;	"Interleukin 13, a T-cell-derived cytokine that regulates human
"Interleukin-13 is a new human lymphokine regulating inflammatory and	monocyte and B-cell function.";
immune responses.";	Proc. Natl. Acad. Sci. U.S.A. 90:3735-3739(1993).
Nature 362:248-250(1993).	[3]
[2]	SEQUENCE FROM N.A.
McKenzie A.N., Culpepper J.A., Waal Malefyt R., Briere F.,	Punnonen J., Aversa G., Sato A., Dang W., Cocks B.G., Menon S.,
de Vries J.E., Banchereau J., Zurawski G.R.;	"Interleukin 13, a T-cell-derived cytokine that regulates human
monocyte and B-cell function.";	Proc. Natl. Acad. Sci. U.S.A. 90:3735-3739(1993).
[3]	SEQUENCE FROM N.A.
Dolganov G., Lewis D.B., Lovett M., Burr J., Bort S., Short D.,	McGurn M., Gibson C.;
Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.	[4]
SEQUENCE FROM N.A.	TISSUE=Blood;
MEDLINE=95237624; PubMed=7721105;	Smirnov D.V., Smirnova M.G., Korobko V.G., Frolova E.I.;
"Tandem arrangement of human genes for interleukin-4 and	interleukin-13: resemblance in their organization.";
Gene 155:277-281(1995).	[5]
SEQUENCE FROM N.A.	Jang J.S., Kim B.E.;
Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.	[6]
3D-STRUCTURE MODELING.	MEDLINE=95132583; PubMed=7530359;
Bamborough P., Duncan D., Richards W.G.;	"Predictive modelling of the 3-D structure of interleukin-13.";
Protein Eng. 7:1077-1082(1994).	[7]





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RA Brown K.D., Zurawski S.M., Mosmann T.R., Zurawski G.;
RT "A family of small inducible proteins secreted by leukocytes are
RT members of a new superfamily that includes leukocyte and
RT fibroblast-derived inflammatory agents, growth factors, and
RT indicators of various activation processes.";
RL J. Immunol. 142:679-687(1989).
CC -!- FUNCTION: CYTOKINE. INHIBITS INFLAMMATORY CYTOKINE PRODUCTION.
CC SYNERGIZES WITH IL2 IN REGULATING INTERFERON-GAMMA SYNTHESIS.
CC MAY BE CRITICAL IN REGULATING INFLAMMATORY AND IMMUNE RESPONSES
CC (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: SECRETED.
CC -!- SIMILARITY: BELONGS TO THE IL-4 / IL-13 FAMILY.
CC -----
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CC -----
DR EMBL; M23504; AAA40149.1; -.
DR PIR; E30552; E30552.
DR HSSP; P35225; 3ITR.
DR MGD; MGI:96541; IL13.
DR InterPro; IPR001325; -.
DR PROSITE; PS00838; INTERLEUKIN_4_13; 1.
KW Cytokine; Glycoprotein; Signal.
FT SIGNAL 1 21 BY SIMILARITY.
FT CHAIN 22 131 INTERLEUKIN-13.
FT DISULFID 51 79 BY SIMILARITY.
FT DISULFID 67 93 BY SIMILARITY.
FT CARBOHYD 42 42 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 52 52 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 75 75 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 131 AA; 14107 MW; 954F93F105713FED CRC64;

Query Match 52.7%; Score 295.5; DB 1; Length 131;
Best Local Similarity 59.2%; Pred. No. 6.6e-25;
Matches 61; Conservative 16; Mismatches 23; Indels 3; Gaps 2;

QY 8 TLKELIEELVNITQNASLCNGSMVSVNLTAGMYCAALESLINVSDCSAIQRTQRLKA 67
Db 32 TLKELIEELSNITQDTPLCNGSMVSVVDLAAGGFCVALDSLNTNISNCNAIYRTQRLHG 91

QY 68 LCSOKPAAGQISSERSRDTKIEVIQLVKNLLTYVRGVYRHGNF 110
Db 92 LCNRK-APTTVSS--LPDTKIEVAHFITKLLSYTKQLFRHGPF 131

RESULT 4
IL13_RAT
ID IL13_RAT STANDARD; PRT; 131 AA.
AC P42203;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE INTERLEUKIN-13 PRECURSOR (IL-13) (T-CELL ACTIVATION PROTEIN P600).
GN IL13 OR IL-13.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Kidney cortex;
RX MEDLINE=94092138; PubMed=7916615;
RA Lakkis F.G., Cruet E.N.;
RT "Cloning of rat interleukin-13 (IL-13) cDNA and analysis of IL-13
RT gene expression in experimental glomerulonephritis.";
RL Biochem. Biophys. Res. Commun. 197:612-618(1993).
CC -!- FUNCTION: CYTOKINE. INHIBITS INFLAMMATORY CYTOKINE PRODUCTION.
```

```
CC SYNERGIZES WITH IL2 IN REGULATING INTERFERON-GAMMA SYNTHESIS.
CC MAY BE CRITICAL IN REGULATING INFLAMMATORY AND IMMUNE RESPONSES
CC (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: SECRETED.
CC -!- SIMILARITY: BELONGS TO THE IL-4 / IL-13 FAMILY.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L26913; AAA16478.1; -.
DR HSSP; P35225; 3ITR.
DR InterPro; IPR001325; -.
DR PROSITE; PS00838; INTERLEUKIN_4_13; 1.
KW Cytokine; Glycoprotein; Signal.
FT SIGNAL 1 21 BY SIMILARITY.
FT CHAIN 22 131 INTERLEUKIN-13.
FT DISULFID 52 80 BY SIMILARITY.
FT DISULFID 68 94 BY SIMILARITY.
FT CARBOHYD 42 42 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 76 76 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 121 121 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 131 AA; 14093 MW; E5008CAB8DE8C201 CRC64;

Query Match 52.4%; Score 294; DB 1; Length 131;
Best Local Similarity 57.9%; Pred. No. 9.5e-25;
Matches 62; Conservative 17; Mismatches 24; Indels 4; Gaps 3;

QY 4 TPSPTLKEELVNITQNO-ASLCNGSMVSVNLTAGMYCAALESLINVSDCSAIQRTQ 62
Db 28 SPPVALRELIEELSNITQDKTSLCNSMWSVDLTAGGFCALLESLTNISSCAIHRTO 87

QY 63 RMLKALCSQKPAAGQISSERSRDTKIEVIQLVKNLLTYVRGVYRHGN 109
Db 88 RILNGLCNQK--ASDVASS-PPDTKIEVAQFISKLLNYSKQLFRYGH 131

RESULT 5
UBF2_XENLA
ID UBF2_XENLA STANDARD; PRT; 701 AA.
AC P25980;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE NUCLEOLAR TRANSCRIPTION FACTOR 2 (UPSTREAM BINDING FACTOR-2) (UBF-2).
GN XUBF-2.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91293106; PubMed=2065665;
RA McStay B., Hu C.H., Pikaard C.S., Reeder R.H.;
RT "xUBF and Rib 1 are both required for formation of a stable
RT polymerase I promoter complex in X. laevis.";
RL EMBO J. 10:2297-2303(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91348289; PubMed=1879565;
RA Bachvarov D., Normandeu M., Moss T.;
RT "Heterogeneity in the Xenopus ribosomal transcription factor xUBF has
RT a molecular basis distinct from that in mammals.";
RL FEBS Lett. 288:55-59(1991).
RN [3]
RP DOMAINS.
```

```
RX MEDLINE=92038986; PubMed=1936987;
RA McStay B., Frazier M.W., Reeder R.H.;
RT "XUBF" contains a novel dimerization domain essential for RNA
RT polymerase I transcription."
RL Genes Dev. 5:1957-1968(1991).
CC -1- FUNCTION: UBF RECOGNIZES THE RIBOSOMAL RNA GENE PROMOTOR AND
CC ACTIVATES TRANSCRIPTION MEDIATED BY RNA POLYMERASE I THROUGH
CC COOPERATIVE INTERACTIONS WITH THE SPECIES-SPECIFIC FACTOR SL1.
CC IT BINDS SPECIFICALLY TO THE UPSTREAM CONTROL ELEMENT.
CC -1- SUBUNIT: XUBF CONSISTS OF 2 POLYPEPTIDES OF 82 AND 85 KDA,
CC ENCODED BY THE SAME OR CLOSELY RELATED GENES.
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- SIMILARITY: CONTAINS 5 HMG BOXES.
CC -----
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```
RX MEDLINE=89057927; PubMed=3057506;
RA Venkatesan M.M., Buysse J.M., Kopecko D.J.;
RT "Characterization of invasion plasmid antigen genes (ipaBCD) from
RT Shigella flexneri."
RL Proc. Natl. Acad. Sci. U.S.A. 85:9317-9321(1988).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=M90T / SEROTYPE 5;
RX MEDLINE=89200844; PubMed=3071655;
RA Baudry B., Kaczorek M., Sansonetti P.J.;
RT "Nucleotide sequence of the invasion plasmid antigen B and C genes
RT (ipaB and ipaC) of Shigella flexneri."
RL Microb. Pathog. 4:345-357(1988).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=2A; PLASMID=230 kb pMYSH6000;
RX MEDLINE=90014179; PubMed=2552264;
RA Sasakawa C., Adler B., Tobe T., Okada N., Nagai S., Komatsu K.,
RA Yoshikawa M.;
RT "Functional organization and nucleotide sequence of virulence
RT Region-2 on the large virulence plasmid in Shigella flexneri 2a."
RL Mol. Microbiol. 3:1191-1201(1989).
RN [4]
RP PARTIAL SEQUENCE OF 20-64 AND 318-335.
RX MEDLINE=89307550; PubMed=2663721;
RA Sankaran K., Ramachandran V., Subrahmanyam Y.V.B.K., Rajarathnam S.,
RA Elango S., Roy R.K.;
RT "Congo red-mediated regulation of levels of Shigella flexneri 2a
RT membrane proteins."
RL Infect. Immun. 57:2364-2371(1989).
CC -1- FUNCTION: ASSOCIATED WITH THE ENTRY OF THE BACTERIA INTO COLONIC
CC EPIHELIAL CELLS.
CC -1- MISCELLANEOUS: SYNTHESIS OF THIS IMMUNOGEN IS REPRESSED AT 30
CC DEGREES CELSIUS AND RESTORED AT 37 DEGREES CELSIUS.
CC -----
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DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE SEPIAPTERIN REDUCTASE (EC 1.1.1.153) (SPR).
GN SPR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=91354248; PubMed=1883349;
RA Ichinose H., Katoh S., Sueoka T., Titani K., Fujita K., Nagatsu T.;
RT "Cloning and sequencing of cDNA encoding human sepiapterin
RT reductase -- an enzyme involved in tetrahydrobiopterin biosynthesis.";
RL Biochem. Biophys. Res. Commun. 179:183-189(1991).
CC -!- FUNCTION: CATALYZES THE FINAL ONE OR TWO REDUCTIONS IN TETRA-
CC HYDROBIOPTERIN BIOSYNTHESIS TO FORM 5,6,7,8-TETRAHYDROBIOPTERIN.
CC -!- CATALYTIC ACTIVITY: 7,8-DIHYDROBIOPTERIN + NADP(+) = SEPIAPTERIN +
CC NADPH.
CC -!- SUBUNIT: HOMODIMER.
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -!- DISEASE: DEPRESSED SYNTHESIS OF TETRAHYDROBIOPTERIN MAY PLAY A
CC ROLE IN A VARIETY OF HUMAN DISEASES.
CC -----
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CC -----
DR EMBL; M76231; AAA60314.1; -.
DR PIR; JQ1176; JQ1176.
DR MIM; 182125; -.
DR InterPro; IPR002198; -.
DR Pfam; PF00106; adh_short; 1.
KW Oxidoreductase; NADP; Acetylation.
FT MOD_RES 1 1 ACETYLVATION (BY SIMILARITY).
FT NP_BIND 13 39 NADP (BY SIMILARITY).
FT DOMAIN 28 32 PTERIN BINDING (POTENTIAL).
SQ SEQUENCE 261 AA; 28048 MW; 9C9BF76212826F47 CRC64;

Query Match 12.7%; Score 71; DB 1; Length 261;
Best Local Similarity 24.7%; Pred. No. 1.8;
Matches 24; Conservative 21; Mismatches 42; Indels 10; Gaps 4;

QY 16 LVNITQNASLNGSMV---WSVNLTAGMYCAALESLINVSDCSAIQRTQRLKALCSQK.72
Db 104 LGDYSKGEVDLSDSQTQNNYWALNLT-SMLCLTSSVLKAFDPSPGLNRTVVNSSLALQ 162
QY 73 PAAG---QISSERSRDTKIEVIQLVK---NLLTYVRG 103
Db 163 PFKGVALYCAGKAARDMLFQVLALEPNVRVLNYAPG 199

RESULT 8
FLHC_SALTY STANDARD; PRT; 192 AA.
AC O52222;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE FLAGELLAR TRANSCRIPTIONAL ACTIVATOR FLHC.
GN FLHC.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=LT2;
RA Toguchi A., Harshey R.M.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX PubMed=10586519;
RA Yanagihara S., Iyoda S., Ohnishi K., Iino T., Kutsukake K.;
RT "Structure and transcriptional control of the flagellar master operon
RT of Salmonella typhimurium.";
RL Genes Genet. Syst. 74:105-111(1999).
CC -!- FUNCTION: TRANSCRIPTIONAL ACTIVATOR. TOGETHER WITH FLHD.IT ACTS AS
CC A COMPOUND SIGMA FACTOR THAT ACTIVATE CLASS 2 FLAGELLAR GENES (BY
CC SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE FLHC FAMILY.
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CC -----
DR EMBL; AF029300; AAB96640.1; -.
DR EMBL; D43640; BAA85315.1; -.
DR StyGene; SG10643; flhc.
KW Transcription regulation; Sigma factor; DNA-directed RNA polymerase;
KW DNA-binding; Flagella.
SQ SEQUENCE 192 AA; 21579 MW; C7334C691ECE3F8D CRC64;

Query Match 12.6%; Score 70.5; DB 1; Length 192;
Best Local Similarity 28.6%; Pred. No. 1.4;
Matches 16; Conservative 10; Mismatches 27; Indels 3; Gaps 1;

QY 31 MVSVNLTAGMYCAALESLINVSDCS---AIQRTQRLKALCSQKPAAGQISSERS 83
Db 65 MTWEQNIHSMFCNAWQFLKLTGCSGVDAAIKAYRLYLEQCQPPEGPLLALTRA 120

RESULT 9
SPRE_RAT
ID SPRE_RAT STANDARD; PRT; 262 AA.
AC P18297;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE SEPIAPTERIN REDUCTASE (EC 1.1.1.153) (SPR).
GN SPR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=90349631; PubMed=2201030;
RA Citron B.A., Milstien S., Gutierrez J.C., Levine R.A., Yanak B.L.,
RA Kaufman S.;
RT "Isolation and expression of rat liver sepiapterin reductase cDNA.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:6436-6440(1990).
RN [2]
RP SEQUENCE.
RX MEDLINE=91083647; PubMed=2260974;
RA Oyama R., Katoh S., Sueoka T., Suzuki M., Ichinose H., Nagatsu T.,
RA Titani K.;
RT "The complete amino acid sequence of the mature form of rat
RT sepiapterin reductase.";
RL Biochem. Biophys. Res. Commun. 173:627-631(1990).
CC -!- FUNCTION: CATALYZES THE FINAL ONE OR TWO REDUCTIONS IN TETRA-
CC HYDROBIOPTERIN BIOSYNTHESIS TO FORM 5,6,7,8-TETRAHYDROBIOPTERIN.
CC -!- CATALYTIC ACTIVITY: 7,8-DIHYDROBIOPTERIN + NADP(+) = SEPIAPTERIN +
CC NADPH.
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```
CC -!- SUBUNIT: HOMODIMER.
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -----
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CC -----
DR EMBL; M36410; AAA42130.1; -.
DR PIR; A36400; A36400.
DR InterPro; IPR002198; -.
DR Pfam; PF00106; adh_short; 1.
KW Oxidoreductase; NADP; Acetylation.
FT MOD_RES 1 1 ACETYLATION.
FT NP_BIND 14 40 NADP (BY SIMILARITY).
FT DOMAIN 29 33 PTERIN BINDING (POTENTIAL).
SQ SEQUENCE 262 AA; 28128 MW; EC992564A0334C61 CRC64;

Query Match 12.6%; Score 70.5; DB 1; Length 262;
Best Local Similarity 23.5%; Pred. No. 2.1;
Matches 24; Conservative 25; Mismatches 42; Indels 11; Gaps 4;

QY 8 TLKELIEELVNITQNASLCSGMVSVNLTAGMYCAALESLINVSDCSAIQRTQRLKA 67
|| : : : || : : ||| : : || : : || : : || : : || : : || : :
Db 104 TLGDVSKGFLNIN----DLAEVNNYWALNLTSLMLCLTTGTLNFAFNSPGLSKTVVNISS 158

QY 68 LCSQKPAAG---QISERSRDTKIEVIQLVK---NLLTYVRG 103
|| : : || : : || : : || : : || : : || : : || : : || : : ||
Db 159 LCALQPFKGLGKAGKAARDMLYQVLAVEEPSVRVLSYAPG 200

RESULT 10
IPAC_SHIDY
ID IPAC_SHIDY STANDARD; PRT; 382 AA.
AC Q03946;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE 42 KDA MEMBRANE ANTIGEN PRECURSOR.
GN IPAC.
OS Shigella dysenteriae.
OG Plasmid Invasion.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Shigella.
OX NCBI_TaxID=622;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CG097;
RX MEDLINE=92114800; PubMed=1766387;
RA Yao R., Palchaudhuri S.;
RT "Nucleotide sequence of the ipaBCD structural genes of Shigella
RT dysenteriae.";
RL Mol. Microbiol. 5:2217-2221(1991).
CC -!- FUNCTION: ASSOCIATED WITH THE ENTRY OF THE BACTERIA INTO COLONIC
CC EPITHELIAL CELLS.
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CC -----
DR EMBL; X60777; CAA43191.1; -.
DR PIR; S15578; S15578.
KW Antigen; Plasmid; Virulence; Membrane; Signal.
FT SIGNAL 1 19 BY SIMILARITY.
FT CHAIN 20 382 42 KDA MEMBRANE ANTIGEN.
```

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SQ SEQUENCE 382 AA; 41098 MW; A22E1D6399EC90BF CRC64;

Query Match 12.5%; Score 70; DB 1; Length 382;
Best Local Similarity 21.7%; Pred. No. 3.7;
Matches 28; Conservative 26; Mismatches 39; Indels 36; Gaps 5;

QY 4 TPSPTLKELE-----ELVNITQNQ-----ASLCNGSMVSVNLTAGMYCAALESLIN 51
:| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 268 SPDLSLDQKIDTQRRTYELNLTLSAQKQKNIGRATMETSAVAGNISTSGRYASALE---- 323

QY 52 VSDCSAIQRTQRLKALCSQKPAAGQISSERSRDTKIEVIQLVKNLLTYVRGVYRH---- 107
: : : : :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 324 -----EEEQLISQASSKQAEASQVSKEASQATN----QLIQKLLNIIDNINQSRSS 372

QY 108 -----GNFR 111
|| |
Db 373 ASQIAGNIR 381

RESULT 11
FTSZ_SYNY3
ID FTSZ_SYNY3 STANDARD; PRT; 430 AA.
AC P73456;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE CELL DIVISION PROTEIN FTSZ.
GN FTSZ OR SLL1633.
OS Synecocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synecocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97061201; PubMed=8905231;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hirose M., Sugita M., Sasamoto S., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K.,
RA Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A.,
RA Yamada M., Yasuda M., Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synecocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions.";
RL DNA Res. 3:109-136(1996).
CC -!- FUNCTION: THIS PROTEIN IS ESSENTIAL TO THE CELL-DIVISION PROCESS.
CC ITS SEEMS TO ASSEMBLE INTO A DYNAMIC RING ON THE INNER SURFACE OF
CC THE CYTOPLASMIC MEMBRANE AT THE PLACE WHERE DIVISION WILL OCCUR,
CC AND THE FORMATION OF THE RING IS THE SIGNAL FOR SEPTATION TO
CC BEGIN. BINDS TO AND HYDROLYZES GTP (BY SIMILARITY).
CC -!- SUBUNIT: AGGREGATE TO FORM A RING-LIKE STRUCTURE (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC. ASSEMBLE AT THE INNER SURFACE
CC OF THE CYTOPLASMIC MEMBRANE (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE FTSZ FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
DR EMBL; D90906; BAA17496.1; -.
DR HSSP; Q57816; IFSZ.
DR InterPro; IPR000158; -.
DR InterPro; IPR003008; -.
DR Pfam; PF00091; tubulin; 1.
DR PRINTS; PRO0423; CELLDVIFTSZ.
DR PROSITE; PS01134; FTSZ_1; 1.
DR PROSITE; PS01135; FTSZ_2; 1.
KW Cell division; Septation; GTP-binding.
FT NP_BIND 159 167 GTP (POTENTIAL).
SQ SEQUENCE 430 AA; 44773 MW; E3C7DD554983FF44 CRC64;
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Db 533 VIRII-----NQVSSDAEEDTNGALMEVLSQVISY 562  
::: |::: || :::: :::  
|::: |::: |::: |

Search completed: May 14, 2001, 06:02:05  
Job time: 43362 sec





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DE INTERLEUKIN-13 PRECURSOR (FRAGMENT).
GN IL-13.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Trigona W.T., Hirano A., Brown W.;
RT "Biological activities of interleukin-13 (IL-13) on bovine
RT lymphocytes: implications for signaling through IL-13Ra1."
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF072807; AAD22748.1; -.
DR HSSP; P35225; 3ITR.
DR INTERPRO; IPR001325; -.
DR PROSITE; PS00838; INTERLEUKIN_4_13; UNKNOWN_1.
FT NON_TER 114
SQ SEQUENCE 114 AA; 12355 MW; D8CC56E5627D030A CRC64;

Query Match 59.1%; Score 331.5; DB 6; Length 114;
Best Local Similarity 72.0%; Pred. No. 3.4e-29;
Matches 67; Conservative 10; Mismatches 15; Indels 1; Gaps 1;

QY 1 SPVTPSPTLKELIEELVNITQNK-ASLCNGSMVWSVNLTAGMYCAALESLINVSDCSAIQ 59
Db 21 SPVPSATALKELIEELVNITQNKVPLCNGSMVWSVNLTSMSYCAALDSLISINCSVIQ 80

QY 60 RTQRMKALCSQKPAAGQISSERSRDTKIEVIQ 92
Db 81 RTKRMNLALCPHKPSAKQVSSEYVRDTKIEVAQ 113

RESULT 3
Q9UDC7 PRELIMINARY; PRT; 49 AA.
AC Q9UDC7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE P600 HOMOLOG.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93027259; PubMed=1408833;
RA Morgan J.G., Dolganov G.M., Robbins S.E., Hinton L.M., Lovett M.;
RT "The selective isolation of novel cDNAs encoded by the regions
RT surrounding the human interleukin 4 and 5 genes."
RL Nucleic Acids Res. 20:5173-5179(1992).
DR HSSP; P35225; 3ITR.
SQ SEQUENCE 49 AA; 5109 MW; 679CD23A190C778E CRC64;

Query Match 15.6%; Score 87.5; DB 4; Length 49;
Best Local Similarity 71.4%; Pred. No. 0.012;
Matches 20; Conservative 1; Mismatches 6; Indels 1; Gaps 1;

QY 2 PVTSPPTLKELIEELVNITQNK-ASLCN 28
Db 22 PVPSTALRELIEELSNITQTQKAPLCN 49

RESULT 4
Q28609 PRELIMINARY; PRT; 275 AA.
AC Q28609;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
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DE PUTATIVE PREPROSPERMINOGEN PRECURSOR.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NEW ZEALAND WHITE; TISSUE=TESTIS;
RX MEDLINE=94368861; PubMed=8086468;
RA Richardson R.T., O'Rand M.G.;
RT "Cloning and sequencing of cDNAs for rabbit preproacrosin and a novel
RT preproacrosin-related cDNA."
RL Biochim. Biophys. Acta 1219:215-218(1994).
DR EMBL; U05203; AAA61629.1; -.
DR HSSP; P00734; 2HNT.
DR INTERPRO; IPR001254; -.
DR PFAM; PF00089; trypsin; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
KW SIGNAL.
FT SIGNAL 1 16 POTENTIAL.
FT CHAIN 17 275 PROSPERMINOGEN.
SQ SEQUENCE 275 AA; 29965 MW; 8FC2467414069C61 CRC64;

Query Match 14.3%; Score 80; DB 6; Length 275;
Best Local Similarity 32.3%; Pred. No. 0.58;
Matches 20; Conservative 11; Mismatches 25; Indels 6; Gaps 2;

QY 5 PSPTLKELIEELVNITQNKASLCNGSMVWSVNLTAGMYCAALESLINVSDCSAIQRTQM 64
Db 190 PSPTLMEARVDLINL-----ELCNSTQWYNGRITASNLGAGYPS-GKIDTCQRQLQQLVEV 243

QY 65 LK 66
Db 244 LK 245

RESULT 5
Q9MUM4 PRELIMINARY; PRT; 415 AA.
AC Q9MUM4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE PUTATIVE PLASTID DIVISION PROTEIN.
GN FTSW.
OS Mesostigma viride.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Chlorophyta; Prasinophyceae;
OC Chlorodendrales; Mesostigmataceae; Mesostigma.
OX NCBI_TaxID=41882;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20150907; PubMed=10688199;
RA Lemieux C., Otis C., Turmel M.;
RT "Ancestral chloroplast genome in Mesostigma viride reveals an early
RT branch of green plant evolution."
RL Nature 403:649-652(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Lemieux C., Otis C., Turmel M.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF166114; AAF43874.1; -.
KW Chloroplast.
SQ SEQUENCE 415 AA; 46813 MW; E35116E9692EC782 CRC64;

Query Match 13.2%; Score 74; DB 8; Length 415;
Best Local Similarity 28.4%; Pred. No. 4.3;
Matches 27; Conservative 18; Mismatches 30; Indels 20; Gaps 4;

QY 16 LVNITQNKASLCNGSMVWSVNLTAGMYCAALESLINVSDCSAI-----QRTQRMKAL 68
Db 16 LVNITQNKASLCNGSMVWSVNLTAGMYCAALESLINVSDCSAI-----QRTQRMKAL 68
```

Db 188 LIQPNLSTASLC-GAIWLVALTAGIHWFYLNLSIGAVTALISLGSQEYQRIISFL 246

QY 69 CSQKPAAGQISSERSRDTKIEVIQLVKNLLTYVRG 103

Db 247 ---NPWANPTSIG-----YQLVQSLLAVGSG 269

RESULT 6

Q98779 ID Q98779 PRELIMINARY; PRT; 150 AA.

AC Q98779;

DT 01-FEB-1997 (TReMBLrel. 02, Created)

DT 01-FEB-1997 (TReMBLrel. 02, Last sequence update)

DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)

DE PHOSPHOPROTEIN (FRAGMENT).

OS Vesicular stomatitis virus.

OC Viruses; ssRNA negative-strand viruses; Mononegavirales;

OC Rhabdoviridae; Vesiculovirus.

OX NCBI\_TaxID=11276;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=0888CRB;

RX MEDLINE=97075113; PubMed=8917539;

RA Rodriguez L.L., Fitch W.M., Nichol S.T.;

RT "Ecological factors rather than temporal factors dominate the evolution of vesicular stomatitis virus.";

RL Proc. Natl. Acad. Sci. U.S.A. 93:13030-13035(1996).

DR EMBL; U39211; AAB50939.1; -.

DR INTERPRO; IPR000224; -.

DR PFAM; PF00922; Phosphoprotein; 1.

FT NON\_TER 1

FT NON\_TER 150

SQ SEQUENCE 150 AA; 16711 MW; 16D11C4E8E8A65E7 CRC64;

Query Match 13.0%; Score 73; DB 14; Length 150;

Best Local Similarity 24.2%; Pred. No. 1.7;

Matches 29; Conservative 19; Mismatches 42; Indels 30; Gaps 6;

QY 2 PVTSPPTLKEIEEL-----VNITQNA-----SLCNGSMVWSVN-----LTAGMY 42

Db 14 PSWTQPVIKENGERSLSLFPVPVGLTQVQTEQWKKTETVCESKYWNLSQCIVTSG-N 72

QY 43 CAALESLINVSDCSAIQRTQRMKALCSQKPAAGQISSERSR-----DTKIEVIQLV 94

Db 73 CLILRGQVMTSDCSSSAKSNRQS--SESFSPNSPEHASRASASPNLWDFKFTVEVQLI 130

RESULT 7

Q9Q8P4 ID Q9Q8P4 PRELIMINARY; PRT; 350 AA.

AC Q9Q8P4;

DT 01-MAY-2000 (TReMBLrel. 13, Created)

DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)

DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)

DE M52L.

GN M052L.

OS Myxoma virus.

OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;

OC Leporipoxvirus.

OX NCBI\_TaxID=10273;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=LAUSANNE;

RX MEDLINE=20032073; PubMed=10562494;

RA Cameron C., Hota-Mitchell S., Chen L., Barrett J., Cao J.X.,

RA Macaulay C., Willer D., Evans D., McFadden G.;

RT "The complete DNA sequence of myxoma virus.";

RL Virology 264:298-318(1999).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=LAUSANNE;

RA Cameron C., Hota-Mitchell S., Chen L., Barrett J., Cao J.-X.,

RA Macaulay C., Willer D., Evans D., McFadden G.;

RL Submitted (JUL-1999) to the EMBL/GenBank/DBDJ databases.

DR EMBL; AFI70726; AAF14940.1; -.

SQ SEQUENCE 350 AA; 39157 MW; 4D9CC2B04ACFCB7F CRC64;

Query Match 13.0%; Score 73; DB 14; Length 350;

Best Local Similarity 22.3%; Pred. No. 4.6;

Matches 29; Conservative 22; Mismatches 37; Indels 42; Gaps 5;

QY 6 SPTLKE-----LIEELVNITQNAQSLCNGSMVWSVN----- 36

Db 45 APTIKENVINGIYFCENNIVVRDIPHLVEILNKLKNSVYVCNSNEFWRLYNSLSRFTH 104

QY 37 -----LTAGMY--CAALESLINVSDCSAIQRTQRMKAL-----CSQKPAAGQISSERSR 85

Db 105 CKSFPTACMYTIIATLSTLVTLVLSNKLHHAADMIESIYLFQAQKPPAQELSD--LLE 162

QY 86 TKIEVIQLVK 95

Db 163 MKYGLINLVQ 172

RESULT 8

Q98791 ID Q98791 PRELIMINARY; PRT; 150 AA.

AC Q98791;

DT 01-FEB-1997 (TReMBLrel. 02, Created)

DT 01-FEB-1997 (TReMBLrel. 02, Last sequence update)

DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)

DE PHOSPHOPROTEIN (FRAGMENT).

OS Vesicular stomatitis virus.

OC Viruses; ssRNA negative-strand viruses; Mononegavirales;

OC Rhabdoviridae; Vesiculovirus.

OX NCBI\_TaxID=11276;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=1286CRB3;

RX MEDLINE=97075113; PubMed=8917539;

RA Rodriguez L.L., Fitch W.M., Nichol S.T.;

RT "Ecological factors rather than temporal factors dominate the evolution of vesicular stomatitis virus.";

RL Proc. Natl. Acad. Sci. U.S.A. 93:13030-13035(1996).

DR EMBL; U39223; AAB50951.1; -.

DR INTERPRO; IPR000224; -.

DR PFAM; PF00922; Phosphoprotein; 1.

FT NON\_TER 1

FT NON\_TER 150

SQ SEQUENCE 150 AA; 16577 MW; E3D1095B842ACFFD CRC64;

Query Match 12.8%; Score 72; DB 14; Length 150;

Best Local Similarity 24.2%; Pred. No. 2.2;

Matches 29; Conservative 17; Mismatches 44; Indels 30; Gaps 6;

QY 2 PVTSPPTLKEIEEL-----VNITQNA-----SLCNGSMVWSVN-----LTAGMY 42

Db 14 PSWTQPVIKENGERSLSLFPVPVGLTQVQTEQWKKTETVCESKYWNLSQCIVTSG-N 72

QY 43 CAALESLINVSDCSAIQRTQRMKALCSQKPAAGQISSERSR-----DTKIEVIQLV 94

Db 73 CLILRGQVMTSDCSSSAKSN--SQSSSESPSPNSPEHASRASASPNLWDLKFTVEVQLI 130

RESULT 9

Q9M3H8 ID Q9M3H8 PRELIMINARY; PRT; 438 AA.

AC Q9M3H8;

DT 01-OCT-2000 (TReMBLrel. 15, Created)

DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)

DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)

DE PUTATIVE UDP-GLYCOSE (FRAGMENT).

OS Cicer arietinum (Chickpea) (Garbanzo).

OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC	Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
OC	Fabales; Fabaceae; Papilionoideae; Cicer.
OX	NCBI_TaxID=3827;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=CV. CASTELLANA; TISSUE=ETIOLATED EPICOTYLS;
RA	Dopico B., Munoz F.J., Labrador E.;
RT	"A putative UDP-Glycose: Flavonoid glycosyltransferase is expressed in
RT	chickpea epicotyls.";
RL	Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AJ400861; CAB88666.1; -
FT	NON_TER 1
SQ	SEQUENCE 438 AA; 48662 MW; 0BB7B805BD66E27C CRC64;
Query Match 12.8%; Score 72; DB 10; Length 438;	
Best Local Similarity 26.7%; Pred. No. 7.7;	
Matches 36; Conservative 21; Mismatches 46; Indels 32; Gaps 7;	
QY	2 PVTSPPTLKEIEELV-----ITQNQASL-----CNGSMVSVNLTAGMYC 43
Db	136 PIKSPGFGARLTEPLVBAEKGGSHGVIVNSFAELDEGYEYENLTGRKVVHVGPTSLMIK 195
QY	44 AALESLINVSDCSAIQRTQRMKALCSQKPA-----GQISSERSRDTKIEV---IQLV 94
Db	196 TTLEKTDNISNGSSTK--HKCLTWLDTKEPSSVVYISFGSLCS-LSNDQLELAKGIEAS 252
QY	95 KNLITYVRGVYRHGN 109
Db	253 KHQFLWV--VHRKGD 265
RESULT 10	
QY	2 PVTSPPTLKEIEEL-----VNITQNQA-----SLCNGSMVWSVN-----LTAGMY 42
Db	14 PSWTQPVIKENGERSLSLFPVGLTQVQTEQWKKTETVCESKYWNLSQCQIVTSG-N 72
QY	43 CAALESLINVSDCSAIQRTQRMKALCSQKPAAGQISSERSR-----DTKIEVIQLV 94
Db	73 CLILRGQVMTSDCSSAKSQN--SGQSSESPSPNSPEHASRASASPNLWDFKFTVQLI 130
Query Match 12.7%; Score 71; DB 14; Length 150;	
Best Local Similarity 24.2%; Pred. No. 2.9;	
Matches 29; Conservative 17; Mismatches 44; Indels 30; Gaps 6;	
QY	2 PVTSPPTLKEIEEL-----VNITQNQA-----SLCNGSMVWSVN-----LTAGMY 42
Db	14 PSWTQPVIKENGERSLSLFPVGLTQVQTEQWKKTETVCESKYWNLSQCQIVTSG-N 72
QY	43 CAALESLINVSDCSAIQRTQRMKALCSQKPAAGQISSERSR-----DTKIEVIQLV 94
Db	73 CLILRGQVMTSDCSSAKSQN--SGQSSESPSPNSPEHASRASASPNLWDFKFTVQLI 130
RESULT 12	
QY	2 PVTSPPTLKEIEEL-----VNITQNQA-----SLCNGSMVWSVN-----LTAGMY 42
Db	14 PSWTQPVIKENGERSLSLFPVGLTQVQTEQWKKTETVCESKYWNLSQCQIVTSG-N 72
QY	43 CAALESLINVSDCSAIQRTQRMKALCSQKPAAGQISSERSR-----DTKIEVIQLV 94
Db	73 CLILRGQVMTSDCSSAKSQN--SGQSSESPSPNSPEHASRASASPNLWDFKFTVQLI 130
Query Match 12.7%; Score 71; DB 14; Length 150;	
Best Local Similarity 24.2%; Pred. No. 2.9;	
Matches 29; Conservative 17; Mismatches 44; Indels 30; Gaps 6;	
QY	2 PVTSPPTLKEIEEL-----VNITQNQA-----SLCNGSMVWSVN-----LTAGMY 42
Db	14 PSWTQPVIKENGERSLSLFPVGLTQVQTEQWKKTETVCESKYWNLSQCQIVTSG-N 72
QY	43 CAALESLINVSDCSAIQRTQRMKALCSQKPAAGQISSERSR-----DTKIEVIQLV 94
Db	73 CLILRGQVMTSDCSSAKSQN--SGQSSESPSPNSPEHASRASASPNLWDFKFTVQLI 130

OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC	Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
OC	Fabales; Fabaceae; Papilionoideae; Cicer.
OX	NCBI_TaxID=3827;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=CV. CASTELLANA; TISSUE=ETIOLATED EPICOTYLS;
RA	Dopico B., Munoz F.J., Labrador E.;
RT	"A putative UDP-Glycose: Flavonoid glycosyltransferase is expressed in
RT	chickpea epicotyls.";
RL	Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AJ400861; CAB88666.1; -
FT	NON_TER 1
SQ	SEQUENCE 438 AA; 48662 MW; 0BB7B805BD66E27C CRC64;
Query Match 12.8%; Score 72; DB 10; Length 438;	
Best Local Similarity 26.7%; Pred. No. 7.7;	
Matches 36; Conservative 21; Mismatches 46; Indels 32; Gaps 7;	
QY	2 PVTSPPTLKEIEELV-----ITQNQASL-----CNGSMVSVNLTAGMYC 43
Db	136 PIKSPGFGARLTEPLVBAEKGGSHGVIVNSFAELDEGYEYENLTGRKVVHVGPTSLMIK 195
QY	44 AALESLINVSDCSAIQRTQRMKALCSQKPA-----GQISSERSRDTKIEV---IQLV 94
Db	196 TTLEKTDNISNGSSTK--HKCLTWLDTKEPSSVVYISFGSLCS-LSNDQLELAKGIEAS 252
QY	95 KNLITYVRGVYRHGN 109
Db	253 KHQFLWV--VHRKGD 265
RESULT 10	
QY	2 PVTSPPTLKEIEEL-----VNITQNQA-----SLCNGSMVWSVN-----LTAGMY 42
Db	14 PSWTQPVIKENGERSLSLFPVGLTQVQTEQWKKTETVCESKYWNLSQCQIVTSG-N 72
QY	43 CAALESLINVSDCSAIQRTQRMKALCSQKPAAGQISSERSR-----DTKIEVIQLV 94
Db	73 CLILRGQVMTSDCSSAKSQN--SGQSSESPSPNSPEHASRASASPNLWDFKFTVQLI 130
Query Match 12.7%; Score 71; DB 14; Length 150;	
Best Local Similarity 24.2%; Pred. No. 2.9;	
Matches 29; Conservative 17; Mismatches 44; Indels 30; Gaps 6;	
QY	2 PVTSPPTLKEIEEL-----VNITQNQA-----SLCNGSMVWSVN-----LTAGMY 42
Db	14 PSWTQPVIKENGERSLSLFPVGLTQVQTEQWKKTETVCESKYWNLSQCQIVTSG-N 72
QY	43 CAALESLINVSDCSAIQRTQRMKALCSQKPAAGQISSERSR-----DTKIEVIQLV 94
Db	73 CLILRGQVMTSDCSSAKSQN--SGQSSESPSPNSPEHASRASASPNLWDFKFTVQLI 130
RESULT 12	
QY	2 PVTSPPTLKEIEEL-----VNITQNQA-----SLCNGSMVWSVN-----LTAGMY 42
Db	14 PSWTQPVIKENGERSLSLFPVGLTQVQTEQWKKTETVCESKYWNLSQCQIVTSG-N 72
QY	43 CAALESLINVSDCSAIQRTQRMKALCSQKPAAGQISSERSR-----DTKIEVIQLV 94
Db	73 CLILRGQVMTSDCSSAKSQN--SGQSSESPSPNSPEHASRASASPNLWDFKFTVQLI 130
Query Match 12.7%; Score 71; DB 14; Length 150;	
Best Local Similarity 24.2%; Pred. No. 2.9;	
Matches 29; Conservative 17; Mismatches 44; Indels 30; Gaps 6;	
QY	2 PVTSPPTLKEIEEL-----VNITQNQA-----SLCNGSMVWSVN-----LTAGMY 42
Db	14 PSWTQPVIKENGERSLSLFPVGLTQVQTEQWKKTETVCESKYWNLSQCQIVTSG-N 72
QY	43 CAALESLINVSDCSAIQRTQRMKALCSQKPAAGQISSERSR-----DTKIEVIQLV 94
Db	73 CLILRGQVMTSDCSSAKSQN--SGQSSESPSPNSPEHASRASASPNLWDFKFTVQLI 130





RC STRAIN-FRIEDLIN;  
RA Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,  
RA Smith D.F.;  
RT "A physical map of the Leishmania major Friedlin genome.";  
RL Genome Res. 8:135-145(1998).  
DR EMBL; AL358652; CAB94012.1; -.  
KW Hypothetical protein.  
SQ SEQUENCE 670 AA; 73399 MW; 46942AE667026D1F CRC64;

Query Match	12.3%;	Score 69;	DB 5;	Length 670;
Best Local Similarity	24.8%;	Pred. NO. 27;		
Matches	27;	Conservative	20;	Mismatches 38;
		Indels	24;	Gaps 5;

Qy	4	TPS-PTLKELEEELVNITQNQASL-----CNGSMVWSVNLTAGMYCAALESLINVSDC	55
		:   :   :   :   :   :   :   :   :   :   :   :	
Dd	367	TPSLVSLLRVWEVVTOIPDLRAPLORLLPFNCTGFFLWCLORYPGLYQSPVES-----	419

**QY**      56 SATQRTQRM LKALCSQ KPAAGQISSERSRDTKTIEVTLVKNLLTYVRGV 104  
             | : : : | : : | : : | : : | : : | : : | : : | : :  
**Dbb**     420 ---QSQQKATRRVCA---LLGCLAVEESNAEKLPA LLKV---LTHDKGV 459

Search completed: May 14, 2001, 06:01:11  
Job time: 43954 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: May 13, 2001, 17:47:35 ; Search time 79.9 seconds  
(without alignments)  
93.007 Million cell updates/sec

Title: US-09-451-527-100  
Perfect score: 658  
Sequence: 1 MALWLTWVIALTCGLGLASP.....QLVKNLLTYVRGVYRHGNER 130

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 390729 seqs, 57163235 residues

Total number of hits satisfying chosen parameters: 390729

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_0401:\*  
1: /cgnl\_8/gcgdata/geneseq/geneseqp/AA1980.DAT.\*  
2: /cgnl\_8/gcgdata/geneseq/geneseqp/AA1981.DAT.\*  
3: /cgnl\_8/gcgdata/geneseq/geneseqp/AA1982.DAT.\*  
4: /cgnl\_8/gcgdata/geneseq/geneseqp/AA1983.DAT.\*  
5: /cgnl\_8/gcgdata/geneseq/geneseqp/AA1984.DAT.\*  
6: /cgnl\_8/gcgdata/geneseq/geneseqp/AA1985.DAT.\*  
7: /cgnl\_8/gcgdata/geneseq/geneseqp/AA1986.DAT.\*  
8: /cgnl\_8/gcgdata/geneseq/geneseqp/AA1987.DAT.\*  
9: /cgnl\_8/gcgdata/geneseq/geneseqp/AA1988.DAT.\*  
10: /cgnl\_8/gcgdata/geneseq/geneseqp/AA1989.DAT.\*  
11: /cgnl\_8/gcgdata/geneseq/geneseqp/AA1990.DAT.\*  
12: /cgnl\_8/gcgdata/geneseq/geneseqp/AA1991.DAT.\*  
13: /cgnl\_8/gcgdata/geneseq/geneseqp/AA1992.DAT.\*  
14: /cgnl\_8/gcgdata/geneseq/geneseqp/AA1993.DAT.\*  
15: /cgnl\_8/gcgdata/geneseq/geneseqp/AA1994.DAT.\*  
16: /cgnl\_8/gcgdata/geneseq/geneseqp/AA1995.DAT.\*  
17: /cgnl\_8/gcgdata/geneseq/geneseqp/AA1996.DAT.\*  
18: /cgnl\_8/gcgdata/geneseq/geneseqp/AA1997.DAT.\*  
19: /cgnl\_8/gcgdata/geneseq/geneseqp/AA1998.DAT.\*  
20: /cgnl\_8/gcgdata/geneseq/geneseqp/AA1999.DAT.\*  
21: /cgnl\_8/gcgdata/geneseq/geneseqp/AA2000.DAT.\*  
22: /cgnl\_8/gcgdata/geneseq/geneseqp/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	658	100.0	130	21 Y58223	Canine interleukin
2	647.5	98.4	131	21 Y58221	Canine interleukin
3	556	84.5	110	21 Y58224	Canine mature inte
4	545.5	82.9	111	21 Y58222	Canine mature inte
5	448	68.1	132	15 R48624	Sequence of human
6	441	67.0	146	13 R27348	Cytokine NC30. R
7	385	58.5	131	15 R48625	Sequence of mouse
8	377.5	57.4	111	17 R92794	Human interleukin-
9	367	55.8	112	13 R27347	Protein with cytok
10	367	55.8	112	17 R92793	Human interleukin-
11	360	54.7	112	13 R27346	Protein with cytok

12	302	45.9	111	17 R92795	Murine P600. Mus
13	81	12.3	20	13 R27345	Cytokine signal pe
14	81	12.3	34	13 R27344	Cytokine signal pe
15	79	12.0	665	21 B38312	Human secreted pro
16	79	12.0	667	21 B38311	Gene 38 human secr
17	79	12.0	1230	18 W15764	TIP120. Rattus ra
18	79	12.0	1230	21 B42180	Human ORFX ORF1944
19	78	11.9	21	20 Y49702	Human interleukin
20	77.5	11.8	634	20 Y21548	Human heparin-bind
21	72.5	11.0	286	21 Y58998	Wheat sulfite redu
22	72	10.9	141	21 G35063	Arabidopsis thalia
23	72	10.9	482	13 R20641	Placental-derived
24	72	10.9	482	17 R77531	Human platelet der
25	72	10.9	482	19 W62026	Recombinantly prod
26	72	10.9	5072	12 R11510	Ryanodine receptor
27	71.5	10.9	718	20 W84067	Drosophila mitofus
28	71	10.8	482	19 W62025	Recombinantly prod
29	70	10.6	237	21 Y84892	A human proliferat
30	70	10.6	330	21 G06262	Arabidopsis thalia
31	70	10.6	407	21 G06261	Arabidopsis thalia
32	69.5	10.6	513	11 R04585	Aquaricine I. The
33	69.5	10.6	513	12 R13181	T.aquaticus Aquari
34	69.5	10.6	513	16 R67653	Aqualysin I. Ther
35	69.5	10.6	980	19 W69741	SAPAP2 protein. H
36	69.5	10.6	980	19 W69743	SAPAP1 protein. H
37	69	10.5	4987	12 R10834	Rianodin receptor.
38	68.5	10.4	221	21 Y91434	Human secreted pro
39	67	10.2	150	16 R85457	Flax rust resistan
40	67	10.2	618	16 R85456	Flax rust resistan
41	67	10.2	673	21 Y58996	Rice sulfite reduc
42	66	10.0	387	20 Y08621	Human secreted pro
43	66	10.0	387	21 Y67312	Human secreted pro
44	66	10.0	477	18 W21643	Grapevine leafroll
45	65.5	10.0	135	21 B41418	Human ORFX ORF1182

ALIGNMENTS

RESULT 1  
Y58223  
ID Y58223 standard; Protein; 130 AA.  
XX  
AC Y58223;  
XX  
DT 14-MAR-2000 (first entry)  
XX  
DE Canine interleukin-13 (IL-13) clone 78.  
XX  
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;  
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine.  
XX  
OS Canis familiaris.  
XX  
PN WO9961618-A2.  
XX  
PD 02-DEC-1999.  
XX  
PF 28-MAY-1999; 99WO-US11942.  
XX  
PR 29-MAY-1998; 98US-0087306.  
XX  
PA (HESK-) HESKA CORP.  
XX  
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;  
XX  
DR WPI; 2000-072623/06.  
DR N-PSDB; 2555561, 2555562, 2555563, 2555564.  
XX  
PT Nucleic acids encoding immunoregulatory proteins. from cats or dogs,  
PT useful for treating or preventing e.g. tumors or autoimmune disease  
XX  
PS Claim 3i; Page 237; 264pp; English.

XX Sequences Y58221-Y58222 and Y58223-Y58224 represent encoded and mature  
CC canine interleukin-13 (IL-13) clones 80 and 78. The invention relates to  
CC canine IL-4, canine or feline Flt-3 ligand, canine or feline CD40,  
CC canine or feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline  
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage  
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these  
CC immunoregulatory proteins. The proteins, their associated  
CC nucleic acids, specific antibodies and inhibitors may be used as  
CC vaccines for therapeutic or prophylactic regulation of an immune  
CC response in animals (particularly cats, dogs, horses and humans).  
CC They may be used to treat autoimmune or infectious diseases including  
CC allergies, tumours, inflammation and graft rejection, and to increase  
CC the response from a co-administered antigen. The nucleotide sequences  
CC can also be used for the recombinant production of a protein, while  
CC nucleotide fragments are useful as probes, as amplification primers and  
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
CC The proteins may be used to raise antibodies and to screen for  
CC modulators of activity, while the antibodies may be used in detection,  
CC and in drug targeting.  
XX  
SQ Sequence 130 AA;

Query Match 100.0%; Score 658; DB 21; Length 130;  
Best Local Similarity 100.0%; Pred. No. 1.9e-68;  
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALWLTVVIALTCGLGLASPSVPTPSPTLKELIEELVNITQNASLNGSMVWSVNLTAG 60  
|||||  
Db 1 malwltvvialtcglglaspsvptpsptlkelielvnitqnaslcnsgsmvwsvnltag 60  
  
QY 61 MYCAALESINVSDCSAIQRTQRMKALCSQKPAAGISSERSRDTKIEVIQLVKNLLTYV 120  
|||||  
Db 61 mycaaleslinvsdcsaigrtqrmkalcscqkpaagissersrdtkieviqlvknlltyv 120  
  
QY 121 RGVYRHGNFR 130  
|||||  
Db 121 rgvyrhgnfr 130

RESULT 2  
Y58221  
ID Y58221 standard; Protein; 131 AA.  
XX Y58221;  
AC Y58221;  
XX  
DT 14-MAR-2000 (first entry)  
XX  
DE Canine interleukin-13 (IL-13) clone 80.  
XX  
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;  
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine.  
XX  
OS Canis familiaris.  
XX  
PN WO9961618-A2.  
XX  
PD 02-DEC-1999.  
XX  
PF 28-MAY-1999; 99WO-US11942.  
XX  
PR 29-MAY-1998; 98US-0087306.  
XX  
PA (HESK-) HESKA CORP.  
XX  
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;  
XX  
XX WPI; 2000-072623/06.  
DR N-PSDB; 255555, 255556, 255557, 255558.  
XX  
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
PT useful for treating or preventing e.g. tumors or autoimmune disease

XX Claim 3i; Page 231; 264pp; English.  
PS  
XX  
CC Sequences Y58221-Y58222 and Y58223-Y58224 represent encoded and mature  
CC canine interleukin-13 (IL-13) clones 80 and 78. The invention relates to  
CC canine IL-4, canine or feline Flt-3 ligand, canine or feline CD40,  
CC canine or feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline  
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage  
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these  
CC immunoregulatory proteins. The proteins, their associated  
CC nucleic acids, specific antibodies and inhibitors may be used as  
CC vaccines for therapeutic or prophylactic regulation of an immune  
CC response in animals (particularly cats, dogs, horses and humans).  
CC They may be used to treat autoimmune or infectious diseases including  
CC allergies, tumours, inflammation and graft rejection, and to increase  
CC the response from a co-administered antigen. The nucleotide sequences  
CC can also be used for the recombinant production of a protein, while  
CC nucleotide fragments are useful as probes, as amplification primers and  
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
CC The proteins may be used to raise antibodies and to screen for  
CC modulators of activity, while the antibodies may be used in detection,  
CC and in drug targeting.  
XX  
SQ Sequence 131 AA;

Query Match 98.4%; Score 647.5; DB 21; Length 131;  
Best Local Similarity 99.2%; Pred. No. 3.2e-67;  
Matches 130; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MALWLTVVIALTCGLGLASPSVPTPSPTLKELIEELVNITQNASLNGSMVWSVNLTAG 60  
|||||  
Db 1 malwltvvialtcglglaspsvptpsptlkelielvnitqnaslcnsgsmvwsvnltag 60  
  
QY 61 MYCAALESINVSDCSAIQRTQRMKALCSQKPAAG-ISSERSRDTKIEVIQLVKNLLTY 119  
|||||  
Db 61 mycaaleslinvsdcsaigrtqrmkalcscqkpaagissersrdtkieviqlvknllty 120  
  
QY 120 RGVYRHGNFR 130  
|||||  
Db 121 rgvyrhgnfr 131

RESULT 3  
Y58224  
ID Y58224 standard; Protein; 110 AA.  
XX Y58224;  
AC Y58224;  
XX  
DT 14-MAR-2000 (first entry)  
XX  
DE Canine mature interleukin-13 (IL-13) clone 78.  
XX  
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;  
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine.  
XX  
OS Canis familiaris.  
XX  
PN WO9961618-A2.  
XX  
PD 02-DEC-1999.  
XX  
PF 28-MAY-1999; 99WO-US11942.  
XX  
PR 29-MAY-1998; 98US-0087306.  
XX  
PA (HESK-) HESKA CORP.  
XX  
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;  
XX  
XX WPI; 2000-072623/06.  
DR N-PSDB; 255565, 255566.  
XX

PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
PT useful for treating or preventing e.g. tumors or autoimmune disease  
XX  
PS Claim 3i; Page 240; 264pp; English.  
XX  
CC Sequences Y58221-Y58222 and Y58223-Y58224 represent encoded and mature  
CC canine interleukin-13 (IL-13) clones 80 and 78. The invention relates to  
CC canine IL-4, canine or feline Flt-3 ligand, canine or feline CD40,  
CC canine or feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline  
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage  
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these  
CC immunoregulatory proteins. The proteins, their associated  
CC nucleic acids, specific antibodies and inhibitors may be used as  
CC vaccines for therapeutic or prophylactic regulation of an immune  
CC response in animals (particularly cats, dogs, horses and humans).  
CC They may be used to treat autoimmune or infectious diseases including  
CC allergies, tumours, inflammation and graft rejection, and to increase  
CC the response from a co-administered antigen. The nucleotide sequences  
CC can also be used for the recombinant production of a protein, while  
CC nucleotide fragments are useful as probes, as amplification primers and  
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
CC The proteins may be used to raise antibodies and to screen for  
CC modulators of activity, while the antibodies may be used in detection,  
CC and in drug targetting.  
XX  
SQ Sequence 110 AA;

Query Match 84.5%; Score 556; DB 21; Length 110;  
Best Local Similarity 100.0%; Pred. No. 9.7e-57;  
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 SPVTPSPTLKELIEELVNITQNQASLCNGSMVWSVNLTAGMYCAALESLINVSDCSAIQR 80  
Db 1 spvtpsptlikelieelvnitqngaslcngsmvwsvnltagmycaaleslinvsdcsaiqr 60  
QY 81 TQRLKALCSQKPAAGISSERSRDTKIEVIQLVKNLLTYVRGVYRHGNFR 130  
Db 61 tqrlmkalcsqkpaagissersrdtkieviqlvknlltyvrgvyrhgnfr 110

RESULT 4  
Y58222  
ID Y58222 standard; Protein; 111 AA.  
XX  
AC Y58222;  
XX  
DT 14-MAR-2000 (first entry)  
XX  
DE Canine mature interleukin-13 (IL-13) clone 80.  
XX  
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;  
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine.  
XX  
OS Canis familiaris.  
XX  
PN WO9961618-A2.  
XX  
PD 02-DEC-1999.  
XX  
PF 28-MAY-1999; 99WO-US11942.  
XX  
PR 29-MAY-1998; 98US-0087306.  
XX  
PA (HESK-) HESKA CORP.  
XX  
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;  
XX WPI; 2000-072623/06.  
DR N-PSDB; Z55559, Z55560.  
XX  
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
PT useful for treating or preventing e.g. tumors or autoimmune disease -

XX Claim 3i; Page 234; 264pp; English.  
PS  
XX  
CC Sequences Y58221-Y58222 and Y58223-Y58224 represent encoded and mature  
CC canine interleukin-13 (IL-13) clones 80 and 78. The invention relates to  
CC canine IL-4, canine or feline Flt-3 ligand, canine or feline CD40,  
CC canine or feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline  
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage  
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these  
CC immunoregulatory proteins. The proteins, their associated  
CC nucleic acids, specific antibodies and inhibitors may be used as  
CC vaccines for therapeutic or prophylactic regulation of an immune  
CC response in animals (particularly cats, dogs, horses and humans).  
CC They may be used to treat autoimmune or infectious diseases including  
CC allergies, tumours, inflammation and graft rejection, and to increase  
CC the response from a co-administered antigen. The nucleotide sequences  
CC can also be used for the recombinant production of a protein, while  
CC nucleotide fragments are useful as probes, as amplification primers and  
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
CC The proteins may be used to raise antibodies and to screen for  
CC modulators of activity, while the antibodies may be used in detection,  
CC and in drug targetting.  
XX  
SQ Sequence 111 AA;

Query Match 82.9%; Score 545.5; DB 21; Length 111;  
Best Local Similarity 99.1%; Pred. No. 1.6e-55;  
Matches 110; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 21 SPVTPSPTLKELIEELVNITQNQASLCNGSMVWSVNLTAGMYCAALESLINVSDCSAIQR 80  
Db 1 spvtpsptlikelieelvnitqngaslcngsmvwsvnltagmycaaleslinvsdcsaiqr 60  
QY 81 TQRLKALCSQKPAAG-ISSERSRDTKIEVIQLVKNLLTYVRGVYRHGNFR 130  
Db 61 tqrlmkalcsqkpaagqissersrdtkieviqlvknlltyvrgvyrhgnfr 111

RESULT 5  
R48624  
ID R48624 standard; Protein; 132 AA.  
XX  
AC R48624;  
XX  
DT 14-SEP-1994 (first entry)  
XX  
DE Sequence of human interleukin-13 (IL-13).  
XX  
KW Interleukin-13; lymphokine; immunological disorder; therapy;  
KW diagnostic.  
XX  
OS Homo sapiens.  
XX  
PN WO9404680-A.  
XX  
PD 03-MAR-1994.  
XX  
PF 18-AUG-1993; 93WO-US07645.  
XX  
PR 21-AUG-1992; 92US-0933416.  
PR 29-JAN-1993; 93US-0010977.  
PR 01-FEB-1993; 93US-0012543.  
XX  
PA (SCHE ) SCHERING CORP.  
XX  
PI Aversa G, Banchemreau J, Briere F, Coffman RL, Cooks BG;  
PI Culpepper, Dang W, De Vries J, De Waal Malefyt R;  
PI Doherty TM, Heath A, Mckenzie A, Punnonen J, Zurawski G;  
XX WPI; 1994-083197/10.  
DR N-PSDB; Q56692.  
XX



PT Purified interleukin-13 proteins and antibodies - obtd. using  
PT mouse gene encoding related protein P600  
XX  
PS Claime 1; Page 126-127; 135pp; English.  
XX  
CC An approx. 400 bp DNA fragment derived from a Pst/PvuII restriction  
CC digest of the mouse P600 cDNA clone was isolated. This fragment,  
CC which encompasses most of the coding region of the mouse P600 cDNA,  
CC was radioactively labelled and hybridised with filter lifts prepd.  
CC from a cDNA library made from a clone of an A10 T cell line. One  
CC clone, designated PA 10.66, was subcloned into M13 and sequenced.  
CC This sequence encodes human IL-13.  
XX  
SQ Sequence 132 AA;  
  
Query Match 68.1%; Score 448; DB 15; Length 132;  
Best Local Similarity 71.0%; Pred. No. 4e-44;  
Matches 93; Conservative 11; Mismatches 25; Indels 2; Gaps 2;  
  
QY 1 MALWLTVVIALTCLGLASPSVPTPSPTLKEIEELVNITQK-ASLCNGSMVWSVNLT 59  
Db 1 mallttvtialtcclgffaspgvpvpstaltrelieelvnitqngkaplcngsmvwsinlta 60  
  
QY 60 GMYCAALESLINVSDCSAIQRTQRMKALCSQKPAAG-ISSERSRDTKIEVIQLVKNNLT 118  
Db 61 gmycaaleslinvsgsaiektqrmlsgfcphkvsagqfsslhvrdtkievagfvkdlll 120  
  
QY 119 YVRGVYRHGNE 129  
Db 121 hlklfregrf 131  
  
RESULT 6  
R27348  
ID R27348 standard; Protein; 146 AA.  
XX  
AC R27348;  
XX  
DT 24-FEB-1993 (first entry)  
XX  
DE Cytokine NC30.  
XX  
KW Interleukin; chemotaxis; immunomodulation; inflammation.  
XX  
FH Key Location/Qualifiers  
FT cleavage\_site 20..21 /note= "putative signal peptide cleavage site"  
FT cleavage\_site 24..25 /note= "putative signal peptide cleavage site"  
FT cleavage\_site 32..33 /note= "putative signal peptide cleavage site"  
FT cleavage\_site 34..35 /note= "putative signal peptide cleavage site"  
FT protein 35..146 /label= NC30  
XX  
PN EP506574-A.  
XX  
PD 30-SEP-1992.  
XX  
PE 27-MAR-1992; 92EP-0400858.  
XX  
PR 29-MAR-1991; 91FR-0003904.  
PR 08-JAN-1992; 92FR-0000137.  
XX  
PA (SNFI) ELF SANOFI.  
XX  
PI Caput D, Ferrara P, Guillemot J, Kaghad M, Labit-le Bouteiller C;  
PI Leplatols P, Magazin M, Minty A;  
XX  
DR WPI; 1992-325841/40.  
DR N-PSDB; Q28947.

XX New cytokine having immunomodulatory activity - useful for  
PT treating tumours and infectious or inflammatory conditions  
PT  
XX  
PS Claim 1; Page 52-53; 78pp; French.  
XX  
CC A novel cytokine produced by T lymphocytes induced by phorbol-2-  
CC myristate-3-acetate and phytohaemagglutinin was coded for by the  
CC sequence in clone pSEI-NC30. A second clone was also identified  
CC (pSEI-NC30bis) which differed only in the identity of codon 41.  
CC The corresponding proteins differ in the amino acid at position 41  
CC which is either Asp (in NC30) or Gly (in NC30bis). The cytokine  
CC acts on monocytes and B lymphocytes and is useful in treatment of  
CC tumours and some infections and inflammatory conditions.  
CC See Q28941-Q28947.  
XX  
SQ Sequence 146 AA;  
  
Query Match 67.0%; Score 441; DB 13; Length 146;  
Best Local Similarity 70.2%; Pred. No. 3e-43;  
Matches 92; Conservative 11; Mismatches 26; Indels 2; Gaps 2;  
  
QY 1 MALWLTVVIALTCLGLASPSVPTPSPTLKEIEELVNITQK-ASLCNGSMVWSVNLT 59  
Db 15 mallttvtialtcclgffaspgvpvpstaltrelieelvnitqngkaplcngsmvwsinlta 74  
  
QY 60 GMYCAALESLINVSDCSAIQRTQRMKALCSQKPAAG-ISSERSRDTKIEVIQLVKNNLT 118  
Db 75 dmycaaleslinvsgsaiektqrmlsgfcphkvsagqfsslhvrdtkievagfvkdlll 134  
  
QY 119 YVRGVYRHGNE 129  
Db 135 hlklfregrf 145  
  
RESULT 7  
R48625  
ID R48625 standard; Protein; 131 AA.  
XX  
AC R48625;  
XX  
DT 14-SEP-1994 (first entry)  
XX  
DE Sequence of mouse P600.  
XX  
KW Interleukin-13; lymphokine; P600; immunological disorder; therapy;  
KW diagnostic.  
XX  
OS Mus musculus.  
XX  
PN WO9404680-A.  
XX  
PD 03-MAR-1994.  
XX  
PE 18-AUG-1993; 93WO-US07645.  
XX  
PR 21-AUG-1992; 92US-0933416.  
PR 29-JAN-1993; 93US-0010977.  
PR 01-FEB-1993; 93US-0012543.  
XX  
PA (SCHE) SCHERING CORP.  
XX  
PI Aversa G, Banchereau J, Briere F, Coffman RL, Cooks BG;  
PI Culpepper, Dang W, De Vries J, De Waal Malefyt R;  
PI Doherty TM, Heath A, Mckenzie A, Punnonen J, Zurawski G;  
XX  
DR WPI; 1994-083197/10.  
DR N-PSDB; Q56693.  
XX  
PT Purified interleukin-13 proteins and antibodies - obtd. using  
PT mouse gene encoding related protein P600  
XX

PS Disclosure; Page 128-129; 135pp; English.

XX

CC An approx. 400 bp DNA fragment derived from a Pst/PvuII restriction

CC digest of the mouse P600 cDNA clone was isolated. This fragment,

CC which encompasses most of the coding region of the mouse P600 cDNA,

CC was radioactively labelled and hybridised with filter lifts prepd.

CC from a cDNA library made from a clone of an A10 T cell line. One

CC clone, designated PA 10.66, was subcloned into M13 and sequenced.

CC This sequence encodes human IL-13.

XX

SQ Sequence 131 AA;

Query Match 58.5%; Score 385; DB 15; Length 131;

Best Local Similarity 58.6%; Pred. NO. 7.8e-37;

Matches 78; Conservative 19; Mismatches 30; Indels 6; Gaps 2;

QY 1 MALWLTVVVIALTCGLGASPSPVTPSP----TLKELIEELVNITQNQASLCNGSMVWSVN 56

Db 1 malwvtavialacigglagpvpvrsvslptlkelieelsnitqdtplcngsmvwsvd 60

QY 57 LTAGMYCAALESILNVSDCSAIQRTQRMKALCSQKPAAGISSERSRDTKIEVIQLVKNL 116

Db 61 laaggfcvaldsltnisncnaiyrtqrlhglcnrkapttvss--lpdtkievahfitkl 118

QY 117 LTYVRGVYRHGNF 129

Db 119 lsytkqlfrhgp 131

RESULT 8

R92794

ID R92794 standard; Protein; 111 AA.

XX

AC R92794;

XX

DT 24-MAY-1996 (first entry)

XX

DE Human interleukin-13 mutein 2.

XX

KW Cytokine; mutein; interleukin-13; IL-13; agonist; antagonist;

KW diagnosis; therapy; cancer; inflammation; degenerative disease.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Misc-difference 11

FT /note= "Glu at position 11 may be replaced by an

FT amidated amino acid, including Lys"

FT

FT Misc-difference 64

FT /note= "Arg at position 64 may be replaced by an

FT acidic amino acid, including Asp"

XX

PN WO9604306-A2.

XX

PD 15-FEB-1996.

XX

PF 31-JUL-1995; 95WO-US08950.

XX

PR 01-AUG-1994; 94US-0284393.

XX

PA (SCHE ) SCHERING CORP.

XX

PI Zurawski G, Zurawski SM;

XX

DR WPI; 1996-129335/13.

XX

PT Mutein(s) of human and murine cytokine(s), esp. interleukin(s) and

PT murine P600 contg. amino acid substitutions. - useful for the

PT diagnosis and treatment of cancer, inflammation, etc.

XX

PS Claim 12; Page 46; 52pp; English.

XX

CC Muteins 1 and 2 (R92793-94) of human interleukin-13 (IL-13) contain

CC amino acid substitutions at amino acid position 11 in helix A and/or

CC at position 64 in helix C. They are obtd. by site-directed

CC mutagenesis of natural IL-13 sequences. The muteins antagonise the

CC activity of IL-13 or IL-4. They have partial cytokine agonist

CC activity, exhibit less than 80% maximal agonist activity of natural

CC IL-2, and/or antagonize cytokine activity by least about 50% when

CC present at a 100-fold excess. They and other cytokine muteins

CC (see also R92790-92, R92795-802) are useful in the screening of

CC cytokine and cytokine receptor levels, and in the diagnosis or

CC treatment of e.g. inflammation, cancer, and degenerative disorders.

XX

SQ Sequence 111 AA;

Query Match 57.4%; Score 377.5; DB 17; Length 111;

Best Local Similarity 59.7%; Pred. NO. 4.6e-36;

Matches 76; Conservative 11; Mismatches 21; Indels 1; Gaps 1;

QY 22 PVTSPPTLKELIEELVNITQNQ-ASLCNGSMVSVNLTAGMYCAALESILNVSDCSAIQR 80

Db 2 pvpstpaltrelieelvnitqnqkplcngsmvwsinltagmycaaleslinvsgcsaiek 61

QY 81 TQRMKALCSQKPAAGISSERSRDTKIEVIQLVKNLTYVRGVYRHGNF 129

Db 62 tqrmksqfcphkvsagfsslhvrdtkievagfvkdllhlkklfregf 110

RESULT 9

R27347

ID R27347 standard; Protein; 112 AA.

XX

AC R27347;

XX

DT 24-FEB-1993 (first entry)

XX

DE Protein with cytokine activity encoded by Nal'.

XX

KW Interleukin; chemotaxis; immunomodulation; inflammation.

XX

PN Ep506574-A.

XX

PD 30-SEP-1992.

XX

PF 27-MAR-1992; 92EP-0400858.

XX

PR 29-MAR-1991; 91FR-0003904.

PR 08-JAN-1992; 92FR-0000137.

XX

PA (SNFI ) ELF SANOFI.

XX

PI Caput D, Ferrara P, Guillemot J, Kaghad M, Labit-le Bouteiller C;

PI Leplatols.P, Magazin M, Minty A;

XX

DR WPI; 1992-325841/40.

DR N-PSDB; Q28944.

XX

PT New cytokine having immunomodulatory activity - useful for

PT treating tumours and infectious or inflammatory conditions

XX

PS Claim 1; Page 60; 78pp; French.

XX

CC This protein is one of two possible forms of a new cytokine

CC produced by T lymphocytes induced by phorbol-2-myristate-3-acetate

CC and phytohaemagglutinin. The proteins differ only in the amino acid

CC at position 41 which is either Asp or Gly. The cytokine acts on

CC monocytes and B lymphocytes and is useful in treatment of tumours

CC and some infections and inflammatory conditions.

CC See Q28941-Q28947.

XX

SQ Sequence 112 AA;







PT treating tumours and infectious or inflammatory conditions  
XX Claim 12; Page 61; 78pp; French.  
PS  
XX  
CC The b2 peptide is a preferred signal peptide to be fused to the  
CC N-terminus of the new cytokine. The last two amino acids (Ser-Pro)  
CC are opt. absent; when absent the signal peptide is designated b1.  
CC See Q28942-Q28947.  
XX  
SQ Sequence 34 AA;  
  
Query Match 12.3%; Score 81; DB 13; Length 34;  
Best Local Similarity 85.0%; Pred. No. 0.019;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 MALWLTVVVIALTCLGLASP 20  
Db 15 mallttvtialtclggfasp 34  
  
RESULT 15  
B38312  
ID B38312 standard; Protein; 665 AA.  
XX B38312;  
AC  
XX  
DT 30-JAN-2001 (first entry)  
XX  
DE Human secreted protein sequence encoded by gene 38 SEQ ID NO:168.  
XX  
KW Human; secreted protein; diagnosis; immunosuppressive; antiarthritic;  
KW antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic;  
KW cerebroprotective; nootropic; neuroprotective; antibacterial; virucide;  
KW fungicide; ophthalmological; gene therapy; autoimmune disease; infection;  
KW hyperproliferative disorder; cardiovascular disorder; angiogenesis;  
KW cerebrovascular disorder; nervous system disorder; ocular disorder;  
KW wound healing; skin aging; food additive; preservative.  
XX  
OS Homo sapiens.  
XX  
PN WO200058469-A1.  
XX  
PD 05-OCT-2000.  
XX  
PF 23-MAR-2000; 2000WO-US07579.  
XX  
PR 26-MAR-1999; 99US-0126509.  
PR 07-JAN-2000; 2000US-0174853.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
PI Rosen CA, Ruben SM, Komatsoulis G;  
XX  
DR WPI; 2000-594642/56.  
XX  
PT Isolated nucleic acid molecule encoding a human secreted protein is  
PT used in preventing, treating or ameliorating a medical condition -  
XX  
PS Disclosure; Page 407-409; 416pp; English.  
XX  
CC The polynucleotide sequences given in C69455 to C69502 encode the human  
CC secreted proteins given in B38203 to B38250. B38251 to B38320 represent  
CC human secreted polypeptide sequences and proteins homologous to them,  
CC which are given in the exemplification of the present invention. Human  
CC secreted proteins have activities based on the tissues and cells the  
CC genes are expressed in. Example of activities include: immunosuppressive;  
CC antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiant;  
CC vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial;  
CC virucide; fungicide; and ophthalmological. The polynucleotides and  
CC polypeptides can be used to prevent, treat or ameliorate a medical  
CC condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs,  
CC chickens or sheep. They are also used in diagnosing a pathological

CC condition or susceptibility to a pathological condition. Disorders which  
CC are diagnosed or treated include autoimmune diseases, hyperproliferative  
CC disorders, cardiovascular disorders, cerebrovascular disorders,  
CC angiogenesis, nervous system disorders, infections caused by bacteria,  
CC viruses and fungi and ocular disorders. The polypeptides can also be used  
CC to aid wound healing and epithelial cell proliferation, to prevent skin  
CC aging due to sunburn, to maintain organs before transplantation, for  
CC supporting cell culture of primary tissues, to regenerate tissues and in  
CC chemotaxis. The polypeptides can also be used as a food additive or  
CC preservative to increase or decrease storage capabilities. C69446 to  
CC C69454 and B38202 represent sequences used in the exemplification of the  
CC present invention.  
XX  
SQ Sequence 665 AA;  
  
Query Match 12.0%; Score 79; DB 21; Length 665;  
Best Local Similarity 31.2%; Pred. NO. 1.9;  
Matches 39; Conservative 19; Mismatches 51; Indels 16; Gaps 5;  
  
QY 5 LTVVIALTCLGLASPPVTPSPTLKELIEELVN-ITQNASLNCNGSMV-----WSV 55  
Db 479 lttvkaltliag--splkidlrpvlgegvpiilasflrknqralklgtlsaldiliknysd 536  
  
QY 56 NLTAGMYCALES---LINVSDCSAIQRTQRMKALCSQKPAAGISSERSRDTKIEVIQL 112  
Db 537 sltaamidavidelpplisesdmhvsqmaifittlakvypss--lskisgslneligl 594  
  
QY 113 VKNLL 117  
Db 595 vrspl 599  
  
Search completed: May 13, 2001, 17:47:36  
Job time: 12336 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: May 13, 2001, 17:48:32 ; Search time 42.06 Seconds  
(without alignments)  
59.377 Million cell updates/sec

Title: US-09-451-527-100  
Perfect score: 658  
Sequence: 1 MALWLTVVIALTCLGLASP.....QLVKNLLTYVRGVYRHGNER 130

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 185757 seqs, 19210857 residues

Total number of hits satisfying chosen parameters: 185757

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents\_AA: \*  
1: /cgnl\_7/ptodata/1/iaa/5A\_COMB.pep: \*  
2: /cgnl\_7/ptodata/1/iaa/5B\_COMB.pep: \*  
3: /cgnl\_7/ptodata/1/iaa/6A\_COMB.pep: \*  
4: /cgnl\_7/ptodata/1/iaa/6B\_COMB.pep: \*  
5: /cgnl\_7/ptodata/1/iaa/PCTUS\_COMB.pep: \*  
6: /cgnl\_7/ptodata/1/iaa/backfiles1.pep: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	448	68.1	132	1 US-08-012-543-2	Sequence 2, Appli
2	448	68.1	132	5 PCT-US93-07645A-2	Sequence 2, Appli
3	448	68.1	132	5 PCT-US93-07645-2	Sequence 2, Appli
4	441	67.0	146	1 US-08-371-121-16	Sequence 16, Appl
5	385	58.5	131	1 US-08-012-543-4	Sequence 4, Appli
6	385	58.5	131	1 US-08-371-121-25	Sequence 25, Appl
7	385	58.5	131	5 PCT-US93-07645A-4	Sequence 4, Appli
8	385	58.5	131	5 PCT-US93-07645-4	Sequence 4, Appli
9	377.5	57.4	111	1 US-08-284-393B-5	Sequence 5, Appli
10	377.5	57.4	111	5 PCT-US95-08950-5	Sequence 5, Appli
11	367	55.8	112	1 US-08-284-393B-4	Sequence 4, Appli
12	367	55.8	112	5 PCT-US95-08950-4	Sequence 4, Appli
13	366.5	55.7	111	1 US-08-284-393B-15	Sequence 15, Appl
14	360	54.7	112	1 US-08-371-121-1	Sequence 1, Appli
15	356	54.1	112	1 US-08-284-393B-14	Sequence 14, Appl
16	302	45.9	111	1 US-08-284-393B-6	Sequence 6, Appli
17	302	45.9	111	5 PCT-US95-08950-6	Sequence 6, Appli
18	295	44.8	111	1 US-08-284-393B-16	Sequence 16, Appl
19	81	12.3	20	1 US-08-371-121-8	Sequence 8, Appli
20	81	12.3	34	1 US-08-371-121-6	Sequence 6, Appli
21	71.5	10.9	718	4 US-09-090-808-2	Sequence 2, Appli
22	70	10.6	18	1 US-08-371-121-7	Sequence 7, Appli
23	70	10.6	32	1 US-08-371-121-5	Sequence 5, Appli
24	67	10.2	1209	5 PCT-US95-04589-107	Sequence 107, App
25	67	10.2	1258	2 US-08-310-912A-107	Sequence 107, App
26	67	10.2	1294	3 US-08-930-996A-10	Sequence 10, Appl
27	66	10.0	477	2 US-08-770-544-16	Sequence 16, Appl

28	65.5	10.0	206	3 US-09-041-889-6	Sequence 6, Appli
29	65.5	10.0	206	3 US-08-837-058-6	Sequence 6, Appli
30	65.5	10.0	426	2 US-08-484-993B-12	Sequence 12, Appl
31	65.5	10.0	426	2 US-08-484-158B-12	Sequence 12, Appl
32	65.5	10.0	426	2 US-08-484-596A-12	Sequence 12, Appl
33	65.5	10.0	426	2 US-08-480-150A-12	Sequence 12, Appl
34	65.5	10.0	426	3 US-08-458-731-12	Sequence 12, Appl
35	65.5	10.0	426	3 US-08-149-223A-12	Sequence 12, Appl
36	64.5	9.8	168	3 US-09-188-579-85	Sequence 85, Appl
37	64.5	9.8	496	2 US-08-696-349-2	Sequence 2, Appli
38	64.5	9.8	496	5 PCT-US96-13156-2	Sequence 2, Appli
39	64	9.7	383	1 US-08-486-037B-2	Sequence 2, Appli
40	64	9.7	1461	2 US-08-993-228-10	Sequence 10, Appl
41	64	9.7	1754	1 US-07-745-206A-13	Sequence 13, Appl
42	64	9.7	1754	2 US-08-311-363-13	Sequence 13, Appl
43	62.5	9.5	228	4 US-08-569-221A-2	Sequence 2, Appli
44	62.5	9.5	848	4 US-08-976-255-10	Sequence 10, Appl
45	62.5	9.5	1589	3 US-08-755-587-189	Sequence 189, App

ALIGNMENTS

RESULT 1  
US-08-012-543-2  
; Sequence 2, Application US/08012543  
; Patent No. 5596072  
; GENERAL INFORMATION:  
; APPLICANT: Culpepper, Janice  
; APPLICANT: McKenzie, Andrew  
; APPLICANT: Dang, Warren  
; APPLICANT: de Waal Malefyt, Rene  
; APPLICANT: Heath, Andrew  
; APPLICANT: Aversa, Gregorio  
; APPLICANT: Briere, Francine  
; APPLICANT: Banchereau, Jacques  
; APPLICANT: de Vries, Jan  
; APPLICANT: Zurawski, Gerard  
; TITLE OF INVENTION: Human Interleukin-13  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/012,543  
; FILING DATE: 01-FEB-1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/933,416  
; FILING DATE: 21-AUG-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0302K1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-852-9196  
; TELEFAX: 415-496-1200  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 132 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-012-543-2

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Query Match 68.1%; Score 448; DB 1; Length 132;
Best Local Similarity 71.0%; Pred. No. 3.8e-47;
Matches 93; Conservative 11; Mismatches 25; Indels 2; Gaps 2;

QY 1 MALWLTVVIALTCGLGSPVTPSPPTLKELIEELVNITQK-ASLCNGSMVWSVNLT 59
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Db 1 MALLTTVIALTCGGFASPGVPVPPSTALRELIEELVNITQKAPLCNGSMVWSINLT 60
   ||| || ||||| ||||| ||| : || || ||||| ||||| ||||| : |||

QY 60 GMYCAALESLINVSDCSAIQRTQRMKALCSQKPAAG-ISSERSRDTKIEVIQLVKNLLT 118
   ||||| ||||| ||||| ||||| ||| : || || ||||| ||||| ||||| : |||
Db 61 GMYCAALESLINVSGCSAIEKTQRMLSGFCPHKVSAGQFSSLHVRDTKIEVAQFVKDLLL 120
   ||||| ||||| ||||| ||||| ||| : || || ||||| ||||| ||||| : |||

QY 119 YVRGVYRHGNF 129
   ::::| | |
Db 121 HLKKLFGREGF 131

RESULT 2
PCT-US93-07645A-2
; Sequence 2, Application PC/TUS9307645A
; GENERAL INFORMATION:
; APPLICANT: Human Interleukin-13
; TITLE OF INVENTION: Human Interleukin-13
; NUMBER OF SEQUENCES: 6
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.5
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07645A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/012543
; FILING DATE: 01-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/010977
; FILING DATE: 29-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/933416
; FILING DATE: 21-AUG-1992
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 132 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US93-07645A-2

Query Match 68.1%; Score 448; DB 5; Length 132;
Best Local Similarity 71.0%; Pred. No. 3.8e-47;
Matches 93; Conservative 11; Mismatches 25; Indels 2; Gaps 2;

QY 1 MALWLTVVIALTCGLGSPVTPSPPTLKELIEELVNITQK-ASLCNGSMVWSVNLT 59
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Db 1 MALLTTVIALTCGGFASPGVPVPPSTALRELIEELVNITQKAPLCNGSMVWSINLT 60
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QY 60 GMYCAALESLINVSDCSAIQRTQRMKALCSQKPAAG-ISSERSRDTKIEVIQLVKNLLT 118
   ||||| ||||| ||||| ||||| ||| : || || ||||| ||||| ||||| : |||
Db 61 GMYCAALESLINVSGCSAIEKTQRMLSGFCPHKVSAGQFSSLHVRDTKIEVAQFVKDLLL 120
   ||||| ||||| ||||| ||||| ||| : || || ||||| ||||| ||||| : |||

QY 119 YVRGVYRHGNF 129
   ::::| | |
Db 121 HLKKLFGREGF 131

RESULT 3
PCT-US93-07645-2
; Sequence 2, Application PC/TUS9307645
; GENERAL INFORMATION:
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; APPLICANT:
; TITLE OF INVENTION: Human Interleukin-13
; NUMBER OF SEQUENCES: 6
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.5
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07645
; FILING DATE: 19930818
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/012543
; FILING DATE: 01-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/010977
; FILING DATE: 29-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/933416
; FILING DATE: 21-AUG-1992
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 132 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US93-07645-2

Query Match 68.1%; Score 448; DB 5; Length 132;
Best Local Similarity 71.0%; Pred. No. 3.8e-47;
Matches 93; Conservative 11; Mismatches 25; Indels 2; Gaps 2;

QY 1 MALWLTVVIALTCGLGSPVTPSPPTLKELIEELVNITQK-ASLCNGSMVWSVNLT 59
   ||| || ||||| ||| || | : ||||| ||||| ||||| ||||| : |||
Db 1 MALLTTVIALTCGGFASPGVPVPPSTALRELIEELVNITQKAPLCNGSMVWSINLT 60
   ||| || ||||| ||||| ||| : || || ||||| ||||| ||||| : |||

QY 60 GMYCAALESLINVSDCSAIQRTQRMKALCSQKPAAG-ISSERSRDTKIEVIQLVKNLLT 118
   ||||| ||||| ||||| ||||| ||| : || || ||||| ||||| ||||| : |||
Db 61 GMYCAALESLINVSGCSAIEKTQRMLSGFCPHKVSAGQFSSLHVRDTKIEVAQFVKDLLL 120
   ||||| ||||| ||||| ||||| ||| : || || ||||| ||||| ||||| : |||

QY 119 YVRGVYRHGNF 129
   ::::| | |
Db 121 HLKKLFGREGF 131

RESULT 4
US-08-371-121-16
; Sequence 16, Application US/08371121
; Patent No. 5652123
; GENERAL INFORMATION:
; APPLICANT: CAPUT, Daniel
; APPLICANT: FERRARA, Pascual
; APPLICANT: GUILLEMOT, Jean-Claude
; APPLICANT: LEPLATOIS, Pascal
; APPLICANT: MINTY, Adrian
; APPLICANT: KAGHAD, Mourad
; APPLICANT: LABIT-LE BOUTEILLER, Christine
; APPLICANT: MAGAZIN, Marilyn
; TITLE OF INVENTION: Protein having a cytokine type
; TITLE OF INVENTION: activity, recombinant DNA coding for this protein,
; TITLE OF INVENTION: transformed cells and microorganisms.
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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Qy 117 LTYVRGVYRHGNF 129  
| : | : : | | |  
Db 119 LSYTKQLFRHGPCF 131

```

RESULT          9
US-08-284-393B-5
; Sequence 5, Application US/08284393B
; Patent No. 5696234
; GENERAL INFORMATION:
; APPLICANT: Zurawski, Sandra M.
; APPLICANT: Zurawski, Gerard
; TITLE OF INVENTION: MUTEINS OF MAMMALIAN CYTOKINES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/284,393B
; FILING DATE: 01-AUG-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0389
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-852-9196
; TELEFAX: 415-496-1200
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 111 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-284-393B-5

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	Query Match	57.4%;	Score 377.5;	DB 1;	Length 111;			
	Best Local Similarity	69.7%;	Pred. No. 1.2e-38;					
	Matches 76;	Conservative 11;	Mismatches 21;	Indels 1;	Gaps 1;			
QY	22	PVTPSP	TLKELIEELVNITQ	NQ-ASLCNGSMVWSVNL	TAGMYCAALES	LINVS	DCSA	IQR 80
			:		:			
Db	2	PVPPST	ALRELIEELVNITQ	NQKAPLCNGSMVWSIN	L	TAGMYCAALES	LINVS	GCSAIEK 61
QY	81	TQRLK	KALCSQKPAAGIS	SRSRDTKIEV	IQLVKNLLTYVRGVYR	HGNF 129		
			:			:  :  :		
Db	62	TQRLSG	FCPHKVSAGFSS	LHVDRDTKIEVA	QFVKDILLHLKKL	FRGFR 110		

RESULT 10  
PCT-US95-08950-5  
; Sequence 5, Application PC/TUS9508950  
; GENERAL INFORMATION:  
; APPLICANT: Zurawski, Sandra M.  
; APPLICANT: Zurawski, Gerard  
; TITLE OF INVENTION: MUTEINS OF MAMMALIAN CYTOKINES  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto

```

; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/08950
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/284,393
; FILING DATE: 01-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0389
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-852-9196
; TELEFAX: 415-496-1200
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 111 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-08950-5

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Query Match      57.4%; Score 377.5; DB 5; Length 111;
Best Local Similarity 69.7%; Pred. NO. 1.2e-38;
Matches 76; Conservative 11; Mismatches 21; Indels 1; Gaps 1;

QY    22 PVTSPSTLKELIEELVNITQN-Q-ASLCNGSMVWSVNLTAGMYCAALESLINVSDCSAIQR 80
      || || -:||:||||| | |||||:||||| | ||||| | |||||
Db     2 PVPPSTALRELIEELVNITQNQKAPLCLCNGSMVWSINLTAGMYCAALESLINVGCSAIEK 61

QY    81 TQRLMKALCSQKPAAGISSERSRDTKIEVIQLVKNLLTYVRGVYRHGNF 129
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Db     62 TQRLMSGFCPHKVVSAGFSLSHVDRDTKIEVAQFVKDLLLLHLKKLFREGRF 110

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RESULT 11  
US-08-284-393B-4  
; Sequence 4, Application US/08284393B  
; Patent No. 5696234  
; GENERAL INFORMATION:  
; APPLICANT: Zurawski, Sandra M.  
; APPLICANT: Zurawski, Gerard  
; TITLE OF INVENTION: MUTEINS OF MAMMALIAN CYTOKINES  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/284,393B  
; FILING DATE: 01-AUG-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34,090





APPLICANT: GUILLEMOT, Jean-Claude  
APPLICANT: LEPLATOIS, Pascal  
APPLICANT: MINTY, Adrian  
APPLICANT: KAGHAD, Mourad  
APPLICANT: LABIT-LE BOUTEILLER, Christine  
APPLICANT: MAGAZIN, Marilyn  
TITLE OF INVENTION: Protein having a cytokine type  
TITLE OF INVENTION: activity, recombinant DNA coding for this protein,  
TITLE OF INVENTION: transformed cells and microorganisms.  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FOLEY & LARDNER  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington, D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/371,121  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/938,161  
FILING DATE: 30-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/FR92/00280  
FILING DATE: 27-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 91 00137  
FILING DATE: 08-JAN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 91 03904  
FILING DATE: 29-MAR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: SAXE, Bernhard D.  
REGISTRATION NUMBER: 28,665  
REFERENCE/DOCKET NUMBER: 16781/383  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 112 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 41  
OTHER INFORMATION: /label= Xaa  
OTHER INFORMATION: /note= "amino acid is Asp or Gly"  
US-08-371-121-1

Query Match 54.7%; Score 360; DB 1; Length 112;  
Best Local Similarity 68.2%; Pred. No. 1.6e-36;  
Matches 75; Conservative 11; Mismatches 22; Indels 2; Gaps 2;  
Qy 22 PVTSPSTLKEIEELVNITQNQ-ASLCNGSMVWSVNLTAGMYCAALESINVSDCSAIQR 80  
Db 2 PVPSTALRELIEELVNITQNQKAPLCNGSMVWSINLTAXMYCAALESINVS GCSAIEK 61  
Qy 81 TQRLMKALCSQKPAAG-ISSERSRDTKIEVIQLVKNLLTYVRGVYRHGNF 129  
Db 62 TQRLMSGFCPHKVSAGQFSSLHVRDTKIEVAQFVKDLLHLKFLFREGF 111

RESULT 15

US-08-284-393B-14  
Sequence 14, Application US/08284393B  
Patent No. 5696234  
GENERAL INFORMATION:  
APPLICANT: Zurawski, Sandra M.  
APPLICANT: Zurawski, Gerard  
TITLE OF INVENTION: MUTEINS OF MAMMALIAN CYTOKINES  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DNAX Research Institute  
STREET: 901 California Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/284,393B  
FILING DATE: 01-AUG-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Ching, Edwin P.  
REGISTRATION NUMBER: 34,090  
REFERENCE/DOCKET NUMBER: DX0389  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-852-9196  
TELEFAX: 415-496-1200  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 112 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-284-393B-14

Query Match 54.1%; Score 356; DB 1; Length 112;  
Best Local Similarity 67.3%; Pred. No. 5e-36;  
Matches 74; Conservative 12; Mismatches 22; Indels 2; Gaps 2;  
Qy 22 PVTSPSTLKEIEELVNITQNQ-ASLCNGSMVWSVNLTAGMYCAALESINVSDCSAIQR 80  
Db 2 PVPSTALRELIEELVNITQNQKAPLCNGSMVWSINLTAGMYCAALESINVS GCSAIEK 61  
Qy 81 TQRLMKALCSQKPAAG-ISSERSRDTKIEVIQLVKNLLTYVRGVYRHGNF 129  
Db 62 TQDMLSGFCPHKVSAGQFSSLHVRDTKIEVAQFVKDLLHLKFLFREGF 111  
Search completed: May 13, 2001, 17:48:33  
Job time: 12136 sec

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Db	15	MALLTTVIALTCLGGFASPGVPVPPSTALRELIELLVNITQNQKAPLCNGSMVWSINLTA	74
QY	60	GMVCAALESLINVSDCSAIQRTQRMKALCSQKPAAG - ISSERSRDTKIEVIQLVKNLLT	118
Db	75	GMVCAALESLINVSGCSAIEKTMRLSGFCPHKVSAGQFSSLHLVRDTKIEVAFVKDLLL	134

Qy 119 YVRGVYRHGNE 129  
:: :: | |  
Db 135 HLKKLFREGRE 145

RESULT 2  
E30552  
T-cell activation protein P600 precursor - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 28-Aug-1989 #sequence\_revision 28-Aug-1989 #text\_change 16-Jul-1999  
C:Accession: E30552  
R:Brown, K.D.; Zurawski, S.M.; Mosmann, T.R.; Zurawski, G.  
J. Immunol. 142, 679-687, 1989  
A:Title: A family of small inducible proteins secreted by leukocytes are members of a new class of various activation processes.  
A:Reference number: A30552; MUID:89093958  
A:Accession: E30552  
A:Molecule type: mRNA  
A:Residues: 1-131 <BRO>  
A:Cross-references: GB:M23504; NID:g5333246; PIDN:AAA40149.1; PID:g5333247  
C:Superfamily: interleukin-13

Query Match	58.5%;	Score 385;	DB 2;	Length 131;
Best Local Similarity	58.6%;	Pred. No. 2.3e-31;		
Matches 78;	Conservative 19;	Mismatches 30;	Indels 6;	Gaps 2;

Qy	1	MALWLTVVVIALTCLGGLASPSVP	PSP----	TLKELIEELVNITQNQASLCNGSMWWSVN	56
Dd	1	MALWVTAVLACLGGLAAGPVPRSVSLPL	TLKELIEELSNIQTDP	PLCNGSMWWSVD	60
Qy	57	LTAGMYCAALESLINVSDCSAIQRTQRM	LKALCSQKPAAGISSERSRDTKIEVIQLVKNL	116	
Dd	61	LAAGGFCAVALDSLTNISNCNAIYRTQR	ILHGLCNRKAPTTVSS--LPDTKIEVAHFITKL	118	
Qy	117	LTYYRGVYRHGNF	129		
Dd	119	LSYTKQLFRHGPF	131		

RESULT 3  
I52290  
interleukin-13 - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 16-Jul-1999  
C:Accession: I52290  
R:Lakkis, F.G.; Cruet, E.N.  
Biochem. Biophys. Res. Commun. 197, 612-618, 1993  
A:Title: Cloning of rat interleukin-13 (IL-13) cDNA and analysis of IL-13 gene expression  
A:Reference number: I52290; MUID:94092138  
A:Accession: I52290  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: mRNA  
A:Residues: 1-131 <RES>  
A:Cross-references: GB:L26913; NID:g438875; PIDN:AAA16478.1; PID:g438876  
C:Genetics:  
A:Gene: IL-13  
C:Superfamily: interleukin-13

Query Match 57.5%; Score 378.5; DB 2; Length 131;  
Best Local Similarity 59.4%; Pred. No. 1e-30;  
Matches 79; Conservative 21; Mismatches 26; Indels 7; Gaps 4;

QY	1	MALWLT	VVIA	LTCL	GGGL	ASPS	PV---	TPSP	TLKE	LIIE	LVNI	TQ-N	ASLC	NGSM	VWSV	55
							:									
Db	1	MALWVT	AVLA	ACLG	GLAT	PGV	RRST	SPPV	ALRE	LIIE	LSNI	TODOK	TSLC	NSSM	VWSV	60

QY	56	NLTAGMYCAALES	LINVSDCSAIQRTORMLKALCSQKPAAGISSERSRDTKIEVQLVKN	115
		:    :      :	:        :       :	
Dd	61	DLTAGGFCAALES	TNISSCNAIHRTORLNLGNLCNQK-ASDVASS-PPDTKIEVAQFISK	118
QY	116	LLTYVRGVYRHGN	128	
		: :  :  :		
Dd	119	LLNYSKQLFRYGH	131	

RESULT 4  
T42735  
TBP-interacting protein TIP120 - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 21-Jul-2000  
C;Accession: T42735  
R;Yogosawa, S.; Makino, Y.; Yoshida, T.; Kishimoto, T.; Muramatsu, M.; Tamura, T.  
Biochem. Biophys. Res. Commun. 229, 612-617, 1996  
A;Title: Molecular cloning of a novel 120-kDa TBP-interacting protein

A;Description: considered to participate in transcription regulation through the inte

Query Match	12.0%;	Score 79;	DB 2;	Length 1230;
Best Local Similarity	31.2%;	Pred. NO. 11;		
Matches 39;	Conservative 19;	Mismatches 51;	Indels 16;	Gaps 5;

QY	5	LTWVIALTCGLGLASPSVPTSPPTLKELEELVN-ITQNQASLNCNGSMV-----WSV	55
		:      :       :   : :     :     :	
Db	626	LTTVKALTLIAG--SPLKIDLRPVLGEGVPTLASFLRKNQRAKGLTSLDILIKNYS	683
		:      :       :   : :     :     :	
QY	56	NLTAGMYCAALES---LINVSDCSAIQRTQRMKALCSQKPAAGISSERSRDTKIEVIQL	112
		:         : :     :           : : :     :	
Db	684	SLTAAMIDAVDELPLPLISESDMHVSQMAISFLTTLAKVYPSS--LSKISGSILNEIIGL	741
		:      :       :   : :     :     :	

RESULT 5  
E83551  
conserved hypothetical protein PA0752 [imported] - Pseudomonas aeruginosa (strain PAO  
C;Species: Pseudomonas aeruginosa  
C;Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000  
C;Accession: E83551  
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.;  
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L  
.; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa  
A;Reference number: A82950; MUID:20437337  
A;Accession: E83551  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-505 <STO>  
A;Cross-references: GB:AE004510; GB:AE004091; NID:g9946634; PIDN:AAG04141.1; GSPDB:GN  
A;Experimental source: strain PA01  
C;Genetics:  
A;Gene: PA0752

Query Match	11.7%;	Score 77;	DB 2;	Length 505;
Best Local Similarity	24.8%;	Pred. No. 6.1;		
Matches	34;	Conservative	25;	Mismatches 42;
				Indels 36;
				Gaps 6;









A;Accession: T38183  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-481 <LY2>  
A;Cross-references: EMBL:254285; PIDN:CAA91073.1; PID:g1008436; GSPDB:GN00066; SPDB:SPAC  
A;Experimental source: strain 972h-; cosmid c22F3  
C;Genetics:  
A;Gene: SPAC22F3.08c  
A;Map position: 1L  
C;Keywords: ATP; P-loop  
F;90-97/Region: nucleotide-binding motif A (P-loop)  
F;192-197/Region: nucleotide-binding motif B  
F;196-199/Region: DEAD motif

Query Match 10.9%; Score 71.5; DB 2; Length 481;  
Best Local Similarity 24.3%; Pred. No. 21;  
Matches 25; Conservative 25; Mismatches 48; Indels 5; Gaps 4;  
QY 25 PSPTLKL-IEELVNITQNASLCSGSMWSV-NLTAGMYCAALESLINVSDCSAIQRTQ 82  
Db 18 PPSIKEKEAKKLQGITKGAQVTGNNPVDPIEEFPEGILCENLKKQ-NITECTTIQR-- 74  
QY 83 RMLKALCSQKPAAGISSERSRDTKIEVIQLVKNLLTYVRGVYR 125  
Db 75 YAIPTIGSKRDLLACAPTGSCKTIAYLFPIQLQLHVPGGYR 117

Search completed: May 13, 2001, 21:48:44  
Job time: 26253 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: May 14, 2001, 06:02:05 ; Search time 44.64 Seconds  
(without alignments)  
99.758 Million cell updates/sec

Title: US-09-451-527-100  
Perfect score: 658  
Sequence: 1 MALWLTVVIALTCLGLASP.....QLVKNLLTYVRGVYRHGNER 130

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %		DB ID	Description
		Match	Length		
1	448	68.1	132	1 IL13_HUMAN	P35225 homo sapien
2	412	62.6	132	1 IL13_BOVIN	Q9xsv9 bos taurus
3	385	58.5	131	1 IL13_MOUSE	P20109 mus musculus
4	378.5	57.5	131	1 IL13_RAT	P42203 rattus norv
5	74.5	11.3	261	1 SPRE_MOUSE	Q64105 mus musculus
6	74.5	11.3	262	1 SPRE_RAT	P18297 rattus norv
7	73.5	11.2	211	1 H1T_PIG	P06348 sus scrofa
8	72	10.9	431	1 ACRO_RABIT	P48038 oryctolagus
9	72	10.9	482	1 TYPH_HUMAN	P19971 homo sapien
10	72	10.9	5032	1 RYNR_HUMAN	P21817 homo sapien
11	71.5	10.9	261	1 SPRE_HUMAN	P35270 homo sapien
12	71.5	10.9	481	1 YA88_SCHPO	Q09775 schizosacch
13	70.5	10.7	207	1 H1T_MACMU	P40286 macaca mula
14	70	10.6	725	1 VR2A_BPT4	P03690 bacterioph
15	69.5	10.6	192	1 FLHC_SALTY	O52222 salmonella
16	69.5	10.6	513	1 AQL1_THEAQ	P08594 thermus aqu
17	69.5	10.6	1037	1 ACRD_ECOLI	P24177 escherichia
18	69	10.5	323	1 GC_RABIT	P01870 oryctolagus
19	69	10.5	5035	1 RYNR_PIG	P16960 sus scrofa
20	69	10.5	5037	1 RYNR_RABIT	P11716 oryctolagus
21	68	10.3	805	1 UBFP5_YEAST	P39944 saccharomyc
22	68	10.3	936	1 FHL1_YEAST	P39521 saccharomyc
23	67.5	10.3	1164	1 KEL1_YEAST	P38853 saccharomyc
24	67	10.2	522	1 TSAW_RICTS	P37919 rickettsia
25	67	10.2	1221	1 TOP2_TRYBB	P12531 trypanosoma
26	66.5	10.1	633	1 DNAK_AGRTO	P50019 agrobacteri
27	66.5	10.1	891	1 YB33_SCHPO	O14338 schizosacch
28	65.5	10.0	206	1 H1T_HUMAN	P22492 homo sapien
29	65.5	10.0	426	1 ZP3_CANFA	P48831 canis famil
30	65.5	10.0	510	1 MUTL_THEMA	P74925 thermotoga
31	65.5	10.0	638	1 DNAK_RHILE	O33528 rhizobium l
32	65.5	10.0	1164	1 FHOS_HUMAN	Q9y613 homo sapien
33	65	9.9	1477	1 A1I3_RAT	P14046 rattus norv

ALIGNMENTS

RESULT 1					
IL13_HUMAN					
ID	IL13_HUMAN	STANDARD;	PRT;	132 AA.	
AC	P35225; O43644;				P24656 autographa
DT	01-FEB-1994 (Rel. 28, Created)				P15473 rattus norv
DT	01-FEB-1994 (Rel. 28, Last sequence update)				P44324 haemophilus
DT	01-OCT-2000 (Rel. 40, Last annotation update)				P42700 xenopus lae
DE	INTERLEUKIN-13 PRECURSOR (IL-13).				P25980 xenopus lae
GN	IL13 OR NC30.				Q12751 saccharomyc
OS	Homo sapiens (Human).				P06758 zymomonas m
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				Q60738 mus musculu
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				P46012 caenorhabdi
OX	NCBI_TaxID=9606;				P54211 dunaliella
RN	[1]				P42609 escherichia
RP	SEQUENCE FROM N.A.				P34528 caenorhabdi
RX	MEDLINE=93211479; PubMed=8096327;				
RA	Minty A.J., Chalon P., Derocq J.M., Dumont X., Guillemot J.C.,				
RA	Kaghad M., Labit C., Leplatois P., Liauzun P., Miloux B.,				
RA	Minty C., Casellas P., Loison G., Lupker J., Shire D., Ferrara P.,				
RA	Caput D.;				
RT	"Interleukin-13 is a new human lymphokine regulating inflammatory and				
RT	immune responses.";				
RL	Nature 362:248-250(1993).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=93234572; PubMed=8097324;				
RA	McKenzie A.N., Culpepper J.A., Waal Malefyt R., Briere F.,				
RA	Punnonen J., Aversa G., Sato A., Dang W., Cocks B.G., Menon S.,				
RA	de Vries J.E., Banchereau J., Zurawski G.R.;				
RT	"Interleukin 13, a T-cell-derived cytokine that regulates human				
RT	monocyte and B-cell function.";				
RL	Proc. Natl. Acad. Sci. U.S.A. 90:3735-3739(1993).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RA	Dolganov G., Lewis D.B., Lovett M., Burr J., Bort S., Short D.,				
RA	McGurn M., Gibson C.;				
RL	Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.				
RN	[4]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Blood;				
RX	MEDLINE=95237624; PubMed=7721105;				
RA	Smirnov D.V., Smirnova M.G., Korobko V.G., Frolova E.I.;				
RT	"Tandem arrangement of human genes for interleukin-4 and				
RT	interleukin-13; resemblance in their organization.";				
RL	Gene 155:277-281(1995).				
RN	[5]				
RP	SEQUENCE FROM N.A.				
RA	Jang J.S., Kim B.E.;				
RL	Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.				
RN	[6]				
RP	3D-STRUCTURE MODELING.				
RX	MEDLINE=95132583; PubMed=7530359;				
RA	Bamborough P., Duncan D., Richards W.G.;				
RT	"Predictive modelling of the 3-D structure of interleukin-13.";				
RL	Protein Eng. 7:1077-1082(1994).				
RN	[7]				











GN ECGF1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
CC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
RC TISSUE=Placenta;  
RX MEDLINE=89181955; PubMed=2467210;  
RA Ishikawa F., Miyazono K., Hellman U., Drexler H., Wernstedt C.,  
RA Hagiwara K., Usuki K., Takaku F., Risau W., Heldin C.-H.;  
RT "Identification of angiogenic activity and the cloning and expression  
of platelet-derived endothelial cell growth factor.";  
RL Nature 338:557-562(1989).  
RN [12]  
RP SEQUENCE FROM N.A.  
RA Finnis C., Goodey A.R., Courtney M., Sleep D.;  
RL Submitted (xxx-1991) to the EMBL/GenBank/DBJ databases.  
RN [13]  
RP SEQUENCE FROM N.A.  
RA Adams M.D., Kerlavage A.R., Fuldner R.A., Phillips C.A.,  
RA Venter J.C.;  
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.  
RN [14]  
RP SEQUENCE OF 149-244 FROM N.A., AND SEQUENCE OF 125-178 AND 236-244.  
RX MEDLINE=92236753; PubMed=1570012;  
RA Furukawa T., Yoshimura A., Sumizawa T., Haraguchi M., Akiyama S.-I.,  
RA Fukui K., Yamada Y.;  
RT "Angiogenic factor.";  
RL Nature 356:668-668(1992).  
RN [15]  
RP PARTIAL SEQUENCE.  
RX MEDLINE=93015908; PubMed=1400349;  
RA Asai K., Nakanishi K., Isobe I., Eksioğlu Y.Z., Hirano A., Hama K.,  
RA Miyamoto T., Kato T.;  
RT "Neurotrophic action of gliostatin on cortical neurons. Identity of  
gliostatin and platelet-derived endothelial cell growth factor.";  
RL J. Biol. Chem. 267:20311-20316(1992).  
RN [16]  
RP FUNCTION.  
RX MEDLINE=92272724; PubMed=1590793;  
RA Usuki K., Saras J., Waltenberger J., Miyazono K., Pierce G.,  
RA Thomason A., Heldin C.-H.;  
RT "Platelet-derived endothelial cell growth factor has thymidine  
phosphorylase activity.";  
RL Biochem. Biophys. Res. Commun. 184:1311-1316(1992).  
RN [17]  
RP VARIANTS MNGIE.  
RX MEDLINE=99123033; PubMed=9924029;  
RA Nishino I., Spinazzola A., Hirano M.;  
RT "Thymidine phosphorylase gene mutations in MNGIE, a human  
mitochondrial disorder.";  
RL Science 283:689-692(1999).  
CC -1- FUNCTION: MAY HAVE A ROLE IN MAINTAINING THE INTEGRITY OF THE  
BLOOD VESSELS. HAS GROWTH PROMOTING ACTIVITY ON ENDOTHELIAL CELLS  
ANGIOGENIC ACTIVITY IN VIVO AND CHEMOTACTIC ACTIVITY ON  
ENDOTHELIAL CELLS IN VITRO.  
CC -1- FUNCTION: CATALYSES THE REVERSIBLE PHOSPHOROLYSIS OF THYMIDINE.  
THE PRODUCED MOLECULES ARE THEN UTILIZED AS CARBON AND ENERGY  
SOURCES OR IN THE RESCUE OF PYRIMIDINE BASES FOR NUCLEOTIDE  
SYNTHESIS.  
CC -1- CATALYTIC ACTIVITY: THYMIDINE + PHOSPHATE = THYMINES + 2-DEOXY-D-  
RIBOSE 1-PHOSPHATE.  
CC -1- PATHWAY: NUCLEOTIDE AND DEOXYRIBONUCLEOTIDE CATABOLISM.  
CC -1- SUBUNIT: HOMODIMER.  
CC -1- DISEASE: DEFECTS IN ECGF1 ARE THE CAUSE OF MITOCHONDRIAL  
NEUROGAstrointestinal ENCEPHALOMyopathy (MNGIE) (ALSO KNOWN AS  
MYONEUROGAstrointestinal ENCEPHALOMyopathy); AN AUTOSOMAL  
RECESSIVE HUMAN DISEASE ASSOCIATED WITH MULTIPLE DELETIONS OF  
SKELETAL MUSCLE MITOCHONDRIAL DNA (MTDNA). IT IS CLINICALLY  
CHARACTERIZED BY ONSET BETWEEN THE SECOND AND FIFTH DECADES OF  
LIFE, PTOSIS, PROGRESSIVE EXTERNAL OPHTHALMOPLAGIA,  
GASTROINTESTINAL DYSMOTILITY (OFTEN PSEUDOObSTRUCTION), DIFFUSE

```

CC LEUKOENCEPHALOPATHY, THIN BODY HABITUS, PERIPHERAL NEUROPATHY, AND
CC MYOPATHY.
CC -!- SIMILARITY: BELONGS TO THE THYMIDINE/PYRIMIDINE-NUCLEOSIDE
CC PHOSPHORYLASES FAMILY.
CC -!- DATABASE: NAME=R&d systems' cytokine source book;
CC WWW="http://www.rndsystems.com/cyl_cat/pdecgf.html".
CC -----
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CC -----
CC
CC EMBL; M63193; AAA60043.1; -.
CC EMBL; U62317; AAB03344.1; -.
CC PIR; S03904; S03904.
CC MIM; 131222; -.
CC MIM; 603041; -.
CC InterPro; IPR000053; -.
CC InterPro; IPR000312; -.
CC Pfam; PF00591; Glycos_transf_3; 1.
CC PROSITE; PS00647; THYMID_PHOSPHORYLASE; 1.
CC Transferrase; Glycosyltransferase; Growth factor; Chemotaxis;
CC Vascularization; Repeat; Polymorphism; Disease mutation.
KW PROPEP 1 10
FT CHAIN 11 482 THYMIDINE PHOSPHORYLASE.
FT REPEAT 265 279 R-V-A-A-A-L-X(5,6)-L-G-R.
FT REPEAT 329 342 R-V-A-A-A-L-X(5,6)-L-G-R.
FT REPEAT 393 401 R-A-L-X-X-A-L-V-L.
FT REPEAT 453 461 R-A-L-X-X-A-L-V-L.
FT VARIANT 145 145 G -> R (IN MNGIE).
FT VARIANT 153 153 /FTid=VAR_007643.
FT VARIANT 153 153 G -> S (IN MNGIE).
FT VARIANT 222 222 /FTid=VAR_007644.
FT VARIANT 222 222 K -> S (IN MNGIE).
FT VARIANT 289 289 /FTid=VAR_007645.
FT VARIANT 397 398 E -> A (IN MNGIE).
FT VARIANT 398 398 /FTid=VAR_007646.
FT VARIANT 471 471 MISSING (IN MNGIE).
FT VARIANT 471 471 /FTid=VAR_007647.
FT VARIANT 471 471 L -> S.
FT CONFLICT 444 444 /FTid=VAR_007648.
FT CONFLICT 452 452 G -> R (IN REF. 3).
FT SEQUENCE 482 AA; 49981 MW; 0652FA132C3BDE28 CRC64;
SO

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
RC TISSUE=Skeletal muscle;  
RX MEDLINE=90130482; PubMed=2298749;  
RA Zorzato F., Fujii J., Otsu K., Phillips M., Green N.M., Lai F.A.,  
RA Meissner G., MacLennan D.H.;  
RA "Molecular cloning of cDNA encoding human and rabbit forms of the  
RT Ca2+ release channel (ryanodine receptor) of skeletal muscle  
RT sarcoplasmic reticulum.";  
RL J. Biol. Chem. 265:2244-2256(1990).  
RN [2]  
RP VARIANT MH CYS-614.  
RX MEDLINE=92128959; PubMed=1774074;  
RA Gillard E.F., Otsu K., Fujii J., Khanna V.K., de Leon S.,  
RA Derdemezi J., Britt B.A., Duff C.L., Worton R.G., McLennan D.H.;  
RA "A substitution of cysteine for arginine 614 in the ryanodine  
RT receptor is potentially causative of human malignant hyperthermia.";  
RL Genomics 11:751-755(1991).  
RN [3]  
RP VARIANT MH ARG-248, AND VARIANTS CYS-471; LEU-1786 AND CYS-2059.  
RX MEDLINE=92372020; PubMed=1354642;  
RA Gillard E.F., Otsu K., Fujii J., Duff C., de Leon S., Khanna V.K.,  
RA Britt B.A., Worton R.G., McLennan D.H.;  
RA "Polymorphisms and deduced amino acid substitutions in the coding  
RT sequence of the ryanodine receptor (RYR1) gene in individuals with  
RT malignant hyperthermia.";  
RL Genomics 13:1247-1254(1992).  
RN [4]  
RP VARIANT CCD HIS-2434.  
RX MEDLINE=94035117; PubMed=8220422;  
RA Zhang Y., Chen H.S., Khanna V.K., de Leon S., Phillips M.S.,  
RA Schappert K., Britt B.A., Brownell A.K.W., MacLennan D.H.;  
RA "A mutation in the human ryanodine receptor gene associated with  
RT central core disease.";  
RL Nat. Genet. 5:46-50(1993).  
RN [5]  
RP VARIANTS CCD CYS-163 AND MET-403.  
RX MEDLINE=94035118; PubMed=8220423;  
RA Quane K.A., Healy J.M.S., Keating K.E., Manning B.M., Couch F.J.,  
RA Palmucci L.M., Doriguzzi C., Fagerlund T.H., Berg K., Ordling H.,  
RA Bendixen D., Mortier W., Linz U., Muller C.R., McCarthy T.V.;  
RA "Mutations in the ryanodine receptor gene in central core disease and  
RT malignant hyperthermia.";  
RL Nat. Genet. 5:51-55(1993).  
RN [6]  
RP VARIANT MH SER-522.  
RX MEDLINE=95130087; PubMed=7829078;  
RA Quane K.A., Keating K.E., Healy J.M.S., Manning B.M.,  
RA Krivosic-Horber R., Krivosic I., Monnier N., Lunardi J.,  
RA McCarthy T.V.;  
RA "Mutation screening of the RYR1 gene in malignant hyperthermia:  
RT detection of a novel Tyr to Ser mutation in a pedigree with  
RT associated central cores.";  
RL Genomics 23:236-239(1994).  
RN [7]  
RP VARIANT MH ARG-341.  
RX MEDLINE=94282042; PubMed=8012359;  
RA Quane K.A., Keating K.E., Manning B.M., Healy J.M.S., Monsieus K.,  
RA Heffron J.J.A., Lehane M., Heytons L., Krivosic-Horber R., Adnet P.,  
RA Ellis F.R., Monnier N., Lunardi J., McCarthy T.V.;  
RA "Detection of a novel common mutation in the ryanodine receptor gene  
RT in malignant hyperthermia: implications for diagnosis and  
RT heterogeneity studies.";  
RL Hum. Mol. Genet. 3:471-476(1994).  
RN [8]  
RP VARIANT MH ARG-2433.  
RX MEDLINE=95152512; PubMed=7849712;  
RA Keating K.E., Quane K.A., Manning B.M., Lehane M., Hartung E.,  
RA Censier K., Urwyler A., Klausnitzer M., Muller C.R., Heffron J.J.A.,  
RA McCarthy T.V.;

RT "Detection of a novel RYR1 mutation in four malignant hyperthermia  
RT pedigrees.";  
RL Hum. Mol. Genet. 3:1855-1858(1994).  
RN [9]  
RP VARIANT MH ARG-2433.  
RX MEDLINE=95187158; PubMed=7881417;  
RA Phillips M.S., Khanna V.K., de Leon S., Frodis W., Britt B.A.,  
RA McLennan D.H.;  
RA "The substitution of Arg for Gly2433 in the human skeletal muscle  
RT ryanodine receptor is associated with malignant hyperthermia.";  
RL Hum. Mol. Genet. 3:2181-2186(1994).  
RN [10]  
RP VARIANT MH ARG-35.  
RX MEDLINE=97219028; PubMed=9066328;  
RA Lynch P.J., Krivosic-Horber R., Reyford H., Monnier N., Quane K.,  
RA Adnet P., Haudecoeur G., Krivosic I., McCarthy T., Lunardi J.;  
RA "Identification of heterozygous and homozygous individuals with the  
RT novel RYR1 mutation Cys35Arg in a large kindred.";  
RL Anesthesiology 86:620-626(1997).  
RN [11]  
RP VARIANT MH LEU-614.  
RX MEDLINE=98051290; PubMed=9389851;  
RA Quane K.A., Ordling H., Keating K.E., Manning B.M., Heine R.,  
RA Bendixen D., Berg K., Krivosic-Horber R., Lehmann-Horn F.,  
RA Fagerlund T., McCarthy T.V.;  
RA "Detection of a novel mutation at amino acid position 614 in the  
RT ryanodine receptor in malignant hyperthermia.";  
RL Br. J. Anaesth. 79:332-337(1997).  
RN [12]  
RP VARIANT MH TRP-552.  
RX MEDLINE=97284075; PubMed=9138151;  
RA Keating K.E., Giblin L., Lynch P.J., Quane K.A., Lehane M.,  
RA Heffron J.J.A., McCarthy T.V.;  
RA "Detection of a novel mutation in the ryanodine receptor gene in an  
RT Irish malignant hyperthermia pedigree: correlation of the IVCT  
RT response with the affected and unaffected haplotypes.";  
RL J. Med. Genet. 34:291-296(1997).  
RN [13]  
RP VARIANTS MH CYS-2162; HIS-2162; MET-2167 AND MET-2205.  
RX MEDLINE=98163444; PubMed=9497245;  
RA Manning B.M., Quane K.A., Ordling H., Urwyler A., Tegazzin V.,  
RA Lehane M., O'Halloran J., Hartung E., Giblin L.M., Lynch P.J.,  
RA Vaughan P., Censier K., Bendixen D., Comi G., Heytens L.,  
RA Monsieus K., Fagerlund T., Wolz W., Heffron J.J.A., Mueller C.R.,  
RA McCarthy T.V.;  
RA "Identification of novel mutations in the ryanodine-receptor gene  
RT (RYR1) in malignant hyperthermia: genotype-phenotype correlation.";  
RL Am. J. Hum. Genet. 62:599-609(1998).  
RN [14]  
RP VARIANTS MH CYS-2458 AND HIS-2458.  
RX MEDLINE=98111378; PubMed=9450902;  
RA Manning B.M., Quane K.A., Lynch P.J., Urwyler A., Tegazzin V.,  
RA Krivosic-Horber R., Censier K., Comi G., Adnet P., Wolz W.,  
RA Lunardi J., Muller C.R., McCarthy T.V.;  
RA "Novel mutations at a CpG dinucleotide in the ryanodine receptor in  
RT malignant hyperthermia.";  
RL Hum. Mutat. 11:45-50(1998).  
RN [15]  
RP VARIANTS MH.  
RX MEDLINE=99415746; PubMed=10484775;  
RA Brandt A., Schleithoff L., Jurkat-Rott K., Klingler W., Baur C.,  
RA Lehmann-Horn F.;  
RA "Screening of the ryanodine receptor gene in 105 malignant  
RT hyperthermia families: novel mutations and concordance with the in  
RT vitro contracture test.";  
RL Hum. Mol. Genet. 8:2055-2062(1999).  
RN [16]  
RP VARIANTS MH LEU-2434 AND HIS-2453.  
RX MEDLINE=99158296; PubMed=10051009;  
RA Barone V., Massa O., Intravaia E., Bracco A., Di Martino A.,  
RA Tegazzin V., Cozzolino S., Sorrentino V.;  
RA "Mutation screening of the RYR1 gene and identification of two novel  
RT mutations in Italian malignant hyperthermia families.";







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CC -!- SIMILARITY: BELONGS TO THE "DEAD" BOX FAMILY HELICASE.
CC -----
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CC -----
CC EMBL; Z54285; CAA91073.1; -.
CC InterPro; IPR000629; -.
CC InterPro; IPR001410; -.
CC InterPro; IPR001650; -.
CC Pfam; PF00270; DEAD; 1.
CC Pfam; PF00271; helicase_C; 1.
CC PROSITE; PS00039; DEAD_ATP_HELICASE; 1.
KW Hypothetical protein; ATP-binding; RNA-binding; Helicase.
FT NP_BIND 90 97 ATP (POTENTIAL).
FT SITE 196 199 DEAD BOX.
SQ SEQUENCE 481 AA; 54026 MW; 872ECAFC106E110A CRC64;

Query Match 10.9%; Score 71.5; DB 1; Length 481;
Best Local Similarity 24.3%; Pred. No. 8.1;
Matches 25; Conservative 25; Mismatches 48; Indels 5; Gaps 4;

QY 25 PSPTLKL-IEELVNITQNQASLCNGSMVSV-NLTAGMYCAALESLINVSDCSAIQRTQ 82
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
18 PQPSIKEKEAKKLGITGKAKVGTGNPNVDPIEEFPEGILCENLKKQ-NITECTTIQR-- 74
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 83 RMLKALCSQKPAAGISSERSRDTKIEVIQLVKNLLTYVRGVYR 125
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
75 YAIPTIGSKRDLACAPTSKGKTIAYLPILQKLQLHVPGGYR 117

RESULT 13
HIT_MACMU STANDARD; PRT; 207 AA.
AC P40286;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE HISTONE H1T.
GN H1T OR H1T.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94230585; PubMed=8175896;
RA Koppel D.A., Wolfe S.A., Fogelfeld L., Grimes S.R.;
RT "Primate testicular histone H1t genes are highly conserved and the
RT human H1t gene is located on chromosome 6.";
RL J. Cell. Biochem. 54:219-230(1994).
CC -!- FUNCTION: HISTONES H1 ARE NECESSARY FOR THE CONDENSATION OF
CC NUCLEOSOME CHAINS INTO HIGHER ORDER STRUCTURES.
CC -!- SUBCELLULAR LOCATION: NUCLEAR.
CC -!- DEVELOPMENTAL STAGE: THIS HISTONE IS A TESTIS-SPECIFIC H1 VARIANT
CC THAT APPEARS DURING MEIOSIS IN SPERMATOGENESIS.
CC -!- SIMILARITY: BELONGS TO THE HISTONE H1/H5 FAMILY.
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CC -----
CC EMBL; M97756; AAA19937.1; -.

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DR HSSP; P08287; IGHC.
DR InterPro; IPR001386; -.
DR Pfam; PF00538; linker_histone; 1.
KW Chromosomal protein; Nuclear protein; DNA-binding; Multigene family;
KW Acetylation; Spermatogenesis; Testis.
FT INIT_MET 0 0 BY SIMILARITY.
FT MOD_RES 1 1 ACETYLATION (BY SIMILARITY).
FT DOMAIN 39 112 GLOBULAR.
SQ SEQUENCE 207 AA; 21962 MW; 8812112C83727705 CRC64;

Query Match 10.7%; Score 70.5; DB 1; Length 207;
Best Local Similarity 25.6%; Pred. No. 3.8;
Matches 30; Conservative 17; Mismatches 31; Indels 39; Gaps 5;

QY 16 GLASPSVPPTPLKELIEELVNITQNQASLCNGSMVSVNLTAGMYCAALESLINVSDC 75
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
30 GLTSASRKAPNLSVSKLITEALSVSQER-----VGMSLAALK----- 66
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 76 SAIQRTQRMKALCSQKPAAGISSERSRD-TKIEVIQLV-KNLLTYVRGVYRHGNFR 130
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
67 -----KALA---AAGYDVEKNNSRIKLSKLSLVKNGILVQTRGTGSGSGSPK 109

RESULT 14
VR2A_BPT4 STANDARD; PRT; 725 AA.
AC P03690;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE RIIA PROTEIN.
GN RIIA.
OS Bacteriophage T4.
OC Viruses; dsDNA viruses, no RNA stage; Tailed phages; Myoviridae;
OC T4-like phages.
OX NCBI_TaxID=10665;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90337270; PubMed=2379817;
RA Daegelen P., Brody E.;
RT "The rIIA gene of bacteriophage T4. I. Its DNA sequence and discovery
RT of a new open reading frame between genes 60 and rIIA.";
RL Genetics 125:237-248(1990).
RN [2]
RP SEQUENCE OF 476-725 FROM N.A.
RX MEDLINE=84267841; PubMed=6748077;
RA Sugino A., Drake J.W.;
RT "Modulation of mutation rates in bacteriophage T4 by a base-pair
RT change a dozen nucleotides removed.";
RL J. Mol. Biol. 176:239-249(1984).
RN [3]
RP SEQUENCE OF 587-725 FROM N.A.
RX MEDLINE=82078066; PubMed=6273585;
RA Pribnow D., Sigurdson D.C., Gold L., Singer B.S., Napoli C.,
RA Brosius J., Dull T.J., Noller H.F.;
RT "rII cistrons of bacteriophage T4. DNA sequence around the
RT intercistronic divide and positions of genetic landmarks.";
RL J. Mol. Biol. 149:337-376(1981).
CC -!- FUNCTION: TRANSCRIBED PRIOR TO REPLICATION. THIS PROTEIN FORM
CC PARTS OF THE REPLICATION COMPLEX AND HAS DNA-BINDING PROPERTIES.
CC -!- SUBCELLULAR LOCATION: ON THE INNER MEMBRANE OF THE HOST SHORTLY
CC AFTER INFECTION.
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CC EMBL; X52686; CAA36911.1; -.

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DR PIR: A04304; Z2BPA4.  
 DR PIR: JU0400; JU0400.  
 KW Early protein; DNA-binding; DNA replication; Inner membrane; Repeat.  
 FT REPEAT 101 179 APPROXIMATE.  
 FT REPEAT 481 559 APPROXIMATE.  
 FT DNA\_BIND 544 570 H-T-H MOTIF (BY SIMILARITY).  
 FT CONFLICT 616 616 D -> H (IN REF. 2).  
 SO SEQUENCE 725 AA; 82893 MW; 2290FE341BB45416 CRC64;

OY 51 MWSVNLTAGMYCALESINVSDCS---AIQRTQRMKALCSQKP 93  
 Db 65 MTWEQNIHSMFCNMQFLTKTGLCSGVDAVIKAYRLLYEQCPQPP 110

Search completed: May 14, 2001, 06:02:08  
 Job time: 43365 sec

Query Match 10.6%; Score 70; DB 1; Length 725;  
 Best Local Similarity 27.0%; Pred. No. 18;  
 Matches 27; Conservative 20; Mismatches 31; Indels 22; Gaps 5;

OY 28 TLKEL-IEELVNITONQSLCNGSVNLTAGMYCALESINVSDCSAIQRTQRMK 86  
 Db 342 TTKNLSYKKMQSMFEPDSKLCNAGVYEVNLD----PRLKRIQSHETSAVASSYRLF- 395  
 OY 87 ALCQKPRAGISSERSRDTKIE-VIOLVKNLTYVGRGVR 125  
 Db 396 -----GINT-----TKINIVIDNIKNRVNIVRGLAR 421

RESULT 15  
 FLHC\_SALTY  
 ID FLHC\_SALTY STANDARD; PRT; 192 AA.  
 AC 052222;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE FLAGELLAR TRANSCRIPTIONAL ACTIVATOR FLHC.  
 GN FLHC.  
 OS Salmoneella typhimurium.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Salmoneella.  
 OX NCBI\_TaxID=602;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-LT2;  
 RA Toguchi A., Harshey R.M.;  
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX Pubmed=10586519;  
 RA Yanagihara S., Iyoda S., Ohnishi K., Iino T., Kutsukake K.;  
 RT "Structure and transcriptional control of the flagellar master operon  
 of Salmoneella typhimurium."  
 RL Genes Genet. Syst. 74:105-111(1999).  
 CC -I- FUNCTION: TRANSCRIPTIONAL ACTIVATOR. TOGETHER WITH FLHD IT ACTS AS  
 A COMPOUND SIGMA FACTOR THAT ACTIVATE CLASS 2 FLAGELLAR GENES (BY  
 SIMILARITY).  
 CC -I- SIMILARITY: BELONGS TO THE FLHC FAMILY.  
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 CC -----  
 DR EMBL: AF029300; AAB96640.1; -  
 DR EMBL: D43640; BAA85315.1; -  
 DR StyGene: SG10643; flhc.  
 KW Transcription regulation; Sigma factor; DNA-directed RNA polymerase;  
 KW DNA-binding; Flagella.  
 SO SEQUENCE 192 AA; 21579 MW; C7334C691ECE3F8D CRC64;

Query Match 10.6%; Score 69.5; DB 1; Length 192;  
 Best Local Similarity 32.6%; Pred. No. 4.4;  
 Matches 15; Conservative 7; Mismatches 21; Indels 3; Gaps 1;



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OM protein - protein search, using sw model

Run on: May 14, 2001, 06:01:11 ; Search time 133.94 Seconds  
(without alignments)  
113.760 Million cell updates/sec

Title: US-09-451-527-100  
Perfect score: 658  
Sequence: 1 MALWLTVVIALTCLGLASP.....QLVKNLLTYVRGVYRHGNFR 130

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_15:

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_unclassified:\*
- 13: sp\_vertebrate:\*
- 14: sp\_virus:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	647.5	98.4	131	6 Q9N0W9	Q9n0w9 canis famil
2	383	58.2	114	6 Q9TV84	Q9tv84 bos taurus
3	157.5	23.9	49	4 Q9UDC7	Q9udc7 homo sapien
4	82.5	12.5	275	6 Q28609	Q28609 oryctolagus
5	79	12.0	1183	4 Q94918	Q94918 homo sapien
6	79	12.0	1230	4 Q9P0H7	Q9p0h7 homo sapien
7	79	12.0	1230	11 P97536	P97536 rattus norv
8	78.5	11.9	1448	5 Q9N949	Q9n949 trypanosoma
9	76.5	11.6	1448	5 Q9N946	Q9n946 trypanosoma
10	74	11.2	336	10 Q9SMD4	Q9smd4 lycopersico
11	73.5	11.2	415	8 Q9MUM4	Q9mun4 mesostigma
12	73.5	11.2	607	10 Q9SI43	Q9si43 arabisdopsis
13	73.5	11.2	649	14 O10619	O10619 helicoverpa
14	73.5	11.2	1806	5 O45657	O45657 caenorhabdi
15	72.5	11.0	150	14 Q98779	Q98779 vesicular s
16	72.5	11.0	438	10 Q9M3H8	Q9m3h8 cicer ariet
17	72.5	11.0	1763	11 Q9JKX5	Q9jkk5 mus musculu
18	72	10.9	5038	4 Q9NPK1	Q9npk1 homo sapien
19	71.5	10.9	150	14 Q98791	Q98791 vesicular s

20	71.5	10.9	718	5 O18412	O18412 drosophila
21	71	10.8	155	11 Q9RLG1	Q9rlg1 rattus norv
22	71	10.8	293	6 Q9TTI0	Q9tti0 sus scrofa
23	71	10.8	586	3 Q9P3A1	Q9p3a1 neurospora
24	71	10.8	589	5 O96661	O96661 trypanosoma
25	70.5	10.7	150	14 Q98780	Q98780 vesicular s
26	70.5	10.7	150	14 Q98787	Q98787 vesicular s
27	70.5	10.7	150	14 Q98789	Q98789 vesicular s
28	70.5	10.7	264	1 Q9YEK5	Q9yek5.aeropyrum p
29	70.5	10.7	1026	10 O49529	O49529 arabisdopsis
30	70.5	10.7	1449	5 Q9N937	Q9n937 trypanosoma
31	70.5	10.7	1811	14 O36184	O36184 plautia sta
32	70	10.6	425	4 Q95810	Q95810 homo sapien
33	70	10.6	474	2 Q9RAC1	Q9rac1 rickettsia
34	70	10.6	475	2 Q9RAC2	Q9rac2 rickettsia
35	70	10.6	475	2 Q9RAC0	Q9rac0 rickettsia
36	70	10.6	475	2 Q9RAB9	Q9rab9 rickettsia
37	70	10.6	482	9 O36165	O36165 bacterioph
38	70	10.6	513	2 O68559	O68559 rickettsia
39	70	10.6	516	2 Q53242	Q53242 rickettsia
40	70	10.6	540	5 Q9W025	Q9w025 drosophila
41	70	10.6	925	10 Q9SIX4	Q9six4 arabisdopsis
42	70	10.6	1063	5 Q9VWL7	Q9vwl7 drosophila
43	70	10.6	1510	5 Q9VX92	Q9vx92 drosophila
44	69.5	10.6	274	14 Q89048	Q89048 vesicular s
45	69.5	10.6	980	11 P97837	P97837 rattus norv

ALIGNMENTS

RESULT 1.  
Q9N0W9  
ID Q9N0W9 PRELIMINARY; PRT; 131 AA.  
AC Q9N0W9;  
DT 01-OCT-2000 (TremBLrel. 15, Created)  
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)  
DT 01-OCT-2000 (TremBLrel. 15, Last annotation update)  
DE INTERLEUKIN-13.  
OS Canis familiaris (Dog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
OX NCBI\_TaxID=9615;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Yang S., Boroughs K.L., McDermott M.J.;  
RT "Canine Interleukin-13: Molecular Cloning of Full-Length cDNA and  
RT Expression of Biologically Active Recombinant Protein.";  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF244915; AAF63204.1; -  
SQ SEQUENCE 131 AA; 14268 MW; 9A142B4D0F80370F CRC64;

Query Match	98.4%	Score	647.5;	DB	6;	Length	131;
Best Local Similarity	99.2%	Pred. No.	3.8e-60;				
Matches	130;	Conservative	0;	Mismatches	0;	Indels	1;
Gaps	1;						
Qy	1	MALWLTVVIALTCLGLASPSVTPSPPTIKELIEELVNITQNQASLNGSMVWSVNLTAG	60				
Db	1	MALWLTVVIALTCLGLASPSVTPSPPTIKELIEELVNITQNQASLNGSMVWSVNLTAG	60				
Qy	61	MYCAALESLINVSDCSAIQRTQRMKALCSQKPAAG-ISSERSRDTKIEVLVKNLLTY	119				
Db	61	MYCAALESLINVSDCSAIQRTQRMKALCSQKPAAG-ISSERSRDTKIEVLVKNLLTY	120				
Qy	120	VRGVYRHGNFR	130				
Db	121	VRGVYRHGNFR	131				
RESULT	2						
Q9TV84							
ID	Q9TV84	PRELIMINARY;	PRT;	114	AA.		



AC Q9TVB4,  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
IDT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)  
DE INTERLEUKIN-13 PRECURSOR (FRAGMENT).  
GN IL-13.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Trigona W.T., Hirano A., Brown W.;  
RT "Biological activities of interleukin-13 (IL-13) on bovine  
RT lymphocytes: implications for signaling through IL-13Ra1."  
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
EMBL; AF072807; AAD22748.1; - .  
DR HSSP; P35225; 3ITR.  
DR INTERPRO; IPR001325; - .  
DR PROSITE; PS00838; INTERLEUKIN\_4\_13; UNKNOWN\_1.  
FT NON\_TER 114 114  
SQ SEQUENCE 114 AA; 12355 MW; D8CC56E5627D030A CRC64;

Query Match	58.2%;	Score 383;	DB 6;	Length 114;
Best Local Similarity	70.8%;	Pred. No. 1.4e-32;		
Matches	80;	Conservative	10;	Mismatches 21;
			Indels	2;
			Gaps	2;

```

Qy 1 MALMLTVIALTCLGGLASPSVPPTPTLKELEELVNITONQ-ASLCNGSMWWSYNLTA 59
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 MALMLTAVIVLICEFGLTSPVPSATALKELEELVNITONQKVPPLCNGSMWWSNLNLS 60

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Oy      60  GMYCALESLINVSDCSAIOQTQRMKLKALCSQKPPA-GISSERSRDTKIEVQ 111
          |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      61  SMYCALDLSLISNCSVIORTKRLNALCPHKPSAKOVSSSEYVRDTKIEVQ 113

```

### RESULT 3

ID	Q9UDC7	PRELIMINARY;	PRT;	49	AA
----	--------	--------------	------	----	----

DT	01-MAY-2000 (TREMBlrel. 13, Created)
DT	01-MAY-2000 (TREMBlrel. 13, last sequence update)
DT	01-OCT-2000 (TREMBlrel. 15, last annotation update)
DE	P600 HOMOLOG.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX	NCBI_TaxID=9606;

RP SEQUENCE FROM N.A.  
RX MEDLINE=93027259; Pubmed=1408833;  
RA Morgan J.G., Dolganov G.M., Robbins S.E., Hinton L.M., Lovett M.;  
RT "The selective isolation of novel cDNAs encoded by the regions  
RT surrounding the human interleukin 4 and 5 genes.";  
RL Nucleic Acids Res. 20:5173-5179(1992).

SQ SEQUENCE 49 AA; 5109 MW; 679CD23A190C778E CRC64;

Query Match	23.98;	Score 157.5;	DB 4;	Length 49;
Best Local Similarity	71.4%;	Pred. No. 1.9e-09;		
Matches 35; Conservative	1;	Mismatches 12;	Indels 1;	Gaps 1;

Qy 1 MALMLTVVIALTCGLGLASPSPVTPSPTLKELIEELVNITQNG-ASLCN 48  
||| ||||| |||| | : ||||| |||| | ||||  
Db 1 MALLLTVVIALACGLGFGDPSGVPSTALRELIEELSNITQTQKAPLCN 49

RESULT	4	
Q28609		
ID	Q28609	
PRELIMINARY;		
PRT;	275	AA

AC Q28609,  
DT 01-NOV-1996 (TREMBLrel, 01, Created)  
DT 01-NOV-1996 (TREMBLrel, 01, Last sequence update)  
DT 01-OCT-2000 (TREMBLrel, 15, Last annotation update)  
DE PUTATIVE PREPROSPERMINOGEN PRECURSOR.  
OS Oryctolagus cuniculus (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
OX NCBI\_TaxID=9986;

RP	SEQUENCE FROM N.A.		
RC	STRAIN=NEW ZEALAND WHITE; TISSUE=TESTIS;		
RX	MEDLINE=94368861; PubMed=8086468;		
RA	Richardson R.T., O'Rand M.G.;		
RT	"Cloning and sequencing of cDNAs for rabbit preproacrosin and a novel		
RL	preproacrosin-related cDNA.";		
DR	Biochim. Biophys. Acta 1219:215-218(1994).		
DR	EMBL: U05203; AAA61629.1; -.		
DR	HSSP: P00734; 2HNT.		
DR	INTERPRO: IPR001254; -.		
DR	PFAM: PF00089; trypsin; 1.		
DR	PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.		
KW	Signal.		
FT	Signal	1	16
FT	CHAIN	17	275
SQ	SEQUENCE	275 AA;	29965 MW; 8FC2467414069C61 CRC64;

Query.Match	12.5%;	Score 82.5;	DB 6;	Length 275;
Best Local Similarity	30.0%;	Pred. No. 0.88;		
Matches	24;	Conservative 12;	Mismatches 35;	Indels 9;
				Gaps 3;

```

QY      10 AATCL---GGLASPSPTPTLKEELIVNTITQNASLNGSMWWSVNLTAGMYCAAL 66
          |||      : ||||| : ||| : : || ||
Db      172 AQTGYVAGMGVYKENAPRPSPTLMEARVDLNL-----ELCNSTQWYNGRITFASNLGAGY 226

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```
QY      67  ESLINVSDCSAIQRTQRM LK 86
          | : | :| :||
Db      227 PS-GKIDTCQRLQQLVEVLK 245
```

## RESULT

ID	094918	PRELIMINARY;	PRT;	1183	AA.
----	--------	--------------	------	------	-----

DT 01-MAY-1999 (TREMBLrel. 10, Created)  
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)  
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)  
DE KIAA0829 PROTEIN (FRAGMENT).  
GN KIAA0829.

OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;

RP SEQUENCE FROM N.A.

RX MEDLINE=99156230; Pubmed=10048485;

RA Nagase T., Ishikawa K., Suyama M., Kikuno R., Hirosewa M.,  
 RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.,  
 RT "Prediction of the coding sequences of unidentified human genes. XII.  
 RT The complete sequences of 100 new cDNA clones from brain which code  
 RT for large proteins in vitro.";  
 RL DNA Res. 5:335-364(1998).

FT	NON_TER	SEQUENCE	AA;	130962 MW;	1FE0EE56C0DFFEE3A CRC64;
SO	1	1183			

Query Match	12.08;	Score 79;	DB 4;	Length 1183;
Best Local Similarity	31.28;	Pred. No. 11;		
Matches	39;	Conservative 19;	Mismatches 51;	Indels 16;
				Gaps 5;



OS Trypanosoma brucei.  
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.  
OX NCBI\_TaxID=5691;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=TREU927;  
RA Hall N., Bowman S., Quail M., Ivens A.C., Kay M.P., Bray-Allen S.,  
RA Lennard N.J., Clark L.N., Harris B.R., Melville S., Lawson D.,  
RA Gerard C., Rajandream M.A., Barrell B.G.;  
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AL359782; CAB95333.1; -  
SQ SEQUENCE 1448 AA; 160479 MW; 688B26228AD2046B CRC64;

Query Match 11.6%; Score 76.5; DB 5; Length 1448;  
Best Local Similarity 29.3%; Pred. No. 24;  
Matches 36; Conservative 18; Mismatches 34; Indels 35; Gaps 7;

QY 13 CLGGLASPSVTPSPTLKELIELVNITONQA--SLCNGSMWWSVNL-----TAGMYCA 64  
DB 557 CLGNL-----PQLKMLDLSGTN-TDNESLRSLSLQTVVSLNLSHCWKMTNVSHIS 606  
QY 65 ALESF--INVSDC-----SAIQRTQRMKALCSQKPAAGISSERSRDTKIEVIQLVKN 115  
DB 607 SLEALNELNSNCIRINAGWEAIEKLQQLHVAI-----LSNTHITDRDISHFSKCKN 658  
QY 116 LLT 118  
DB 659 LVT 661

RESULT 10  
Q9SMD4 PRELIMINARY; PRT; 336 AA.  
AC Q9SMD4;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)  
DE CYCD3,3 PROTEIN.  
CN CYCD3,3.  
OS Lycopersicon esculentum (Tomato).  
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
OC Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I;  
OC Solanales; Solanaceae; Solanum.  
OX NCBI\_TaxID=4081;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CV. UC82B;  
RA Kvarnheden A., Yao J.L., O'Brien I., Morris B.;  
RT "differential expression of three D3 cyclin genes during tomato fruit  
set and development."  
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AJ002590; CAB60838.1; -  
DR INTERPRO: IPR000553; -  
DR PFAM: PF00134; cyclin; 1.  
SQ SEQUENCE 336 AA; 38687 MW; 5BBA8F6DD0852031 CRC64;

Query Match 11.2%; Score 74; DB 10; Length 336;  
Best Local Similarity 23.9%; Pred. No. 8.5;  
Matches 37; Conservative 24; Mismatches 54; Indels 40; Gaps 9;

QY 4 WLTVTIALTCLGLASPSVTPSPTLKEL-IEEL-----VNITQNASLNGSMWWSVN- 56  
DB 125 WMNQLVAVTCL-SLAAYVEETDVPPLLDLQVEESGFLESKTIQRMEMLILSTLKKMNP 183  
QY 57 -----LTAGM-----YCALE-----SLINVS-----CSAIQRTQRMKALCS 90  
DB 184 VTFPSFLDFTRRLGLKHLCLSLLEFLRCEKVLVTTDDRFITGYLPSAMASATMLHVIDR 243  
QY 91 QKPAAGISSERSRDTKIEVIQLVKNLLTYVGVYR 125  
DB 244 LKPCIG---EKYQDQLGLIGIVKE---KVEGCYR 272

RESULT 11  
Q9MUM4 PRELIMINARY; PRT; 415 AA.  
AC Q9MUM4;  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)  
DE PUTATIVE PLASTID DIVISION PROTEIN.  
GN FTSW.  
OS Mesostigma viride.  
OC Chloroplast.  
OC Eukaryota; Viridiplantae; Chlorophyta; Prasinophyceae;  
OC Chlorodendrales; Mesostigmataceae; Mesostigma.  
OX NCBI\_TaxID=41882;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20150907; PubMed=1068199;  
RA Lemieux C., Otis C., Turmel M.;  
RT "Ancestral chloroplast genome in Mesostigma viride reveals an early  
branch of green plant evolution."  
RL Nature 403:649-652(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Lemieux C., Otis C., Turmel M.;  
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF166114; AAF43874.1; -  
KW Chloroplast.  
SQ SEQUENCE 415 AA; 46813 MW; E35116E9692EC782 CRC64;

Query Match 11.2%; Score 73.5; DB 8; Length 415;  
Best Local Similarity 28.7%; Pred. No. 12;  
Matches 27; Conservative 19; Mismatches 29; Indels 19; Gaps 4;

QY 36 LVNITQNASLNGSMWWSVNLTAGMYCALESLINVSDCSAI-----QRTQMLKAL 88  
DB 188 LIQPNLSTASLC-GAIIMLVALTAGIHWFYLSILSIGAVTALISLGSQETQRRISFL 246  
QY 89 CSQKPAAGISSERSRDTKIEVIQLVKNLLTYVVG 122  
DB 247 ---NPWANPITSIG-----YQLVQSLAVGSG 269

RESULT 12  
Q9SI43 PRELIMINARY; PRT; 607 AA.  
AC Q9SI43;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)  
DE PUTATIVE METHYLMALONATE SEMI-ALDEHYDE DEHYDROGENASE.  
GN AT2G14170.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;  
OX NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CV. COLUMBIA;  
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,  
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,  
RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,  
RA Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,  
RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,  
RA Copenhaver G.P., Preuss D., Niernan W.C., White O., Eisen J.A.,  
RA Salzberg S.L., Fraser C.M., Venter J.C.;  
RT "Sequence and analysis of chromosome II of Arabidopsis thaliana."  
RL Nature 402:761-768(1999).  
DR EMBL: AC007197; AAD25855.1; -  
DR HSSP; P56533; 1A4S.





DR	PFAM; PF00922; phosphoprotein; 1.
FT	NON_TER 1 1
FT	NON_TER 150 150
SO	SEQUENCE 150 AA; 16711 MW; 16D11C4E8E8A65E7 CRC64;

Query Match	11.0%;	Score 72.5;	DB 14;	Length 150;
Best Local Similarity	24.28;	Pred. NO. 4.9;		
Matches	29;	Conservative	20;	Mismatches 40;
			Indels	31;
			Gaps	6;

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QY 22 PYTPSPTLKELIEEL-----VNITQNOA-----SLCNGSMWVSVN---LTAGMY 62
      | :||| | | :||| | :|| | :||
Db 14 PSWTQPIKENGGERSLSLFPVGLTQVQTEQWKKTIEYVCESSKXWNLSECQIVTSG-N 72
      | :||| | :||| | :||| | :|||
QY 63 CAALSLINVSDCSAIQRTQRMKLKALCSQKPAAGTSSERSR-----DTKIEVIQLV 113
      | : |||| :|| :| :| :| :|
Db 73 CLILRGQVMTSDCCSSAKSQNSRQS--SESPSPSNSEPHASRASASPMLDFKFTVEQVLI 130
      | :||| :|| :| :| :| :|
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Search completed: May 14, 2001, 06:01:15  
Job time: 43958 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: May 13, 2001, 17:47:36 ; Search time 79.9 Seconds  
(without alignments)  
78.698 Million cell updates/sec

Title: US-09-451-527-105  
Perfect score: 556  
Sequence: 1 SPVTPSPTLKELIELVNIT.....QLVKNLLTYVRGVYRHGNFR 110

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 390729 seqs, 57163235 residues

Total number of hits satisfying chosen parameters: 390729

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_0401.\*  
1: /cgnl\_8/gcgdata/geneseq/geneseqp/AA1980.DAT.\*  
2: /cgnl\_8/gcgdata/geneseq/geneseqp/AA1981.DAT.\*  
3: /cgnl\_8/gcgdata/geneseq/geneseqp/AA1982.DAT.\*  
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5: /cgnl\_8/gcgdata/geneseq/geneseqp/AA1984.DAT.\*  
6: /cgnl\_8/gcgdata/geneseq/geneseqp/AA1985.DAT.\*  
7: /cgnl\_8/gcgdata/geneseq/geneseqp/AA1986.DAT.\*  
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13: /cgnl\_8/gcgdata/geneseq/geneseqp/AA1992.DAT.\*  
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15: /cgnl\_8/gcgdata/geneseq/geneseqp/AA1994.DAT.\*  
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17: /cgnl\_8/gcgdata/geneseq/geneseqp/AA1996.DAT.\*  
18: /cgnl\_8/gcgdata/geneseq/geneseqp/AA1997.DAT.\*  
19: /cgnl\_8/gcgdata/geneseq/geneseqp/AA1998.DAT.\*  
20: /cgnl\_8/gcgdata/geneseq/geneseqp/AA1999.DAT.\*  
21: /cgnl\_8/gcgdata/geneseq/geneseqp/AA2000.DAT.\*  
22: /cgnl\_8/gcgdata/geneseq/geneseqp/AA2001.DAT.\*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	556	100.0	110	21 Y58224	Canine mature inte
2	556	100.0	130	21 Y58223	Canine interleukin
3	545.5	98.1	111	21 Y58222	Canine mature inte
4	545.5	98.1	131	21 Y58221	Canine interleukin
5	377.5	67.9	111	17 R92794	Human interleukin-
6	367	66.0	112	13 R27347	protein with cyto
7	367	66.0	112	17 R92793	Human interleukin-
8	367	66.0	132	15 R48624	Sequence of human
9	360	64.7	112	13 R27346	Protein with cyto
10	360	64.7	146	13 R27348	Cytokine NC30. R
11	302	54.3	131	15 R48625	Sequence of mouse

12	299	53.8	111	17	R92795	Murine P600. Mus
13	75	13.5	634	20	Y21548	Human heparin-bind
14	72	12.9	5072	12	R11510	Ryanodine receptor
15	70	12.6	330	21	G06262	Arabidopsis thalia
16	70	12.6	407	21	G06261	Arabidopsis thalia
17	69	12.4	286	21	Y58998	Wheat sulfite redu
18	69	12.4	4987	12	R10834	Rianodin receptor.
19	67	12.1	21	20	Y49702	Human interleukin
20	67	12.1	673	21	Y58996	Rice sulfite reduc
21	65	11.7	197	21	G31561	Arabidopsis thalia
22	65	11.7	213	21	G31560	Arabidopsis thalia
23	65	11.7	300	21	G31559	Arabidopsis thalia
24	65	11.7	514	21	G55503	Arabidopsis thalia
25	65	11.7	602	21	G55502	Arabidopsis thalia
26	65	11.7	620	21	G55501	Arabidopsis thalia
27	65	11.7	1015	21	G41796	Arabidopsis thalia
28	65	11.7	1074	21	G41795	Arabidopsis thalia
29	65	11.7	1100	21	G41794	Arabidopsis thalia
30	65	11.7	5035	13	R25450	Arabidopsis thalia
31	64	11.5	383	13	R28947	MH mutant porcine
32	64	11.5	383	18	W07698	Alcohol dehydrogen
33	64	11.5	383	19	W80730	Zymomonas mobilis
34	64	11.5	504	20	W93429	Z. mobilis alcohol
35	64	11.5	1461	19	W64468	A. thaliana EL3 pr
36	63.5	11.4	168	21	B35513	Human secreted pro
37	63.5	11.4	168	21	B32216	Baculovirus RNA ba
38	63.5	11.4	621	20	Y21549	RNA baculovirus ph
39	63.5	11.4	2548	20	Y05781	Porcine heparin-bi
40	62.5	11.2	150	16	R85457	Human myosin IXa.
41	62.5	11.2	220	21	G06263	Flax rust resistan
42	62.5	11.2	401	21	G51250	Arabidopsis thalia
43	62.5	11.2	404	21	G51249	Arabidopsis thalia
44	62.5	11.2	534	21	B42909	Arabidopsis thalia
45	62.5	11.2	570	21	Y51174	Human ORFX ORF2673
						Human brain PARP2

ALIGNMENTS

RESULT 1  
Y58224  
ID Y58224 standard; Protein; 110 AA.  
XX  
AC Y58224;  
XX  
DT 14-MAR-2000 (first entry)  
XX  
DE Canine mature interleukin-13 (IL-13) clone 78.  
XX  
DE Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;  
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine.  
XX  
OS Canis familiaris.  
XX  
PN WO9961618-A2.  
XX  
PD 02-DEC-1999.  
XX  
PF 28-MAY-1999; 99WO-US11942.  
XX  
PR 29-MAY-1998; 98US-0087306.  
XX  
PA (HESK-) HESKA CORP.  
XX  
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;  
XX  
DR WPI; 2000-072623/06.  
XX  
DR N-PSDB; 255565, 255566.  
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
PT useful for treating or preventing e.g. tumors or autoimmune disease  
XX  
PS Claim 3i; Page.240; 264pp; English.

XX Sequences Y58221-Y58222 and Y58223-Y58224 represent encoded and mature  
CC canine interleukin-13 (IL-13) clones 80 and 78. The invention relates to  
CC canine IL-4, canine or feline Flt-3 ligand, canine or feline CD40,  
CC canine IL-4, canine or feline Flt-3 ligand, canine or feline CD40,  
CC canine or feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline  
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage  
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these  
CC immunoregulatory proteins. The proteins, their associated  
CC nucleic acids, specific antibodies and inhibitors may be used as  
CC vaccines for therapeutic or prophylactic regulation of an immune  
CC response in animals (particularly cats, dogs, horses and humans).  
CC They may be used to treat autoimmune or infectious diseases including  
CC allergies, tumours, inflammation and graft rejection, and to increase  
CC the response from a co-administered antigen. The nucleotide sequences  
CC can also be used for the recombinant production of a protein, while  
CC nucleotide fragments are useful as probes, as amplification primers and  
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
CC The proteins may be used to raise antibodies and to screen for  
CC modulators of activity, while the antibodies may be used in detection,  
CC and in drug targeting.

XX  
SQ Sequence 110 AA;

Query Match 100.0%; Score 556; DB 21; Length 110;  
Best Local Similarity 100.0%; Pred. No. 1.2e-61;  
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SPVTPSPTLKELIEELVNTQNOASLNGSMWVSVNLTAGMYCAALESILNVSDCSAIQR 60  
|||||  
DB 1 spvtspstlkelieelvnltqngaslcngsmwsvnltagmycaalesilnvsdcsaigr 60

OY 61 TQRMKALCSQKPAAGISSERSRDTKIEVIQLVKNLITYRGVYRHGNFR 110  
|||||  
DB 61 tqrmkalcsgkpaagissersrdtkieivqlvknltlyrvgyrghgnfr 110

RESULT 2

ID Y58223 standard; Protein; 130 AA.

XX  
AC Y58223;

DT 14-MAR-2000 (first entry)

DE Canine interleukin-13 (IL-13) clone 78.

KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;  
immunoregulation; tumour; cancer; autoimmune disease; vaccine.

OS Canis familiaris.

PN WO9961618-A2.

PD 02-DEC-1999.

PF 28-MAY-1999; 99WO-US11942.

PR 29-MAY-1998; 98US-0087306.

PA (HESK-) HESKA CORP.

PI Slim G, Yang S, Dreitz MJ, Wonderling RS;

DR WPI; 2000-072623/06.

DR N-PSDB; 255561, 255562, 255563, 255564.

PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
useful for treating or preventing e.g. tumors or autoimmune disease

PS Claim 3i; Page 237; 264pp; English.

CC Sequences Y58221-Y58222 and Y58223-Y58224 represent encoded and mature

CC canine interleukin-13 (IL-13) clones 80 and 78. The invention relates to  
CC canine IL-4, canine or feline Flt-3 ligand, canine or feline CD40,  
CC canine or feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline  
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage  
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these  
CC immunoregulatory proteins. The proteins, their associated  
CC nucleic acids, specific antibodies and inhibitors may be used as  
CC vaccines for therapeutic or prophylactic regulation of an immune  
CC response in animals (particularly cats, dogs, horses and humans).  
CC They may be used to treat autoimmune or infectious diseases including  
CC allergies, tumours, inflammation and graft rejection, and to increase  
CC the response from a co-administered antigen. The nucleotide sequences  
CC can also be used for the recombinant production of a protein, while  
CC nucleotide fragments are useful as probes, as amplification primers and  
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
CC The proteins may be used to raise antibodies and to screen for  
CC modulators of activity, while the antibodies may be used in detection,  
CC and in drug targeting.

XX  
SQ Sequence 130 AA;

Query Match 100.0%; Score 556; DB 21; Length 130;  
Best Local Similarity 100.0%; Pred. No. 1.5e-61;  
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SPVTPSPTLKELIEELVNTQNOASLNGSMWVSVNLTAGMYCAALESILNVSDCSAIQR 60  
|||||  
DB 21 spvtspstlkelieelvnltqngaslcngsmwsvnltagmycaalesilnvsdcsaigr 80

OY 61 TQRMKALCSQKPAAGISSERSRDTKIEVIQLVKNLITYRGVYRHGNFR 110  
|||||  
DB 81 tqrmkalcsgkpaagissersrdtkieivqlvknltlyrvgyrghgnfr 130

RESULT 3

ID Y58222 standard; Protein; 111 AA.

XX  
AC Y58222;

DT 14-MAR-2000 (first entry)

DE Canine mature interleukin-13 (IL-13) clone 80.

KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;  
immunoregulation; tumour; cancer; autoimmune disease; vaccine.

OS Canis familiaris.

PN WO9961618-A2.

PD 02-DEC-1999.

PF 28-MAY-1999; 99WO-US11942.

PR 29-MAY-1998; 98US-0087306.

PA (HESK-) HESKA CORP.

PI Slim G, Yang S, Dreitz MJ, Wonderling RS;

DR WPI; 2000-072623/06.

DR N-PSDB; 255559, 255560.

PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
useful for treating or preventing e.g. tumors or autoimmune disease

PS Claim 3i; Page 234; 264pp; English.

CC Sequences Y58221-Y58222 and Y58223-Y58224 represent encoded and mature

CC canine interleukin-13 (IL-13) clones 80 and 78. The invention relates to  
canine IL-4, canine or feline Flt-3 ligand, canine or feline CD40,

CC canine or feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline  
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage  
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these  
CC immunoregulatory proteins. The proteins, their associated  
CC nucleic acids, specific antibodies and inhibitors may be used as  
CC vaccines for therapeutic or prophylactic regulation of an immune  
CC response in animals (particularly cats, dogs, horses and humans).  
CC They may be used to treat autoimmune or infectious diseases including  
CC allergies, tumours, inflammation and graft rejection, and to increase  
CC the response from a co-administered antigen. The nucleotide sequences  
CC can also be used for the recombinant production of a protein, while  
CC nucleotide fragments are useful as probes, as amplification primers and  
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
CC The proteins may be used to raise antibodies and to screen for  
CC modulators of activity, while the antibodies may be used in detection,  
CC and in drug targeting.  
XX  
SQ Sequence 111 AA;  
  
Query Match 98.1%; Score 545.5; DB 21; Length 111;  
Best Local Similarity 99.1%; Pred. No. 2.5e-60;  
Matches 110; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
  
QY 1 SPVTPSPTLKEIEELVNITQNQASLCNGSMVWSVNLTAGMYCAALESLINVSDCSAIQR 60  
|||||  
Db 1 spvtpsptlkeieelvnitqnqaslcngsmvsvnltagmycaaleslinvsdcsaigr 60  
  
QY 61 TQRLKALCSQKPAAG-ISSERSRDTKIEVIQLVKNLLTYVRGVYRHGNFR 110  
|||||  
Db 61 tqrlkalcsqkpaagqissersrdtkieviqlvknlltyvrgvyrhgnfr 111  
  
RESULT 4  
Y58221  
ID Y58221 standard; Protein; 131 AA.  
XX  
AC Y58221;  
XX  
DT 14-MAR-2000 (first entry)  
XX  
DE Canine interleukin-13 (IL-13) clone 80.  
XX  
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;  
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine.  
XX  
OS Canis familiaris.  
XX  
PN WO9961618-A2.  
XX  
PD 02-DEC-1999.  
XX  
PF 28-MAY-1999; 99WO-US11942.  
XX  
PR 29-MAY-1998; 98US-0087306.  
XX  
PA (HESK-) HESKA CORP.  
XX  
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;  
XX  
DR WPI; 2000-072623/06.  
DR N-PSDB; 255555, 255556, 255557, 255558.  
XX  
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
PT useful for treating or preventing e.g. tumors or autoimmune disease -  
XX  
PS Claim 3i; Page 231; 264pp; English.  
XX  
CC Sequences Y58221-Y58222 and Y58223-Y58224 represent encoded and mature  
CC canine interleukin-13 (IL-13) clones 80 and 78. The invention relates to  
CC canine IL-4, canine or feline Flt-3 ligand, canine or feline CD40,  
CC canine or feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline  
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage

CC colony-stimulating factor (GM-CSF), and nucleotides which encode these  
CC immunoregulatory proteins. The proteins, their associated  
CC nucleic acids, specific antibodies and inhibitors may be used as  
CC vaccines for therapeutic or prophylactic regulation of an immune  
CC response in animals (particularly cats, dogs, horses and humans).  
CC They may be used to treat autoimmune or infectious diseases including  
CC allergies, tumours, inflammation and graft rejection, and to increase  
CC the response from a co-administered antigen. The nucleotide sequences  
CC can also be used for the recombinant production of a protein, while  
CC nucleotide fragments are useful as probes, as amplification primers and  
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
CC The proteins may be used to raise antibodies and to screen for  
CC modulators of activity, while the antibodies may be used in detection,  
CC and in drug targeting.  
XX  
SQ Sequence 131 AA;  
  
Query Match 98.1%; Score 545.5; DB 21; Length 131;  
Best Local Similarity 99.1%; Pred. No. 3.2e-60;  
Matches 110; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
  
QY 1 SPVTPSPTLKEIEELVNITQNQASLCNGSMVWSVNLTAGMYCAALESLINVSDCSAIQR 60  
|||||  
Db 21 spvtpsptlkeieelvnitqnqaslcngsmvsvnltagmycaaleslinvsdcsaigr 80  
  
QY 61 TQRLKALCSQKPAAG-ISSERSRDTKIEVIQLVKNLLTYVRGVYRHGNFR 110  
|||||  
Db 81 tqrlkalcsqkpaagqissersrdtkieviqlvknlltyvrgvyrhgnfr 131  
  
RESULT 5  
R92794  
ID R92794 standard; Protein; 111 AA.  
XX  
AC R92794;  
XX  
DT 24-MAY-1996 (first entry)  
XX  
DE Human interleukin-13 mutein 2.  
XX  
KW Cytokine; mutein; interleukin-13; IL-13; agonist; antagonist;  
KW diagnosis; therapy; cancer; inflammation; degenerative disease.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 11 /note= "Glu at position 11 may be replaced by an  
FT amidated amino acid, including Lys"  
FT Misc-difference 64 /note= "Arg at position 64 may be replaced by an  
FT acidic amino acid, including Asp"  
XX  
PN WO9604306-A2.  
XX  
PD 15-FEB-1996.  
XX  
PF 31-JUL-1995; 95WO-US08950.  
XX  
PR 01-AUG-1994; 94US-0284393.  
XX  
PA (SCHE ) SCHERING CORP.  
XX  
PI Zurawski G, Zurawski SM;  
XX  
DR WPI; 1996-129335/13.  
XX  
PT Mutein(s) of human and murine cytokine(s), esp. interleukin(s) and  
PT murine P600 contg. amino acid substitutions. - useful for the  
PT diagnosis and treatment of cancer, inflammation, etc.  
XX  
PS Claim 12; Page 46; 52pp; English.





Best Local Similarity 69.1%; Pred. No. 4.8e-38;  
Matches 76; Conservative 11; Mismatches 21; Indels 2; Gaps 2;

Qy	2	PVTPSPTLKELIEELVNITQNQ-ASLCNGSMVWSVNLTAGMYCAALESINVSDCSAIQR	60
		:   :        :   :     :     :     :     :     :     :	
Db	2	PVPpStalrelieelvnitgnqkplcngsmvwsinltagmycaalesinvsqcsaiek	61

Qy	61	TQRLKALCSQPAAG-ISSERSDTKIEVIQLVKNLTFVRGVYRHGNF	109
		+ :                :     :   :	
Db	62	tqrlmsgfcphkvsagqfsslhvrdtkievagfvkdllhlklkfregrf	111

RESULT	8
R48624	
ID	R48624 standard; Protein; 132 AA.
XX	
AC	R48624;
XX	
DT	14-SEP-1994 (first entry)
XX	
DE	Sequence of human interleukin-13 (IL-13).
XX	
KW	Interleukin-13; lymphokine; immunological disorder; therapy; diagnostic.

CC An approx. 400 bp DNA fragment derived from a pst/PvuII restriction  
CC digest of the mouse P600 cDNA clone was isolated. This fragment,  
CC which encompasses most of the coding region of the mouse P600 cDNA,  
CC was radioactively labelled and hybridised with filter lifts prepd.  
CC from a cDNA library made from a clone of an A10 T cell line. One  
CC clone, designated PA 10.56, was subcloned into M13 and sequenced.  
CC This sequence encodes human IL-13.

Query Match	66.0%;	Score 367;	DB 15;	Length 132;
Best Local Similarity	69.1%;	Pred. No. 6e-38;		
Matches 76;	Conservative 11;	Mismatches 21;	Indels 2;	Gaps 2;

[illegible]

QY	61	TQRLKALCSQKPAAG-ISSERSRDTKIEVIQLVKNLITYVRGVYRHGNF	109
		:                      :: :	
Db	82	tqrlmsgfcphkvsagfsslhvrdtkievagfvkdllhlkklfregfrf	131

RESULT 9  
R27346  
ID R27346 standard; Protein; 112 AA.

PI Caput D, Ferrara P, Guillemot J, Kaghad M, Labit-le Bouteiller C;  
PI Leplatols P, Magazin M, Minty A;  
XX  
DR WPI; 1992-325841/40.  
DR N-PSDB; Q28943.

PT New cytokine having immunomodulatory activity - useful for  
PT treating tumours and infectious or inflammatory conditions  
XX  
PS Claim 1; Page 60; 78pp; French.

This protein is one of two possible forms of a new cytokine produced by T lymphocytes induced by phorbol-12-myristate-13-acetate and phytohaemagglutinin. The proteins differ only in the amino acid at position 41 which is either Asp or Gly. The cytokine acts on monocytes and B lymphocytes and is useful in treatment of tumours and some infections and inflammatory conditions.  
See Q28941-028947.

Query Match	64.7%;	Score 360;	DB 13;	Length 112;
Best Local Similarity	68.2%;	Pred. No. 3.6e-37;		
Matches 75;	Conservative 11;	Mismatches 22;	Indels 2;	Gaps 2;

QY	2	PVTPSPTLKELIEELVNITQNO-ASLCSNGSMVWSVNLTAGMYCAALESlinvSDCSAIQR	60
		:                      :                      :	
Db	2	pvpptalrelieelvnitgnqkplcngsmvwsintadmycaaleslinvsgcsaiek	61
QY	61	TQRLKALCSQKPAAG-ISSERSRDTKIEIVQLVKNLLTYVRGVYRHGNF	109
		-                       :    :	
Db	62	tqrlmsgfcphkvsagqfsslhvrdtkievagfvkdlllhkkklfreqrf	111

RESULT 10  
R27348  
ID R27348 standard; Protein; 146 AA.

XX	
XX	Interleukin; chemotaxis; immunomodulation; inflammation.
KW	
XX	
FH	Key Location/Qualifiers

FT	Cleavage_site	20..21	"putative signal peptide cleavage site"
FT	/note=	24..25	"putative signal peptide cleavage site"
FT	cleavage_site	/note=	32..33 "putative signal peptide cleavage site"
FT	cleavage_site	/note=	34..35 "putative signal peptide cleavage site"
FT	protein	35..146	/label= NC30
XX	EP506574-A.		
PD	30-SEP-1992.		
XX			
PF	27-MAR-1992;	92EP-0400858.	
XX			
PR	29-MAR-1991;	91FR-0003904.	
PR	08-JAN-1992;	92FR-0000137.	
XX			
PA	(SNFI ) ELF SANOFI.		
XX			
PI	Caput D, Ferrara P, Guillemot J, Kaghad M, Labit-Je Bouteiller C;		
PI	Lepatois P, Magazin M, Minty A;		
DR	WPI; 1992-325841/40.		
XX	N-PSDB; Q28947.		
PT	New cytokine having immunomodulatory activity - useful for		
PT	treating tumours and infectious or inflammatory conditions		
XX			
PS	Claim 1; Page 52-53; 78pp; French.		
XX			
CC	A novel cytokine produced by T lymphocytes induced by phorbol-2-		
CC	myristate-3-acetate and phytohaemagglutinin was coded for by the		
CC	sequence in clone PSE1-NC30. A second clone was also identified		
CC	(PSE1-NC30bis) which differed only in the identity of codon 41.		
CC	The corresponding proteins differ in the amino acid at position 41		
CC	which is either Asp (in NC30) or Gly (in NC30bis). The cytokine		
CC	acts on monocytes and B lymphocytes and is useful in treatment of		
CC	tumours and some infections and inflammatory conditions.		
CC	See Q28941-Q28947.		
XX			
SQ	Sequence 146 AA;		
Query Match                      64.7%; Score 360; DB 13; Length 146;			
Best Local Similarity    68.2%; Pred. No. 5,1e-37;			
Matches    75; Conservative    11; Mismatches    22; Indels    2; Gaps    2;			
OY	2 PYTPSPTLKELELVNITONQ-ASLCNGSMWWSVNLTFAGMYCALESILNVSDCSAIGR 60		
Db	36 pypststalreelleelvnltgnqkplcngsmwmslnltadmycaaleslinvsgcsalek 95		
OY	61 TORMIKALCSOKPAAG-ISSERSRDTKIEVTQLVKNLTTYVRGYVRHGNE 109		
Db	96 tqrmisgfcphkvssagqfsslhvrdtkievagfvkdlllhkkrlfregrf 145		
RESULT 11			
ID	R48625		
AC	R48625 standard; Protein; 131 AA.		
DT	14-SEP-1994 (first entry)		
DE	Sequence of mouse P600.		
KW	Interleukin-13; lymphokine; P600; immunological disorder; therapy;		
OS	Mus musculus.		

[illegible]

```
PF 31-JUL-1995; 95WO-US08950.
XX
PR 01-AUG-1994; 94US-0284393.
XX
PA (SCHE ) SCHERING CORP.
XX
PI Zurawski G, Zurawski SM;
XX
DR WPI; 1996-129335/13.
XX
PT Mutein(s) of human and murine cytokine(s), esp. interleukin(s) and
PT murine P600 contg. amino acid substitutions. - useful for the
PT diagnosis and treatment of cancer, inflammation, etc.
XX
PS Claim 12; Page 46; 52pp; English.
XX
CC Muteins of mouse P600 (R92795) contain amino acid substitutions at
CC amino acid position 67 in helix C. They are obtd. by site-directed
CC mutagenesis of natural P600 sequences. The muteins antagonise the
CC activity of IL-13 or IL-4. They have partial cytokine agonist
CC activity, exhibit less than 80% maximal agonist activity of natural
CC IL-2, and/or antagonize cytokine activity by least about 50% when
CC present at a 100-fold excess. They and other cytokine muteins
CC (see also R92790-94, R92796-802) are useful in the screening of
CC cytokine and cytokine receptor levels, and in the diagnosis or
CC treatment of e.g. inflammation, cancer, and degenerative disorders.
XX
SQ Sequence 111 AA;

Query Match 53.8%; Score 299; DB 17; Length 111;
Best Local Similarity 57.8%; Pred. NO. 1.4e-29;
Matches 59; Conservative 17; Mismatches 24; Indels 2; Gaps 1;

QY 8 TLKELIEELVNITQNASLCSNGSMVSVNLTAGMYCAALESLINVSDCSAIQRTQRLKA 67
Db 12 tlkelieelsnitqdetplcngsmvsvdlaaggfcvaldslnisncnaiyrtqrlhg 71

QY 68 LCSQKPAAGISSERSRDTKIEVIQLVKNLLTYVRGVYRHGNF 109
Db 72 lcnrkaptvss--lpdtkievahfitkllsytkqlfrhgp 111

RESULT 13
Y21548
ID Y21548 standard; Protein; 634 AA.
XX
AC Y21548;
XX
DT 03-AUG-1999 (first entry)
XX
DE Human heparin-binding protein (HBP).
XX
KW Heparin-binding protein; HBP; apoptosis; Islets of Langerhans; beta cell;
KW endothelial cell; nerve cell; azurophil granule; chemoattractant; cancer;
KW polymorphonuclear leukocyte; monocyte; neurodegenerative disorder; human;
KW neuromuscular disorder; human immunodeficiency virus; ischemic stroke;
KW proteoglycan; mitochondrial matrix targeting protein; viral infection;
KW apoptosis inhibitor; immune-mediated glomerulonephritis.
XX
OS Homo sapiens.
XX
PN WO926647-A1.
XX
PD 03-JUN-1999.
XX
PF 20-NOV-1998; 98WO-DK00510.
XX
PR 03-DEC-1997; 97DK-0001394.
PR 20-NOV-1997; 97DK-0001324.
XX
PA (NOVO ) NOVO-NORDISK AS.
XX
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PI Flodgaard HJ;
XX
DR WPI; 1999-347615/29.
DR N-PSDB; X60692.
XX
PT Modulating or decreasing apoptosis in cells useful for treating
PT neurodegenerative disorders and neuromuscular disorders
XX
PS Claim 4; Page 10; 74pp; English.
XX
CC The invention relates to a new method of modulating or decreasing
CC apoptosis in mammalian beta cells of Islets of Langerhans, endothelial
CC cells or nerve cells. The method comprises administering a mammalian
CC heparin-binding protein (HBP) which in a glycosylated form has: (i) a
CC molecular weight of 28 kDa; (ii) is produced in the azurophil granules
CC of polymorphonuclear leukocytes; and (iii) is a chemoattractant for
CC monocytes. The new protein is useful for preventing or treating a
CC disorder (preferably in human patients) resulting from apoptosis of
CC mammalian cells, including insufficient functioning of insulin production
CC or insulin action, a neurodegenerative disorder, a neuromuscular
CC disorder, human immunodeficiency virus and ischemic stroke. Compositions
CC (a) comprising HBP and a proteoglycan which binds the HBP; and (b)
CC comprising the HBP and a protein which is a mammalian mitochondrial
CC matrix targeting protein and which binds to the HBP are useful for
CC modulating or decreasing apoptosis in mammalian beta cells of Islets of
CC Langerhans, endothelial cells or nerve cells. Unlike prior inhibitors,
CC the new apoptosis inhibitor does not cause disorders associated with the
CC inhibition of apoptosis such as cancer, autoimmune disorders such as
CC systemic lupus erythematosus, immune-mediated glomerulonephritis, and
CC viral infections. The present sequence represents a mature human HBP.
XX
SQ Sequence 634 AA;

Query Match 13.5%; Score 75; DB 20; Length 634;
Best Local Similarity 27.2%; Pred. No. 1.4;
Matches 25; Conservative 16; Mismatches 23; Indels 28; Gaps 4;

QY 40 GMYCAALESLINVSDCSA-----IQTRMLKALCSQK---PAAGISSER----- 81
Db 79 glyalaleilehisalaargphevalmetthralaalaserccyspheglnsrglnasn 138

QY 82 -----SRDTKIEVIQLVKNLLTYVRGVYR 105
Db 139 rglyvaiserthrvalvallegl--yalatyr 168

RESULT 14
R11510
ID R11510 standard; Protein; 5072 AA.
XX
AC R11510;
XX
DT 17-JUN-1991 (first entry)
XX
DE Ryanodine receptor deduced from cDNA clone.
XX
KW Malignant hyperthermia; hypermetabolic syndrome; inhalation;
KW anaesthetics; probe; calcium release channel; sarcoplasmic;
KW reticulum.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1629..1632
FT Peptide 1742..1748
FT Peptide 3119..3130
FT Peptide 3196..3210
FT Active-site 3981..3985
FT /label= phosphorylation site
FT 4315..4318
FT /label= phosphorylation site
XX
```













OY 61 TQRLKALCSQKPAAGISSERSRDTKIEVIQLVKNLTYVRGVYRHGNE 109  
||||| | :||| | ||||| | :||| : : :|||  
Db 62 TQRLSGFCPHKVSAGFSSLHVDTKIEVAQFVKDLLHLKLFREGRE 110

## RESULT 2

PCT-US95-08950-5

Sequence 5, Application PC/TUS9508950

GENERAL INFORMATION:

APPLICANT: Zurawski, Sandra M.

APPLICANT: Zurawski, Gerard

TITLE OF INVENTION: MUTAINS OF MAMMALIAN CYTOKINES

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: DNAX Research Institute

STREET: 901 California Avenue

CITY: Palo Alto

STATE: California

COUNTRY: USA

ZIP: 94304-1104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/08950

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/284,393

FILING DATE: 01-AUG-1994

ATTORNEY/AGENT INFORMATION:

NAME: Ching, Edwin P.

REGISTRATION NUMBER: 34,090

REFERENCE/DOCKET NUMBER: DX0389

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-852-9196

TELEFAX: 415-496-1200

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 111 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

PCT-US95-08950-5

Query Match 67.9%; Score 377.5; DB 5; Length 111;

Best Local Similarity 69.7%; Pred. No. 2.9e-41;

Matches 76; Conservative 11; Mismatches 21; Indels 1; Gaps 1;

OY 2 PVTSPPTLKELELVNITQNO-ASLCNGSMVSVNLTAGMYCALESINVSDCSAIOR 60  
||| | :||||| | ||||| | :||||| : : :|||  
Db 2 PVPSTALRELIELVNITQNO-KAPLCNGSMVSVNLTAGMYCALESINVS-GCSAIEK 61

OY 61 TQRLKALCSQKPAAGISSERSRDTKIEVIQLVKNLTYVRGVYRHGNE 109  
||||| | :||| | ||||| | :||| : : :|||  
Db 62 TQRLSGFCPHKVSAGFSSLHVDTKIEVAQFVKDLLHLKLFREGRE 110

## RESULT 3

US-08-284-393B-4

Sequence 4, Application US/08284393B

Patent No. 5696234

GENERAL INFORMATION:

APPLICANT: Zurawski, Sandra M.

APPLICANT: Zurawski, Gerard

TITLE OF INVENTION: MUTAINS OF MAMMALIAN CYTOKINES

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: DNAX Research Institute

STREET: 901 California Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/284,393B

FILING DATE: 01-AUG-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Ching, Edwin P.

REGISTRATION NUMBER: 34,090

REFERENCE/DOCKET NUMBER: DX0389

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-852-9196

TELEFAX: 415-496-1200

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 112 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-284-393B-4

Query Match 66.0%; Score 367; DB 1; Length 112;

Best Local Similarity 69.1%; Pred. No. 6.5e-40;

Matches 76; Conservative 11; Mismatches 21; Indels 2; Gaps 2;

OY 2 PVTSPPTLKELELVNITQNO-ASLCNGSMVSVNLTAGMYCALESINVSDCSAIOR 60  
||| | :||||| | ||||| | :||||| : : :|||  
Db 2 PVPSTALRELIELVNITQNO-KAPLCNGSMVSVNLTAGMYCALESINVS-GCSAIEK 61

OY 61 TQRLKALCSQKPAAG-ISSERSRDTKIEVIQLVKNLTYVRGVYRHGNE 109  
||||| | :||| | ||||| | :||| : : :|||  
Db 62 TQRLSGFCPHKVSAGFSSLHVDTKIEVAQFVKDLLHLKLFREGRE 111

## RESULT 4

PCT-US95-08950-4

Sequence 4, Application PC/TUS9508950

GENERAL INFORMATION:

APPLICANT: Zurawski, Sandra M.

APPLICANT: Zurawski, Gerard

TITLE OF INVENTION: MUTAINS OF MAMMALIAN CYTOKINES

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: DNAX Research Institute

STREET: 901 California Avenue

CITY: Palo Alto

STATE: California

COUNTRY: USA

ZIP: 94304-1104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/08950

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/284,393

FILING DATE: 01-AUG-1994

ATTORNEY/AGENT INFORMATION:

NAME: Ching, Edwin P.

; NAME: Ching, Edwin P.  
 ; REGISTRATION NUMBER: 34,090  
 ; REFERENCE/DOCKET NUMBER: DX0302K1  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 415-852-9196  
 ; TELEFAX: 415-496-1200  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:

RESULT 7  
PCT-US93-07645-2  
; Sequence 2, Application PC/TUS9307645  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: Human Interleukin-13  
; NUMBER OF SEQUENCES: 6







QY 2 PVTSPFLKELIELVNITONQ-ASLNGSMWWSVNLTAGMYCALESILINVSDCSAIOR 60  
DB 2 PVPSTALRKELIELVNITONQAPLNGSMWWSVNLTAGMYCALESILINVS GCSAIEK 61  
QY 61 TQRMKALCSQKPAAG-ISSERSRDTKIEVIOQLVKNLITYRGVYRHGNE 109  
DB 62 TQDMLSGFCPHKVSAGQSSLHVVDTKIEVAQFVKDLHLKKLFREGRE 111

RESULT 12  
US-08-012-543-4  
; Sequence 4, Application US/08012543  
; Patent No. 5596072  
; GENERAL INFORMATION:  
; APPLICANT: Culpepper, Janice  
; APPLICANT: McKenzie, Andrew  
; APPLICANT: Dang, Warren  
; APPLICANT: de Waal Malefyt, Rene  
; APPLICANT: Heath, Andrew  
; APPLICANT: Aversa, Gregorio  
; APPLICANT: Briere, Francine  
; APPLICANT: Bancheureau, Jacques  
; APPLICANT: de Vries, Jan  
; APPLICANT: Zurawski, Gerard  
; TITLE OF INVENTION: Human Interleukin-13  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DMAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentln Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/012,543  
; FILING DATE: 01-FEB-1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/933,416  
; FILING DATE: 21-AUG-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0302K1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-852-9196  
; TELEFAX: 415-496-1200  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 131 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-012-543-4

Query Match 54.3%; Score 302; DB 1; Length 131;  
Best Local Similarity 58.8%; Pred. No. 2e-31;  
Matches 60; Conservative 16; Mismatches 24; Indels 2; Gaps 1;

QY 8 TLKELIELVNITONQASLNGSMWWSVNLTAGMYCALESILINVSDCSAIORMLKA 67  
DB 32 TLKELIELSNITQDQPLCNGSMWWSVDLAAGFCVALDSLITNISNCNAIYRTQRIHIG 91  
QY 68 LCSQKPAAGISSERSRDTKIEVIOQLVKNLITYRGVYRHGNE 109  
DB 92 LCNRAKPTTVSS-LPDTKIEVAHFITKLLSYTKQLFRHGPF 131

RESULT 13  
US-08-371-121-25  
; Sequence 25, Application US/08371121  
; Patent No. 5652123  
; GENERAL INFORMATION:  
; APPLICANT: CAPUT, Daniel  
; APPLICANT: FERRARA, Pascual  
; APPLICANT: GUILLEMOT, Jean-Claude  
; APPLICANT: LEPLATOIS, Pascal  
; APPLICANT: MINY, Adrian  
; APPLICANT: KAGHAD, Mourad  
; APPLICANT: LABIT-LE BOUTEILLER, Christine  
; APPLICANT: MAGAZIN, Marilyn  
; TITLE OF INVENTION: Protein having a cytokine type  
; TITLE OF INVENTION: activity, recombinant DNA coding for this protein,  
; TITLE OF INVENTION: transformed cells and microorganisms.  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FOLEY & LARDNER  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington, D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentln Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/371,121  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/938,161  
; FILING DATE: 30-NOV-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/FR92/00280  
; FILING DATE: 27-MAR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 91 00137  
; FILING DATE: 08-JAN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 91 03904  
; FILING DATE: 29-MAR-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SAXE, Bernhard D.  
; REGISTRATION NUMBER: 28,665  
; REFERENCE/DOCKET NUMBER: 16781/383  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 672-5300  
; TELEFAX: (202) 672-5399  
; TELEX: 904136  
; INFORMATION FOR SEQ ID NO: 25:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 131 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-371-121-25

Query Match 54.3%; Score 302; DB 1; Length 131;  
Best Local Similarity 58.8%; Pred. No. 2e-31;  
Matches 60; Conservative 16; Mismatches 24; Indels 2; Gaps 1;

QY 8 TLKELIELVNITONQASLNGSMWWSVNLTAGMYCALESILINVSDCSAIORMLKA 67  
DB 32 TLKELIELSNITQDQPLCNGSMWWSVDLAAGFCVALDSLITNISNCNAIYRTQRIHIG 91  
QY 68 LCSQKPAAGISSERSRDTKIEVIOQLVKNLITYRGVYRHGNE 109  
DB 92 LCNRAKPTTVSS-LPDTKIEVAHFITKLLSYTKQLFRHGPF 131

FILING DATE: 21-AUG-1992



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: May 13, 2001, 21:48:44 ; Search time 64.5 Seconds  
(without alignments)  
117.202 Million cell updates/sec

Title: US-09-451-527-105  
Perfect score: 556  
Sequence: 1 SPVTPSPTLKELIEELVNIT.....QLVKNLLTYVRGVYRHGNFR 110  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 198801 segs, 68722935 residues  
Total number of hits satisfying chosen parameters: 198801  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries  
Database : PIR\_67:\*

- 1: pir1:\*
- 2: pir2:\*
- 3: pir3:\*
- 4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	367	66.0	146	1 A47481	interleukin-13 pre
2	302	54.3	131	2 E30552	T-cell activation
3	294.5	53.0	131	2 I52290	interleukin-13 - r
4	72	12.9	5032	1 A35041	ryanodine receptor
5	71.5	12.9	261	2 JQ1176	sepiapterin reduct
6	71.5	12.9	481	2 S62423	ATP-dependent RNA
7	71	12.8	262	2 A36024	sepiapterin reduct
8	70.5	12.7	1811	2 T00035	nonstructural poly
9	70	12.6	725	1 Z2BPA4	rapid lysis protei
10	69.5	12.5	431	2 S47538	acrosin (EC 3.4.21
11	69	12.4	261	2 S52110	sepiapterin reduct
12	69	12.4	5035	1 I46646	ryanodine receptor
13	69	12.4	5037	2 B35041	ryanodine receptor
14	68	12.2	805	2 S50277	ubiquitin-specific
15	68	12.2	936	2 S43738	transcription acti
16	67.5	12.1	1164	2 S46769	hypothetical prote
17	67.5	12.1	2626	2 T31099	myosin-RhoGAP prot
18	67	12.1	1221	2 A44978	DNA topoisomerase
19	66.5	12.0	323	1 GHRB	Ig gamma chain C r
20	66	11.9	398	2 T27254	hypothetical prote
21	65.5	11.8	516	2 H72427	DNA mismatch repai
22	65	11.7	336	2 H82920	conserved hypothet
23	65	11.7	475	2 T20165	hypothetical prote
24	65	11.7	655	2 T51792	hypothetical prote
25	65	11.7	1274	2 T19508	hypothetical prote
26	65	11.7	1477	2 A29952	alpha-1 proteinase
27	64.5	11.6	139	2 C64028	hypothetical prote
28	64.5	11.6	168	2 T41891	phosphotyrosine ph
29	64.5	11.6	211	1 HSPGLT	histone Hit - pig

ALIGNMENTS

RESULT 1  
A47481  
Interleukin-13 precursor - human  
N:Contains: interleukin 13, short form  
C:Species: Homo sapiens (man)  
C:Date: 21-Jan-1994 #sequence\_revision 06-Dec-1996 #text\_change 22-Jun-1999  
C:Accession: I38060; I38061; A47481  
R:Minty, A.J.; Chalon, P.; Derocq, J.M.; Dumont, X.; Guillemot, J.C.; Kaghad, M.; Lab  
a, P.; Caput, D.  
Nature 362, 248-250, 1993  
A:Title: Interleukin-13 is a new human lymphokine regulating inflammatory and immune  
A:Reference number: I38060; MUID:93211479  
A:Accession: I38060  
A:Status: translated from GB/EMBL/DDBJ  
A:Molecule type: mRNA  
A:Residues: 1-146 <RES>  
A:Cross-references: EMBL:X69079; NID:g297787; PIDN:CAA48823.1; PID:g580330  
A:Accession: I38061  
A:Status: translated from GB/EMBL/DDBJ  
A:Molecule type: mRNA  
A:Residues: 15-146 <RE2>  
A:Cross-references: EMBL:X69079; NID:g297787; PIDN:CAA48824.1; PID:g673420  
R:McKenzie, A.N.; Culpepper, J.A.; de Waal Malefyt, R.; Briere, F.; Punnonen, J.; Ave  
Proc. Natl. Acad. Sci. U.S.A. 90, 3735-3739, 1993  
A:Title: Interleukin 13, a T-cell-derived cytokine that regulates human monocyte and  
A:Reference number: A47481; MUID:93234572  
A:Accession: A47481  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 15-146 <MCK>  
A:Cross-references: GB:I06801; NID:g186275; PIDN:AAA36107.1; PID:g186276  
A:Experimental source: Con A-activated CD8+ T-cell clone, A10  
A:Note: sequence extracted from NCBI backbone (NCBIP:129773)  
C:Genetics:  
A:Gene: GDB:IL13; P600; NC30  
A:Cross-references: GDB:I38171; OMIM:147683  
A:Map position: 5q31-5q31  
C:Superfamily: interleukin-13  
C:Keywords: alternative initiators; cytokine; glycoprotein  
F:I-146/Product: interleukin-13 precursor, long splice form #status predicted <PRL>  
F:I-24/Domain: signal sequence #status predicted <SIG>  
F:I5-146/Product: interleukin-13 precursor, short splice form #status predicted <PRS>  
F:25-146/Product: interleukin-13 #status predicted <MAT>  
F:52,63,71,86/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 66.0%; Score 367; DB 1; Length 146;  
Best Local Similarity 69.1%; Pred. No. 1.3e-31;  
Matches 76; Conservative 11; Mismatches 21; Indels 2; Gaps 2;  
QY 2 PVTPSPTLKELIEELVNITQNQ-ASLCNGSMVWSVNLTAGMYCAALESLINVSDCSAIQR 60  
|| || |:||||||||||||| | |||||||:||||||||||||| |||:::











Db 99 INNAATLGDVSKGFLNVN-----DLAEVNNYWALNLTS-MCLTSGTLNADFQDSPGLSKTV 153

QY 63 RMLKALCSQKPAAG-----ISSERSDRTKIEVIQLVK---NLLTYVRG 102

Db 154 VNISSLCALQPKYKGWGLYCAGKAARDMLYQVLAAEPSVRVLSYAPG 200

RESULT 12

I46646

ryanodine receptor, skeletal muscle - pig

N;Alternate names: calcium release channel protein

C;Species: Sus scrofa domestica (domestic pig)

C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999

C;Accession: I46646; I46645; S31395; I47133; S26624; A37105; I47212; S18135

R;Fujii, J.; Otsu, K.; Zorzato, F.; De Leon, S.; Khanna, V.K.; Weiler, J.E.; O'Brien, P.

Science 253, 448-451, 1991

A;Title: Identification of a mutation in porcine ryanodine receptor associated with malignant hyperthermia

A;Reference number: I46645; MUID:91320118

A;Accession: I46646

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-5035 <FUJ>

A;Cross-references: GB:M91452; NID:g164647; PIDN:AAA31119.1; PID:g164648

A;Accession: I46645

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-614,'C',616-5035 <FU2>

A;Cross-references: GB:M91451; NID:g164645; PIDN:AAA31118.1; PID:g164646

R;Leeb, T.; Brem, G.; Brenig, B.

submitted to the EMBL Data Library, November 1992

A;Description: Genomic Organization of porcine skeletal muscle ryanodine receptor gene

A;Reference number: S31395

A;Accession: S31395

A;Molecule type: DNA

A;Residues: 1542-2643 <LEE>

A;Cross-references: EMBL:X69465

R;Leeb, T.; Schmoelzl, S.; Brem, G.; Brenig, B.

Genomics 18, 349-354, 1993

A;Title: Genomic organization of the porcine skeletal muscle ryanodine receptor (RYR1) gene

A;Reference number: A48915; MUID:94117003

A;Contents: annotation

R;Harbitz, I.; Kristensen, T.; Bosnes, M.; Kran, S.; Davies, W.

Anim. Genet. 23, 395-402, 1992

A;Title: DNA sequence of the skeletal muscle calcium release channel cDNA and verification

A;Reference number: I47133; MUID:93036581

A;Accession: I47133

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 2-2091,'A',2093-3494,'L',3496-4163,'S',4165-4182,'R',4184-4411,'W',4413-4971

A;Cross-references: EMBL:X62880; NID:g1936; PIDN:CAA44674.1; PID:g1937

R;Harbitz, I.; Kristensen, T.; Kran, T.; Davies, W.

submitted to the EMBL Data Library, August 1992

A;Reference number: S26624

A;Accession: S26624

A;Molecule type: DNA

A;Residues: 482-706 <HAW>

A;Cross-references: EMBL:X68247

R;Harbitz, I.; Chowdhary, B.; Thomsen, P.D.; Davies, W.; Kaufmann, U.; Kran, S.; Gustavsson

Genomics 8, 243-248, 1990

A;Title: Assignment of the porcine calcium release channel gene, a candidate for the malignant hyperthermia

A;Reference number: A37105; MUID:91065640

A;Accession: A37105

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 4785-4971,'R',4973-5035 <HA2>

A;Cross-references: GB:M32501; NID:g164428; PIDN:AAA31022.1; PID:g164429

R;Ledbetter, M.W.; Preiner, J.K.; Louis, C.F.; Mickelson, J.R.

J. Biol. Chem. 269, 31544-31551, 1994

A;Title: Tissue distribution of ryanodine receptor isoforms and alleles determined by reverse transcription-polymerase chain reaction

A;Reference number: A55660; MUID:95081095

A;Accession: I47212

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 516-676 <LED>

A;Cross-references: EMBL:U15965; NID:g562095; PIDN:AAA60467.1; PID:g562096

C;Genetics:

A;Gene: RYR1

A;Introns: 527/1; 559/1; 598/3; 643/2; 1570/3; 1646/2; 1850/3; 1939/3; 2006/3; 2044/1

A;Note: the list of introns may be incomplete

C;Superfamily: ryanodine receptor; transcription initiation factor sigma region 1 homolog

C;Keywords: calcium channel

Query Match 12.4%; Score 69; DB 1; Length 5035;

Best Local Similarity 20.3%; Pred. No. 2.4e+02;

Matches 25; Conservative 26; Mismatches 44; Indels 28; Gaps 4;

QY 9 LKELIEELVNITQNQASLCNGSMVSVN-----LTAGMYCAALES--LINVSDCS 56

Db 522 LYEILASLIRGNRANCALFSNNLDWLVSKLDRLEASSGILEVLYCVLIESPEVLNIIQEN 581

QY 57 AIQ-----RTQRLKALCSQKPAAGISSERSRDTKIE-----VIQLVKNLLTYV 100

Db 582 HIKSIISLLDKHGRNHKVLVDLCSLCVCNGVAVRSNQDLITENLLPGRELLQTNLINYV 641

QY 101 RGV 103

Db 642 TSI 644

RESULT 13

B35041

ryanodine receptor, skeletal muscle - rabbit

N;Alternate names: calcium-release channel protein; junctional channel complex

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 27-Jul-1990 #sequence\_revision 10-Mar-1994 #text\_change 20-Aug-1999

C;Accession: S04654; B35041; A36181; S53794; S32504

R;Takeshima, H.; Nishimura, S.; Matsumoto, T.; Ishida, H.; Kangawa, K.; Minamino, N.; Nature 339, 439-445, 1989

A;Title: Primary structure and expression from complementary DNA of skeletal muscle ryanodine receptor

A;Reference number: S04654; MUID:89262082

A;Accession: S04654

A;Molecule type: mRNA

A;Residues: 1-5037 <TAK>

A;Cross-references: EMBL:X15750; NID:g1709; PIDN:CAA33762.1; PID:g1710

A;Note: part of this sequence was confirmed by protein sequencing

R;Zorzato, F.; Fujii, J.; Otsu, K.; Phillips, M.; Green, N.M.; Lai, F.A.; Meissner, G.

J. Biol. Chem. 265, 2244-2256, 1990

A;Title: Molecular cloning of cDNA encoding human and rabbit forms of the Ca(2+) released channel

A;Reference number: A35041; MUID:90130482

A;Accession: B35041

A;Status: not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-66,'Y',68-2014,'D',2016-3246,'E',3248-3480,3486-4497,'LE',4498-4521,'Q',4748-4758,'N',4760-5037 <ZOR>

R;Marks, A.R.; Tempst, P.; Hwang, K.S.; Taubman, M.B.; Inui, M.; Chadwick, C.; Fleischer

Proc. Natl. Acad. Sci. U.S.A. 86, 8683-8687, 1989

A;Title: Molecular cloning and characterization of the ryanodine receptor/junctional ryanodine receptor

A;Reference number: A36181; MUID:90046857

A;Accession: A36181

A;Status: nucleic acid sequence not shown; not compared with conceptual translation

A;Molecule type: mRNA; protein

A;Residues: 'X',1223-1235,'XX',1238-1251;1334-1348;1566-1569,'X',1571,'X',1573;1597-1-4679,'X',4681-4689,'X',4691-4693,'X',4695,'X',4697-4700 <MAR>

A;Note: the proteolytic fragments sequenced here from the junctional channel complex

R;Varsanyi, M.; Meyer, H.E.

Biol. Chem. Hoppe-Seyler 376, 45-49, 1995

A;Title: Sarcoplasmic reticular Ca(2+) release channel is phosphorylated at serine 28

A;Reference number: S53794; MUID:95336639

A;Accession: S53794

A;Molecule type: protein

A;Residues: 2841-2852 <VAR>

R;Takeshima, H.; Nishimura, S.; Nishi, M.; Ikeda, M.; Sugimoto, T.

FEBS Lett. 322, 105-110, 1993

A;Title: A brain-specific transcript from the 3'-terminal region of the skeletal muscle







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OM protein - protein search, using sw model

Run on: May 14, 2001, 06:02:08 ; Search time 44.64 Seconds  
(without alignments)  
84.411 Million cell updates/sec

Title: US-09-451-527-105  
Perfect score: 556  
Sequence: 1 SPVTPSPPTLKELIEELVNIT.....QLVKNLLTYVRGVYRHGNER 110

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	367	66.0	132	1 IL13_HUMAN	P35225 homo sapien
2	345	62.1	132	1 IL13_BOVIN	Q9XSV9 bos taurus
3	302	54.3	131	1 IL13_MOUSE	P20109 mus musculus
4	294.5	53.0	131	1 IL13_RAT	P42203 rattus norv
5	72	12.9	5032	1 RYNR_HUMAN	P21817 homo sapien
6	71.5	12.9	261	1 SPRE_HUMAN	P35270 homo sapien
7	71.5	12.9	481	1 YA88_SCHPO	Q09775 schizosacch
8	71	12.8	262	1 SPRE_RAT	P18297 rattus norv
9	70	12.6	725	1 VR2A_BPT4	P03690 bacterioph
10	69.5	12.5	192	1 FLHC_SALTY	O52222 salmonella
11	69.5	12.5	431	1 ACRO_RABIT	P48038 oryctolagus
12	69	12.4	261	1 SPRE_MOUSE	Q64105 mus musculus
13	69	12.4	5035	1 RYNR_PIG	P16960 sus scrofa
14	69	12.4	5037	1 RYNR_RABIT	P11716 oryctolagus
15	68	12.2	805	1 UBP5_YEAST	P39944 saccharomyc
16	68	12.2	936	1 FHL1_YEAST	P39521 saccharomyc
17	67.5	12.1	1164	1 KEL1_YEAST	P38853 saccharomyc
18	67	12.1	1221	1 TOP2_TRYBB	P12531 trypanosoma
19	66.5	12.0	323	1 GC_RABIT	P01870 oryctolagus
20	65.5	11.8	510	1 MUTL1_THEMA	P74925 thermotoga
21	65.5	11.8	638	1 DNAK_RHILE	O33528 rhizobium i
22	65	11.7	1477	1 A113_RAT	P14046 rattus norv
23	64.5	11.6	211	1 H1T_PIG	P06348 sus scrofa
24	64.5	11.6	701	1 UBF2_XENLA	P25980 xenopus lae
25	64	11.5	382	1 ADH2_ZYMMO	P06758 zymomonas m
26	64	11.5	503	1 ZNT1_MOUSE	Q60738 mus musculus
27	63.5	11.4	168	1 PTP_NPVAC	P24656 autographa
28	63.5	11.4	1004	1 YG21_YEAST	P53067 saccharomyc
29	63.5	11.4	1234	1 MFD_MYCTU	P96380 mycobacteri
30	63	11.3	507	1 ZNT1_RAT	Q62720 rattus norv
31	63	11.3	758	1 SC18_YEAST	P18759 saccharomyc
32	62.5	11.2	491	1 G6PD_RHIME	Q923s2 rhizobium m
33	62.5	11.2	952	1 YK15_CAEEL	P46012 caenorhabdi

34	62	11.2	171	1 TOXS_VIBPA	Q05939 vibrio para
35	62	11.2	192	1 FLHC_ECOLI	P11165 escherichia
36	62	11.2	774	1 LON1_BACSU	P37945 bacillus su
37	62	11.2	830	1 VP41_CAEEL	Q19954 caenorhabdi
38	62	11.2	1037	1 ACRD_ECOLI	P24177 escherichia
39	62	11.2	3329	1 BRC2_MOUSE	P97929 mus musculu
40	61.5	11.1	522	1 TMA2_XENLA	P52171 xenopus lae
41	61.5	11.1	677	1 UBF1_XENLA	P25979 xenopus lae
42	61.5	11.1	724	1 PAL2_PEA	Q04593 pisum sativ
43	61.5	11.1	901	1 MSH5_YEAST	Q12175 saccharomyc
44	61.5	11.1	1189	1 SCII_CHICK	Q90988 gallus gall
45	61.5	11.1	1351	1 RPOM_YEAST	P13433 saccharomyc

ALIGNMENTS

RESULT	1
IL13_HUMAN	
ID	IL13_HUMAN STANDARD; PRT; 132 AA.
AC	P35225; O43644;
DT	01-FEB-1994 (Rel. 28, Created)
DT	01-FEB-1994 (Rel. 28, Last sequence update)
DT	01-OCT-2000 (Rel. 40, Last annotation update)
DE	INTERLEUKIN-13 PRECURSOR (IL-13).
GN	IL13 OR NC30.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=93211479; PubMed=8096327;
RA	Minty A.J., Chalon P., Derocq J.M., Dumont X., Guillemot J.C.,
RA	Kaghad M., Labit C., Leplatois P., Liauzun P., Miloux B.,
RA	Minty C., Casellas P., Loison G., Lupker J., Shire D., Ferrara P.,
RA	Caput D.;
RT	"Interleukin-13 is a new human lymphokine regulating inflammatory and
RT	immune responses.";
RL	Nature 362:248-250(1993).

```
RP VARIANT GLN-130.
RX MEDLINE=20164293; PubMed=10699178;
RA Heinemann A., Mao X.-Q., Akaiwa M., Kreomer R.T., Gao P.-S.,
RA Ohshima K., Umeshita R., Abe Y., Braun S., Yamashita T., Roberts M.H.,
RA Sugimoto R., Arima K., Arinobu Y., Yu B., Kruse S., Enomoto T.,
RA Dake Y., Kawai M., Shimazu S., Sasaki S., Adra C.N., Kitaichi M.,
RA Inoue H., Yamauchi K., Tomichi N., Kurimoto F., Hamasaki N.,
RA Hopkin J.M., Izuhara K., Shirakawa T., Deichmann K.A.;
RT "Genetic variants of IL-13 signalling and human asthma and atopy.";
RT Hum. Mol. Genet. 9:549-559(2000).
CC -1- FUNCTION: CYTOKINE. INHIBITS INFLAMMATORY CYTOKINE PRODUCTION.
CC SYNERGIZES WITH IL2 IN REGULATING INTERFERON-GAMMA SYNTHESIS.
CC MAY BE CRITICAL IN REGULATING INTERFERON-GAMMA SYNTHESIS.
CC -1- SUBCELLULAR LOCATION: SECRETED.
CC -1- POLYMORPHISM: GLN AT POSITION 130 IS A SIGNIFICANT RISK FACTOR FOR
CC ASTHMA DEVELOPMENT.
CC -1- SIMILARITY: BELONGS TO THE IL-4 / IL-13 FAMILY.
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CC -----
DR EMBL: L06801; AAA36107.1; -
DR EMBL: X69079; CAA48824.1; -
DR EMBL: X69079; CAA48823.1; ALT_INIT.
DR EMBL: U31120; AAB01681.1; -
DR EMBL: U10307; AAA83738.1; -
DR EMBL: AF043334; AAC03535.1; -
DR PIR: A47481; A47481.
DR PDB: 3ITS; 26-JAN-95.
DR PDB: 3ITS; 26-JAN-95.
DR MIM: 147683; -
DR InterPro: IPR001325; -
DR PROSITE: PS00838; INTERLEUKIN_4_13; 1.
KW Cytokine; Glycoprotein; Signal; 3D-structure; Polymorphism.
FT SIGNAL 1 20
FT CHAIN 21 132 INTERLEUKIN-13.
FT DISULFID 48 76
FT DISULFID 64 90
FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 49 49 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 57 57 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 130 130 R->Q.
FT FTID=VAR_010037.
FT CONFLICT 45 45 A->R (IN REF. 4).
FT CONFLICT 87 87 S->G (IN REF. 5).
FT CONFLICT 98 98 MISSING (IN REF. 4).
SQ SEQUENCE 132 AA; 14319 MW; 123F1DCAB87FD78B CRC64;

Query Match 66.0%; Score 367; DB 1; Length 132;
Best Local Similarity 69.1%; Pred. No. 4.3e-33;
Matches 76; Conservative 11; Mismatches 21; Indels 2; Gaps 2;

QY 2 PVTPSPTLKELIEELVNTQNO-ASLCNGSMWVSNLTAGMYCALESILNVSDCSAIO 60
ID IL13_MOUSE STANDARD; PRT; 131 AA.
AC P20109;
DT 01-FEB-1991 (Rel. 17, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE INTERLEUKIN-13 PRECURSOR (IL-13) (T-CELL ACTIVATION PROTEIN P600).
GN IL13 OR IL-13.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89093958; PubMed=2521353;

RESULT 2
ID IL13_BOVIN STANDARD; PRT; 132 AA.
AC Q9XSV9;
DT 30-MAY-2000 (Rel. 39, Created)
```

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DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE INTERLEUKIN-13 PRECURSOR (IL-13).
GN IL13.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Bultkamp J., Jann O., Fries R.;
RT "The bovine interleukin-13 gene: genomic organization, chromosomal
RT location and evolution of the promoter.";
RL Submitted (JAN-1999) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: CYTOKINE. INHIBITS INFLAMMATORY CYTOKINE PRODUCTION.
CC SYNERGIZES WITH IL2 IN REGULATING INTERFERON-GAMMA SYNTHESIS. MAY
CC BE CRITICAL IN REGULATING INFLAMMATORY AND IMMUNE RESPONSES (BY
CC SIMILARITY).
CC -1- SUBCELLULAR LOCATION: SECRETED.
CC -1- SIMILARITY: BELONGS TO THE IL-4 / IL-13 FAMILY.
CC -----
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CC -----
DR EMBL: AJ132441; CAB46636.1; -
DR PROSITE: PS00838; INTERLEUKIN_4_13; 1.
KW Cytokine; Glycoprotein; Signal.
FT SIGNAL 1 20
FT CHAIN 21 132 BY SIMILARITY.
FT DISULFID 48 76 INTERLEUKIN-13.
FT DISULFID 64 90 BY SIMILARITY.
FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 49 49 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 57 57 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 75 75 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 132 AA; 14623 MW; 723BD42375C161F3 CRC64;

Query Match 62.1%; Score 345; DB 1; Length 132;
Best Local Similarity 64.9%; Pred. No. 1.1e-30;
Matches 72; Conservative 16; Mismatches 21; Indels 2; Gaps 2;

QY 1 SPVTPSPTLKELIEELVNTQNO-ASLCNGSMWVSNLTAGMYCALESILNVSDCSAIO 59
ID IL13_MOUSE STANDARD; PRT; 131 AA.
AC P20109;
DT 01-FEB-1991 (Rel. 17, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE INTERLEUKIN-13 PRECURSOR (IL-13) (T-CELL ACTIVATION PROTEIN P600).
GN IL13 OR IL-13.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89093958; PubMed=2521353;

RESULT 3
ID IL13_MOUSE STANDARD; PRT; 131 AA.
AC P20109;
DT 01-FEB-1991 (Rel. 17, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE INTERLEUKIN-13 PRECURSOR (IL-13) (T-CELL ACTIVATION PROTEIN P600).
GN IL13 OR IL-13.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89093958; PubMed=2521353;
```



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RA Brown K.D., Zurawski S.M., Mosmann T.R., Zurawski G.;
RT "A family of small inducible proteins secreted by leukocytes are
RT members of a new superfamily that includes leukocyte and
RT fibroblast-derived inflammatory agents, growth factors, and
RT indicators of various activation processes.";
RL J. Immunol. 142:679-687(1989).
CC -!- FUNCTION: CYTOKINE. INHIBITS INFLAMMATORY CYTOKINE PRODUCTION.
CC SYNERGIZES WITH IL2 IN REGULATING INTERFERON-GAMMA SYNTHESIS.
CC MAY BE CRITICAL IN REGULATING INFLAMMATORY AND IMMUNE RESPONSES
CC (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: SECRETED.
CC -!- SIMILARITY: BELONGS TO THE IL-4 / IL-13 FAMILY.
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CC -----
CC DR EMBL; M23504; AAA40149.1; -.
CC DR PIR; E30552; E30552.
CC DR HSSP; P35225; 3ITR.
CC DR MGD; MGI:96541; I113.
CC DR InterPro; IPR001325; -.
CC DR PROSITE; PS00838; INTERLEUKIN_4_13; 1.
CC KW Cytokine; Glycoprotein; Signal.
CC FT SIGNAL 1 21 BY SIMILARITY.
CC FT CHAIN 22 131 INTERLEUKIN-13.
CC FT DISULFID 51 79 BY SIMILARITY.
CC FT DISULFID 67 93 BY SIMILARITY.
CC FT CARBOHYD 42 42 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 52 52 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 75 75 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SQ SEQUENCE 131 AA; 14107 MW; 954F93F105713FED CRC64;

Query Match 54.3%; Score 302; DB 1; Length 131;
Best Local Similarity 58.8%; Pred. No. 5e-26;
Matches 60; Conservative 16; Mismatches 24; Indels 2; Gaps 1;

QY 8 TLKELIEELVNITQNASLNGSMVSVNLTAGMYCAALESLINVSDCSAIQRTQMLKA 67
Db 32 TLKELIEELSNITQDQTPLCNGSMVSVDLAAGGFCVALDSLNTNISCNAIYRTQRLHG 91

QY 68 LCSQKPAAGISSERSRDTKIEVIQLVKNLLTYVRGVYRHGNF 109
Db 92 LCNRKAPTTSVSS--LPDTKIEVAHFITKLSYTKQLFRHGPF 131

RESULT 4
IL13_RAT
ID IL13_RAT STANDARD; PRT; 131 AA.
AC P42203;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE INTERLEUKIN-13 PRECURSOR (IL-13) (T-CELL ACTIVATION PROTEIN P600).
GN IL13 OR IL-13.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Kidney cortex;
RX MEDLINE=94092138; PubMed=7916615;
RA Lakkis F.G., Cruet E.N.;
RT "Cloning of rat interleukin-13 (IL-13) cDNA and analysis of IL-13
RL gene expression in experimental glomerulonephritis.";
RL Biochem. Biophys. Res. Commun. 197:612-618(1993).
CC -!- FUNCTION: CYTOKINE. INHIBITS INFLAMMATORY CYTOKINE PRODUCTION.
```

```
CC SYNERGIZES WITH IL2 IN REGULATING INTERFERON-GAMMA SYNTHESIS.
CC MAY BE CRITICAL IN REGULATING INFLAMMATORY AND IMMUNE RESPONSES
CC (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: SECRETED.
CC -!- SIMILARITY: BELONGS TO THE IL-4 / IL-13 FAMILY.
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CC -----
CC DR EMBL; L26913; AAA16478.1; -.
CC DR HSSP; P35225; 3ITR.
CC DR InterPro; IPR001325; -.
CC DR PROSITE; PS00838; INTERLEUKIN_4_13; 1.
CC KW Cytokine; Glycoprotein; Signal.
CC FT SIGNAL 1 21 BY SIMILARITY.
CC FT CHAIN 22 131 INTERLEUKIN-13.
CC FT DISULFID 52 80 BY SIMILARITY.
CC FT DISULFID 68 94 BY SIMILARITY.
CC FT CARBOHYD 42 42 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 76 76 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 121 121 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SQ SEQUENCE 131 AA; 14093 MW; E5008CAB8DE8C201 CRC64;

Query Match 53.0%; Score 294.5; DB 1; Length 131;
Best Local Similarity 58.5%; Pred. No. 3.3e-25;
Matches 62; Conservative 18; Mismatches 23; Indels 3; Gaps 3;

QY 4 TPSPTLKEELVNITQNQ-ASLNGSMVSVNLTAGMYCAALESLINVSDCSAIQRTQ 62
Db 28 SPPVALRELIEELSNITQDQKTSLCNSSMVSVDLTAGGCAALESNTNISCNAIHRQTQ 87

QY 63 RMLKALCSQKPAAGISSERSRDTKIEVIQLVKNLLTYVRGVYRHGN 108
Db 88 RILNGLCNQK-ASDVASS-PPDTKIEVAQFISKLLNYSKQLFRYGH 131

RESULT 5
RYNR_HUMAN
ID RYNR_HUMAN STANDARD; PRT; 5032 AA.
AC P21817;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE RYANODINE RECEPTOR, SKELETAL MUSCLE (SKELETAL MUSCLE CALCIUM RELEASE
DE CHANNEL).
GN RYR1 OR RYDR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Skeletal muscle;
RX MEDLINE=90130482; PubMed=2298749;
RA Zorzato F., Fujii J., Otsu K., Phillips M., Green N.M., Lai F.A.,
RA Meissner G., MacLennan D.H.;
RT "Molecular cloning of cDNA encoding human and rabbit forms of the
RT Ca2+ release channel (ryanodine receptor) of skeletal muscle
RT sarcoplasmic reticulum.";
RL J. Biol. Chem. 265:2244-2256(1990).
RN [2]
RP VARIANT MH CYS-614.
RX MEDLINE=92128959; PubMed=1774074;
RA Gillard E.F., Otsu K., Fujii J., Khanna V.K., de Leon S.,
RA Dardemazi J., Britt B.A., Duff C.L., Worton R.G., McLennan D.H.;
RT "A substitution of cysteine for arginine 614 in the ryanodine
```

RT receptor is potentially causative of human malignant hyperthermia.";  
 RL Genomics 11:751-755(1991).  
 RN [3]  
 RP VARIANT MH ARG-248, AND VARIANTS CYS-471; LEU-1786 AND CYS-2059.  
 RX MEDLINE=92372020; PubMed=1354642;  
 RA Gillard E.F., Otsu K., Fujii J., Duff C., de Leon S., Khanna V.K.,  
 RA Britt B.A., Morton R.G., McLennan D.H.;  
 RT "Polymorphisms and deduced amino acid substitutions in the coding  
 RT sequence of the ryanodine receptor (RYR1) gene in individuals with  
 RT malignant hyperthermia.";  
 RL Genomics 13:1247-1254(1992).  
 RN [4]  
 RP VARIANT CCD HIS-2434.  
 RX MEDLINE=94035117; PubMed=8220422;  
 RA Zhang Y., Chen H.S., Khanna V.K., de Leon S., Phillips M.S.,  
 RA Schappert K., Britt B.A., Brownell A.K.W., MacLennan D.H.;  
 RT "A mutation in the human ryanodine receptor gene associated with  
 RT central core disease.";  
 RL Nat. Genet. 5:46-50(1993).  
 RN [5]  
 RP VARIANTS CCD CYS-163 AND MET-403.  
 RX MEDLINE=94035118; PubMed=8220423;  
 RA Quane K.A., Healy J.M.S., Keating K.E., Manning B.M., Couch F.J.,  
 RA Palmucci L.M., Doriguzzi C., Fagerlund T.H., Berg K., Ordling H.,  
 RA Bendixen D., Mortier W., Linz U., Muller C.R., McCarthy T.V.;  
 RT "Mutations in the ryanodine receptor gene in central core disease and  
 RT malignant hyperthermia.";  
 RL Nat. Genet. 5:51-55(1993).  
 RN [6]  
 RP VARIANT MH SER-522.  
 RX MEDLINE=95130087; PubMed=7829078;  
 RA Quane K.A., Keating K.E., Healy J.M.S., Manning B.M.,  
 RA Krivosic-Horber R., Krivosic I., Monnier N., Lunardi J.,  
 RA McCarthy T.V.;  
 RT "Mutation screening of the RYR1 gene in malignant hyperthermia:  
 RT detection of a novel Tyr to Ser mutation in a pedigree with  
 RT associated central cores.";  
 RL Genomics 23:236-239(1994).  
 RN [7]  
 RP VARIANT MH ARG-341.  
 RX MEDLINE=94282042; PubMed=8012359;  
 RA Quane K.A., Keating K.E., Manning B.M., Healy J.M.S., Monsieurs K.,  
 RA Heffron J.J.A., Lehane M., Heytons L., Krivosic-Horber R., Adnet P.,  
 RA Ellis F.R., Monnier N., Lunardi J., McCarthy T.V.;  
 RT "Detection of a novel common mutation in the ryanodine receptor gene  
 RT in malignant hyperthermia: implications for diagnosis and  
 RT heterogeneity studies.";  
 RL Hum. Mol. Genet. 3:471-476(1994).  
 RN [8]  
 RP VARIANT MH ARG-2433.  
 RX MEDLINE=95152512; PubMed=7849712;  
 RA Keating K.E., Quane K.A., Manning B.M., Lehane M., Hartung E.,  
 RA Censier K., Urwyler A., Klausnitzer M., Muller C.R., Heffron J.J.A.,  
 RA McCarthy T.V.;  
 RT "Detection of a novel RYR1 mutation in four malignant hyperthermia  
 RT pedigrees.";  
 RL Hum. Mol. Genet. 3:1855-1858(1994).  
 RN [9]  
 RP VARIANT MH ARG-2433.  
 RX MEDLINE=95187158; PubMed=7881417;  
 RA Phillips M.S., Khanna V.K., de Leon S., Frodis W., Britt B.A.,  
 RA McLennan D.H.;  
 RT "The substitution of Arg for Gly2433 in the human skeletal muscle  
 RT ryanodine receptor is associated with malignant hyperthermia.";  
 RL Hum. Mol. Genet. 3:2181-2186(1994).  
 RN [10]  
 RP VARIANT MH ARG-35.  
 RX MEDLINE=97219028; PubMed=9066328;  
 RA Lynch P.J., Krivosic-Horber R., Reyford H., Monnier N., Quane K.,  
 RA Adnet P., Haudecoeur G., Krivosic I., McCarthy T., Lunardi J.;  
 RT "Identification of heterozygous and homozygous individuals with the  
 RT novel RYR1 mutation Cys35Arg in a large kindred.";  
 RL Anesthesiology 86:620-626(1997).

RN [11]  
 RP VARIANT MH LEU-614.  
 RX MEDLINE=98051290; PubMed=9389851;  
 RA Quane K.A., Ordling H., Keating K.E., Manning B.M., Heine R.,  
 RA Bendixen D., Berg K., Krivosic-Horber R., Lehmann-Horn F.,  
 RA Fagerlund T., McCarthy T.V.;  
 RT "Detection of a novel mutation at amino acid position 614 in the  
 RT ryanodine receptor in malignant hyperthermia.";  
 RL Br. J. Anaesth. 79:332-337(1997).  
 RN [12]  
 RP VARIANT MH TRP-552.  
 RX MEDLINE=97284075; PubMed=9138151;  
 RA Keating K.E., Giblin L., Lynch P.J., Quane K.A., Lehane M.,  
 RA Heffron J.J.A., McCarthy T.V.;  
 RT "Detection of a novel mutation in the ryanodine receptor gene in an  
 RT Irish malignant hyperthermia pedigree: correlation of the IVCT  
 RT response with the affected and unaffected haplotypes.";  
 RL J. Med. Genet. 34:291-296(1997).  
 RN [13]  
 RP VARIANTS MH CYS-2162; HIS-2162; MET-2167 AND MET-2205.  
 RX MEDLINE=98163444; PubMed=9497245;  
 RA Manning B.M., Quane K.A., Ordling H., Urwyler A., Tegazzin V.,  
 RA Lehane M., O'Halloran J., Hartung E., Giblin L.M., Lynch P.J.,  
 RA Vaughan P., Censier K., Bendixen D., Comi G., Heytens L.,  
 RA Monsieurs K., Fagerlund T., Wolz W., Heffron J.J.A., Mueller C.R.,  
 RA McCarthy T.V.;  
 RT "Identification of novel mutations in the ryanodine-receptor gene  
 RT (RYR1) in malignant hyperthermia: genotype-phenotype correlation.";  
 RL Am. J. Hum. Genet. 62:599-609(1998).  
 RN [14]  
 RP VARIANTS MH CYS-2458 AND HIS-2458.  
 RX MEDLINE=9811378; PubMed=9450902;  
 RA Manning B.M., Quane K.A., Lynch P.J., Urwyler A., Tegazzin V.,  
 RA Krivosic-Horber R., Censier K., Comi G., Adnet P., Wolz W.,  
 RA Lunardi J., Muller C.R., McCarthy T.V.;  
 RT "Novel mutations at a CpG dinucleotide in the ryanodine receptor in  
 RT malignant hyperthermia.";  
 RL Hum. Mutat. 11:45-50(1998).  
 RN [15]  
 RP VARIANTS MH.  
 RX MEDLINE=99415746; PubMed=10484775;  
 RA Brandt A., Schleithoff L., Jurkat-Rott K., Klingler W., Baur C.,  
 RA Lehmann-Horn F.;  
 RT "Screening of the ryanodine receptor gene in 105 malignant  
 RT hyperthermia families: novel mutations and concordance with the in  
 RT vitro contracture test.";  
 RL Hum. Mol. Genet. 8:2055-2062(1999).  
 RN [16]  
 RP VARIANTS MH LEU-2434 AND HIS-2453.  
 RX MEDLINE=99158296; PubMed=10051009;  
 RA Barone V., Massa O., Intravala E., Bracco A., Di Martino A.,  
 RA Tegazzin V., Cozzolino S., Sorrentino V.;  
 RT "Mutation screening of the RYR1 gene and identification of two novel  
 RT mutations in Italian malignant hyperthermia families.";  
 RL J. Med. Genet. 36:115-118(1999).  
 RN [17]  
 RP VARIANTS MH CYS-2453.  
 RX MEDLINE=20081079; PubMed=10612851;  
 RA Gencik M., Gencik A., Mortier W., Epplen J.T.;  
 RT "Novel mutation in the RYR1 gene (R2454C) in a patient with malignant  
 RT hyperthermia.";  
 RL Hum. Mutat. 15:122-122(2000).  
 CC -I- FUNCTION: COMMUNICATION BETWEEN TRANSVERSE-TUBULES AND  
 CC SARCOPLASMIC RETICULUM. CONTRACTION OF SKELETAL MUSCLE IS  
 CC TRIGGERED BY RELEASE OF CA++ FROM SR FOLLOWING DEPOLARIZATION OF  
 CC T-TUBULES.  
 CC -I- SUBUNIT: HOMOTETRAMER (POTENTIAL).  
 CC -I- DISEASE: A DEFICIENCY IN THE RYANODINE RECEPTOR MAY BE THE CAUSE  
 CC OF MALIGNANT HYPERTHERMIA (MH) AND OF CENTRAL CORE DISEASE OF  
 CC MUSCLE (CCD). MH IS AN AUTOSOMAL DOMINANT DISORDER OF SKELETAL  
 CC MUSCLE AND IS ONE OF THE MAIN CAUSES OF DEATH DUE TO ANESTHESIA.  
 CC IN SUSCEPTIBLE PEOPLE, AN MH EPISODE CAN BE TRIGGERED BY ALL  
 CC COMMONLY USED INHALATIONAL ANESTHETICS SUCH AS HALOTHANE AND BY











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AC Q64105; Q63996;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE SEPIAPTERIN REDUCTASE (EC 1.1.1.153) (SPR).
GN SPR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95178553; PubMed=7873607;
RA Ota A., Ichinose H., Nagatsu T.;
RT "Mouse sepiapterin reductase: an enzyme involved in the final step of
RT tetrahydrobiopterin biosynthesis. Primary structure deduced from the
RT cDNA sequence."
RL Biochim. Biophys. Acta 1260:320-322(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=129;
RC MEDLINE=99227131; PubMed=10209270;
RA Lee S.W., Park I.Y., Hahn Y., Lee J.E., Seong C.S., Chung J.H.,
RA Park Y.S.;
RT "Cloning of mouse sepiapterin reductase gene and characterization of
RT its promoter region."
RL Biochim. Biophys. Acta 1445:165-171(1999).
RN [3]
RP SEQUENCE OF 209-261 FROM N.A.
RX MEDLINE=94136218; PubMed=8304109;
RA Maier J., Schott K., Werner T., Bacher A., Ziegler I.;
RT "Northern blot analysis of sepiapterin reductase mRNA in mammalian
RT cell lines and tissues."
RL Adv. Exp. Med. Biol. 338:195-198(1993).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (1.25 ANGSTROMS).
RX MEDLINE=98070299; PubMed=9405351;
RA Auerbach G., Herrmann A., Gutlich M., Fischer M., Jacob U., Bacher A.,
RA Huber R.;
RT "The 1.25-A crystal structure of sepiapterin reductase reveals its
RT binding mode to pterins and brain neurotransmitters."
RL EMBO J. 16:7219-7230(1997).
CC -1- FUNCTION: CATALYZES THE FINAL ONE OR TWO REDUCTIONS IN TETRA-
CC HYDROBIOPTERIN BIOSYNTHESIS TO FORM 5,6,7,8-TETRAHYDROBIOPTERIN.
CC -1- CATALYTIC ACTIVITY: 7,8-DIHYDROBIOPTERIN + NADP(+) = SEPIAPTERIN +
CC NADPH.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
DR EMBL; S77493; AAB33611.1; -
DR EMBL; U78077; AAC69364.1; -
DR EMBL; U78076; AAC69364.1; JOINED.
DR EMBL; S71375; -; NOT_ANNOTATED_CDS.
DR PDB; 1SEP; 13-JAN-99.
DR PDB; 1OAA; 16-FEB-99.
DR PDB; 1NAS; 30-MAR-99.
DR MGD; MGI:103078; Spr.
DR InterPro; IPR002198; -.
DR Pfam; PF00106; adh_short; 1.
KW Oxidoreductase; NADP; 3D-structure.
FT NP_BIND 14 40 NADP (BY SIMILARITY).
FT DOMAIN 29 33 PTERIN BINDING (POTENTIAL).
FT CONFLICT 4 4 D -> G (IN REF. 2).
SQ SEQUENCE 261 AA; 27883 MW; 102294EA39CB8AEC CRC64;

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Query Match 12.4%; Score 69; DB 1; Length 261;
Best Local Similarity 21.5%; Pred. No. 2.6;
Matches 23; Conservative 26; Mismatches 46; Indels 12; Gaps 4;

QY 3 VTPSPTLKELIEELVNTQNASLNGSMVSVNLTAGMYCALESILNVSDCSAIQRTQ 62
   :|:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 99 INNAATLGDVSKGFLNVN---DLAEVNNYVALNLTS-MLCLTSGTLNARQDSPGLSKTV 153
   :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 63 RMLKALCSQKPAAG----ISSERSRDTKIEVQLVK--NLITYVRG 102
   :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 154 VNISSLCALQPKYKGMGLYCAGKAARDMLYVLAEPSPVRLSYAPG 200

RESULT 13
RYNR_PIG STANDARD; PRT; 5035 AA.
AC P16960;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE RYANODINE RECEPTOR, SKELETAL MUSCLE (SKELETAL MUSCLE CALCIUM RELEASE
DE CHANNEL).
GN RYR1 OR CRC.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NORWEGIAN LANDRACE; TISSUE=Skeletal muscle;
RX MEDLINE=93036581; PubMed=1329581;
RA Harbitz I., Kristensen T., Bosnes M., Kran S., Davies W.;
RT "DNA sequence of the skeletal muscle calcium release channel cDNA and
RT verification of the Arg615-->Cys615 mutation, associated with porcine
RT malignant hyperthermia, in Norwegian landrace pigs."
RL Anim. Genet. 23:395-402(1992).
RN [2]
RP SEQUENCE OF 1129-2801 FROM N.A.
RA Brenig B.;
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 1129-2643 FROM N.A.
RC STRAIN=GERMAN LANDRACE; TISSUE=Liver;
RX MEDLINE=94117003; PubMed=8288238;
RA Leeb T., Schmolzl S., Brem G., Brenig B.;
RT "Genomic organization of the porcine skeletal muscle ryanodine
RT receptor (RYR1) gene coding region 4624 to 7929."
RL Genomics 18:349-354(1993).
RN [4]
RP SEQUENCE OF 4785-5035 FROM N.A.
RX MEDLINE=91065640; PubMed=2174405;
RA Harbitz I., Chowdhary B., Thomsen P.D., Davies W., Kaufman U.,
RA Kran S., Gustavsson I., Christensen K., Hauge J.G.;
RT "Assignment of the porcine calcium release channel gene, a candidate
RT for the malignant hyperthermia locus, to the 6p11-->q21 segment of
RT chromosome 6."
RL Genomics 8:243-248(1990);
CC -1- FUNCTION: COMMUNICATION BETWEEN TRANSVERSE-TUBULES AND
CC SARCOPLASMIC RETICULUM. CONTRACTION OF SKELETAL MUSCLE IS
CC TRIGGERED BY RELEASE OF CA++ FROM SR FOLLOWING DEPOLARIZATION OF
CC T-TUBULES.
CC -1- SUBUNIT: HOMOTETRAMER (POTENTIAL).
CC -1- MISCELLANEOUS: THE CALCIUM RELEASE CHANNEL IS MODULATED BY CA++,
CC MG++, ATP, AND CALMODULIN.
CC -1- MISCELLANEOUS: THE CALCIUM RELEASE CHANNEL ACTIVITY RESIDES IN THE
CC C-TERMINAL REGION WHILE THE REMAINING PART OF THE PROTEIN
CC CONSTITUTES THE 'FOOT' STRUCTURE SPANNING THE JUNCTIONAL GAP
CC BETWEEN THE SR AND THE T-TUBULE. IT IS POSSIBLE THAT THE FOOT
CC STRUCTURE INTERACTS WITH THE CYTOPLASMIC REGION OF THE
CC DIHYDROPYRIDINE RECEPTOR.
CC -1- MISCELLANEOUS: RYANODINE IS AN ALKALOID THAT BINDS TO THE
CC CA-RELEASE CHANNEL IN JUNCTIONAL SR AND MODULATES ITS ACTIVITY.

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: May 14, 2001, 06:01:15 ; Search time 133.94 Seconds  
(without alignments)  
96.259 Million cell updates/sec

Title: US-09-451-527-105  
Perfect score: 556  
Sequence: 1 SPVTPSPTLKELIEELVNIT.....QLVKNLITYVGVYRHGNER 110

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SP TREMBL\_15:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phase:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_unclassified:\*
- 13: sp\_vertebrate:\*
- 14: sp\_virus:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	545.5	98.1	131	6 Q9N0W9	Q9n0w9 canis famil
2	316	56.8	114	6 Q9TV84	Q9tv84 bos taurus
3	87.5	15.7	49	4 Q9UDC7	Q9udc7 homo sapien
4	80	14.4	275	6 Q28609	Q28609 oryctolagus
5	73.5	13.2	415	8 Q9MUM4	Q9mum4 mesostigma
6	73.5	13.2	607	10 Q9SI43	Q9si43 arabidopsis
7	72.5	13.0	150	14 Q98779	Q98779 vesicular s
8	72.5	13.0	438	10 Q9M3H8	Q9m3h8 cicer ariet
9	72.5	13.0	1763	11 Q9JKX5	Q9jkkx5 mus musculu
10	72	12.9	5038	4 Q9NPK1	Q9npk1 homo sapien
11	71.5	12.9	150	14 Q98791	Q98791 vesicular s
12	71	12.8	155	11 Q9R1G1	Q9rlg1 rattus norv
13	71	12.8	589	5 Q96661	Q96661 trypanosoma
14	71	12.8	649	14 O10619	O10619 helicoverpa
15	70.5	12.7	150	14 Q98780	Q98780 vesicular s
16	70.5	12.7	150	14 Q98787	Q98787 vesicular s
17	70.5	12.7	150	14 Q98789	Q98789 vesicular s
18	70.5	12.7	1811	14 O36184	O36184 plautia sta
19	70	12.6	482	9 O36165	O36165 bacterioph

20	70	12.6	1448	5 Q9N949	Q9n949 trypanosoma
21	70	12.6	1510	5 Q9VX92	Q9vx92 drosophila
22	69.5	12.5	274	14 Q89048	Q89048 vesicular s
23	69.5	12.5	1520	4 O15087	O15087 homo sapien
24	69.5	12.5	1781	4 Q9UKX0	Q9ukx0 homo sapien
25	69.5	12.5	1890	4 Q9UKW3	Q9ukw3 homo sapien
26	69.5	12.5	2073	4 Q9UKW2	Q9ukw2 homo sapien
27	69	12.4	1128	6 P79271	P79271 sus scrofa
28	69	12.4	5035	6 Q29105	Q29105 sus scrofa
29	68	12.2	198	4 Q9UBB1	Q9ubb1 homo sapien
30	68	12.2	1448	5 Q9N946	Q9n946 trypanosoma
31	67.5	12.1	150	14 Q98778	Q98778 vesicular s
32	67.5	12.1	2626	11 Q9Z1N3	Q9z1n3 rattus norv
33	67	12.1	815	5 Q9W3N6	Q9w3n6 drosophila
34	67	12.1	837	5 Q9NFR8	Q9nfr8 drosophila
35	67	12.1	1102	11 Q9JHG7	Q9jhg7 mus musculu
36	66.5	12.0	350	14 Q9Q8P4	Q9q8p4 myxoma viru
37	66.5	12.0	471	14 Q70156	Q70156 human immun
38	66.5	12.0	1112	10 Q9SSP2	Q9ssp2 arabidopsis
39	66	11.9	398	5 O45966	O45966 caenorhabdi
40	65.5	11.8	150	14 Q98790	Q98790 vesicular s
41	65.5	11.8	478	2 Q9KXF0	Q9kxf0 escherichia
42	65.5	11.8	478	9 Q9MCT4	Q9mct4 bacterioph
43	65.5	11.8	483	9 Q9T1M4	Q9t1m4 bacterioph
44	65	11.7	284	2 Q9XBM2	Q9xbm2 acidaminoco
45	65	11.7	300	10 Q9SLJ6	Q9slj6 arabidopsis

ALIGNMENTS

RESULT 1

Q9N0W9

ID Q9N0W9 PRELIMINARY; PRT; 131 AA.

AC Q9N0W9;

DT 01-OCT-2000 (TReMBLrel. 15, Created)

DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)

DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)

DE INTERLEUKIN-13.

OS Canis familiaris (Dog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

OX NCBI\_TaxID=9615;

RN [1]

RP SEQUENCE FROM N.A.

RA Yang S., Boroughs K.L., McDermott M.J.;

RT "Canine Interleukin-13: Molecular Cloning of Full-Length cDNA and Expression of Biologically Active Recombinant Protein.";

RL Submitted (MAR-2000) to the EMBL/GenBank/DBBJ databases.

DR EMBL; AF244915; AAF63204.1; -.

SQ SEQUENCE 131 AA; 14268 MW; 9A142B4D0F80370F CRC64;

Query Match 98.1%; Score 545.5; DB 6; Length 131;  
Best Local Similarity 99.1%; Pred. No. 3.8e-53;  
Matches 110; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 SPVTPSPTLKELIEELVNITQNQASLCNGSMVSVNLTAGMYCAALESINVSDCSAIQR 60  
|||||

Db 21 SPVTPSPTLKELIEELVNITQNQASLCNGSMVSVNLTAGMYCAALESINVSDCSAIQR 80  
|||||

QY 61 TQRLKALCSQKPAAG-ISSERSRDTKIEVIQLVKNLLTYVGVYRHGNER 110  
|||||

Db 81 TQRLKALCSQKPAAGQISSERSRDTKIEVIQLVKNLLTYVGVYRHGNER 131  
|||||

RESULT 2

Q9TV84

ID Q9TV84 PRELIMINARY; PRT; 114 AA.

AC Q9TV84;

DT 01-MAY-2000 (TReMBLrel. 13, Created)

DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)

DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)

```

DE INTERLEUKIN-13 PRECURSOR (FRAGMENT).
GN IL-13.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Trigona W.T., Hirano A., Brown W.;
RT "Biological activities of interleukin-13 (IL-13) on bovine
RL lymphocytes: implications for signaling through IL-13ra1."
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF072807; AAD22748.1; -.
DR HSSP; P35225; 3ITR.
DR INTERPRO; IPR001325; -.
DR PROSITE; PS00838; INTERLEUKIN_4_13; UNKNOWN_1.
FT NON_TER 114 114
SQ SEQUENCE 114 AA; 12355 MW; D8CC56E5627D030A CRC64;

```

Query Match	56.8%;	Score 316;	DB 6;	Length 114;
Best Local Similarity	71.0%;	Pred. No. 1.1e-27;		
Matches	66;	Conservative	10;	Mismatches 15;
			Indels	2;
			Gaps	2;

```
Oy      1 SPVTPSPPTLKELIEELVNITONQ-ASLCNGSMWWSNLTAGMYCAALESILINVSDCSAIQ 59
        ||| : ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     21 SPVP SATALKE L I E E LV N I T O N Q V P L C N G S M W W S N L T T S M Y C A L D S L I S T N C S V I Q 80
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Qy	60	RTQRMKALCSQKPAA-GISSERSRDTKIEVIQ	91
	11:111 111	11:1 111 111111	↓
Db	81	RTKRMALALCPHKPSAKQVSSEIYRDTKIEVAQ	113

RESULT 3  
09UDC7

ID	Q9UDC7	PRELIMINARY;	PRT;	49 AA.
AC	Q9UDC7;			
DT	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT	01-OCT-2000 (TREMBLrel. 15, Last annotation update)			
DE	P600 HOMOLOG.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=93027259; PubMed=1408833;			
RA	Morgan J.G., Dolganov G.M., Robbins S.E., Hinton L.M., Lovett M.;			
RT	"The selective isolation of novel cDNAs encoded by the regions			
RT	surrounding the human interleukin 4 and 5 genes.";			
RL	Nucleic Acids Res. 20:5173-5179(1992).			
DR	HSSP: P35225; 3ITR.			
SO	SEQUENCE 49 AA; 5109 MW; 679CD23A190C778E CRC64;			

Query Match	15.78;	Score 87.5;	DB 4;	Length 49;
Best Local Similarity	71.48;	Pred. No. 0.011;		
Matches 20;	Conservative 1;	Mismatches 6;	Indels 1;	Gaps 1;

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OY      2 PVTPSPTELKELIEELVNITONQ-ASLCN 28
        || | | :|:||||| | | | | | | |
DB     22 PVPSTALRELIEELSNTOTOKAPLNCN 49
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RESULT	4	
Q28609		
ID	Q28609	PRELIMINARY; PRT; 275 AA

DT	01-NOV-1996 (TREMBlrel. 01, Created)
DT	01-NOV-1996 (TREMBlrel. 01, last sequence update)
DT	01-OCT-2000 (TREMBlrel. 15, last annotation update)

DE	PUTATIVE PREPROSPERMINOGEN PRECURSOR.
OS	Oryctolagus cuniculus (Rabbit).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX	NCBI_TaxID=9986;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=NEW ZEALAND WHITE; TISSUE=TESTIS;
RC	MEDLINE=94368861; PubMed=8086468;
RA	Richardson R.T., O'Rand M.G.;
RT	"Cloning and sequencing of cDNAs for rabbit preproacrosin and a novel
RT	preproacrosin-related cDNA.";
RL	Biochim. Biophys. Acta 1219:215-218(1994).
DR	EMBL; U05203; AAA61629.1; -.
DR	HSSP: P00734; 2HNT.
DR	INTERPRO: IPR001254; -.
DR	PFAM: PF00089; trypsin; 1.
DR	PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
KW	Signal.
FT	SIGNAL
FT	CHAIN
FT	1 16 POTENTIAL.
FT	17 275 PROSPERMINOGEN.
SO	SEQUENCE 275 AA; 29965 MW; 8FC2467414069C61 CRC64;

Query Match	14.48;	Score 80;	DB 6;	Length 275;
Best Local Similarity	32.38;	Pred. No. 0.53;		
Matches	20;	Conservative 11;	Mismatches 25;	Indels 6;
				Gaps 2;

```
OY      5 PSPTLKEELIIELVNITQNCASLCNGSMVSVNLTAGMYCAALESILINSDCSAIORTQM 64
        ||||| | :|:| :||: ::|| | | : | :|: :
Db     190 PSPTLMEARVDLINL-----ELCNSIQWYINGRITASNLCAGYPS-GKIDTCQRLOOLEVEY 243
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QY	65	LK	66
Db	244	LK	245

RESULT	5		
ID	Q9MUM4	PRELIMINARY;	PRT; 415 AA.
AC	Q9MUM4;		
DT	01-OCT-2000 (TREMBLrel. 15, Created)		
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)		
DT	01-OCT-2000 (TREMBLrel. 15, Last annotation update)		
DE	PUTATIVE PLASTID DIVISION PROTEIN.		
GN	FTSW.		
OS	Mesostigma viride.		
OG	Chloroplast.		
OC	Eukaryota; Viridiplantae; Chlorophyta; Prasinophyceae;		
OC	Chlorodendrales; Mesostigmataceae; Mesostigma.		
OX	NCBI_TaxID=41882;		
RN	[1]		
RX	SEQUENCE FROM N.A.		
RP	MEDLINE=20150907; Pubmed=10688199;		
RA	Lemieux C., Otis C., Turmel M.;		
RT	"Ancestral chloroplast genome in Mesostigma viride reveals an early		
RT	branch of green plant evolution.";		
RL	Nature 403:649-652(2000).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RA	Lemieux C., Otis C., Turmel M.;		
RL	Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF166114; AAF43874.1; .		
KW	Chloroplast.		
SEQUENCE	415 AA;	46813 MW;	E35116E9692EC782 CRC64;

Query Match	13.28;	Score 73.5;	DB 8;	Length 415;
Best Local Similarity	28.78;	Pred. No. 4.5;		
Matches 27;	Conservative 19;	Mismatches 29;	Indels 19;	Gaps 4;

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0y      16 LVNITONQASLCNGSMVWSVNLTAGMYCAALESLINVSDCSAI-----QRTORMLKAL 68
      | : | | | | : : : | | | | | : | : : : | : : : | : | : : |

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Db 188 LIQPNLSTASLC-GAIIWLVALTAGIHWFYLSILSIGAVTALISLGSQEQYQRIISFL 246

QY 69 CSQKPAAGISSERSRDTKIEVIQLVKNLITYVRG 102

Db 247 ---NPWANPTSIG-----YQLVQSLLAVGSG 269

RESULT 6

Q9SI43

ID Q9SI43 PRELIMINARY; PRT; 607 AA.

AC Q9SI43;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)

DE PUTATIVE METHYLMALONATE SEMI-ALDEHYDE DEHYDROGENASE.

GN AT2G14170.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;

OC Brassicales; Brassicaceae; Arabidopsis.

OX NCBI\_TaxID=3702;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CV. COLUMBIA;

RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,

RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,

RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,

RA Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,

RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,

RA Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,

RA Salzberg S.L., Fraser C.M., Venter J.C.;

RA "Sequence and analysis of chromosome II of Arabidopsis thaliana.";

RL Nature 402:761-768(1999).

DR EMBL; AC007197; AAD25855.1; -.

DR HSSP; P56533; 1A4S.

DR INTERPRO; IPR001064; -.

DR INTERPRO; IPR02086; -.

DR PFAM; PF00171; aldedh; 1.

DR PROSITE; PS00070; ALDEHYDE\_DEHYDR\_CYS; UNKNOWN\_1.

DR PROSITE; PS00225; CRYSTALLIN\_BETAGAMMA; UNKNOWN\_1.

SQ SEQUENCE 607 AA; 65926 MW; 0257A3606B31165C CRC64;

Query Match 13.2%; Score 73.5; DB 10; Length 607;

Best Local Similarity 26.4%; Pred. No. 7;

Matches 23; Conservative 16; Mismatches 31; Indels 17; Gaps 4;

QY 39 AGMYCAALESLINVSDCSA-----IQRTQMLKALCSQKPAAGISSERSRDTKIEVIQLV 93

Db 387 AGQRCMALSTVFVVGDAKSWEDKLVERA-KALKVTCGSEPDADLGPVISKQAKERICRLI 445

QY 94 KN-----LLTYVRGV-----YRHGNF 109

Db 446 QSGVDDGAKLLDGRDIVVPGYKGNF 472

RESULT 7

Q98779

ID Q98779 PRELIMINARY; PRT; 150 AA.

AC Q98779;

DT 01-FEB-1997 (TrEMBLrel. 02, Created)

DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)

DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)

DE PHOSPHOPROTEIN (FRAGMENT).

OS Vesicular stomatitis virus.

OC Viruses; ssRNA negative-strand viruses; Mononegavirales;

OC Rhabdoviridae; Vesiculovirus.

OX NCBI\_TaxID=11276;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=0888CRB;

RX MEDLINE=97075113; PubMed=8917539;

RA Rodriguez L.L., Fitch W.M., Nichol S.T.;

RT "Ecological factors rather than temporal factors dominate the

RT evolution of vesicular stomatitis virus.";

RL Proc. Natl. Acad. Sci. U.S.A. 93:13030-13035(1996).

DR EMBL; U39211; AAB50939.1; -.

DR INTERPRO; IPR000224; -.

DR PFAM; PF00922; Phosphoprotein; 1.

FT NON\_TER 1

FT NON\_TER 150

SQ SEQUENCE 150 AA; 16711 MW; 16D11C4E8E8A65E7 CRC64;

Query Match 13.0%; Score 72.5; DB 14; Length 150;

Best Local Similarity 24.2%; Pred. No. 1.8;

Matches 29; Conservative 20; Mismatches 40; Indels 31; Gaps 6;

QY 2 PVTSPPTLKEELIEEL-----VNITQNQA-----SLCNGSMVWSVN----LTAGMY 42

Db 14 PSWTQPVIKENGGERSLSLFPPVGLTQVQTEQWKKTITVCESSKYWNLSQCIVTSG-N 72

QY 43 CAALESLINVSDCSAIQRTQMLKALCSQKPAAGISSERSR-----DTKIEVIQLV 93

Db 73 CLILRGQVMTSDCSSAKSQNSRQS--SESPSPNSPEHASRASASPNLWDFKFTEVQLI 130

RESULT 8

Q9M3H8

ID Q9M3H8 PRELIMINARY; PRT; 438 AA.

AC Q9M3H8;

DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)

DE PUTATIVE UDP-GLYCOSE (FRAGMENT).

OS Cicer arietinum (Chickpea) (Garbanzo).

OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;

OC Fabales; Fabaceae; Papilionoideae; Cicer.

OX NCBI\_TaxID=3827;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CV. CASTELLANA; TISSUE=ETIOLATED EPICOTYLS;

RA Dopico B., Munoz F.J., Labrador E.;

RT "A putative UDP-Glycose: Flavonoid glycosyltransferase is expressed in

RT chickpea epicotyls.";

RL Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.

DR EMBL; AJ400861; CAB88666.1; -.

FT NON\_TER 1

SQ SEQUENCE 438 AA; 48662 MW; 0BB7B805BD66E27C CRC64;

Query Match 13.0%; Score 72.5; DB 10; Length 438;

Best Local Similarity 26.1%; Pred. No. 6.2;

Matches 35; Conservative 20; Mismatches 48; Indels 31; Gaps 6;

QY 2 PVTSPPTLKEELIEELVN-----ITQNQASL-----CNGSMVWSVNLTAGMYC 43

Db 136 PIKPSPGFARLTPLEAVEAKSGHGVIVNSFAELDEGYTEYYENLTGRKVHWVHGPTSLMIK 195

QY 44 AALESLINVSDCSAIQRTQMLKALCSQKPA-----GISSERSRDTKIEV---IQLVK 94

Db 196 TTLEKTDNISNGSSTK--HKCLTWLDTKEPSSVVYISFGSLCSLSNDQLELAKGIEASK 253

QY 95 NLLTYVRGVYRHGN 108

Db 254 HQFLWV--VHRKGD 265

RESULT 9

Q9JKX5

ID Q9JKX5 PRELIMINARY; PRT; 1763 AA.

AC Q9JKX5;

DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)





Best Local Similarity 21.1%; Pred. No. 2.8;  
Matches 26; Conservative 25; Mismatches 44; Indels 28; Gaps 4;  
QY 9 LKELIEELVNITQNASLCSNGSMVSVN-----LTAGMYCAALES--LINVSDCS 56  
Db 1 LYELLASLRGNRTNCALFSTNLDWLVSCLDRLEASSGILEVLYCVLIESPEVLNIQEN 60  
QY 57 AIQ-----RTQMLKALCSQKPAAGISSERSRDTKIE-----VIQLVKNLLTYV 100  
Db 61 HIKSIISLLDKHGRNHKVLVDVLCVVCNGVAVRSNQDLITENLLPGRELLQTNLINIV 120  
QY 101 RGV 103  
Db 121 TSI 123

RESULT 13  
ID O96661 PRELIMINARY; PRT; 589 AA.  
AC O96661;  
DT 01-MAY-1999 (TReMBLrel. 10, Created)  
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)  
DE 01-JUN-2000 (TReMBLrel. 14, Last annotation update)  
DE PF20 HOMOLOG.  
GN TWD1.  
OS Trypanosoma brucei.  
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.  
OX NCBI\_TaxID=5691;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=427;  
RA Hsu C.L., Lin Y.T., Huang J.D.;  
RT "A novel gene encoding a protein with WD40 repeat and leucine zipper motifs from Trypanosoma brucei";  
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF101480; AAC83819.1; -.  
DR INTERPRO; IPR001680; -.  
DR PFAM; PF00400; WD40; 7.  
DR PRINTS; PR00320; GPROTEINBRPT.  
DR PROSITE; PS00678; WD\_REPEATS; UNKNOWN\_4.  
SQ SEQUENCE 589 AA; 65481 MW; 2053B920666F51BF CRC64;

Query Match 12.8%; Score 71; DB 5; Length 589;  
Best Local Similarity 22.9%; Pred. No. 13;  
Matches 24; Conservative 23; Mismatches 40; Indels 18; Gaps 3;  
QY 14 EELVNITQNASLCSNGSMVSVNLTAGMYCAALESLINVSDCSA-----IQRTQRL 65  
Db 456 DKTVSLWDVNRANCCSQTLYGHNRNAVQSV--TTVGPTTNVATCDADGVVMLWDTRRMEQHL 513  
QY 66 KALCSQKPAAGISSER-----SRDTKIEVIQLVKNLLTYVRG 102  
Db 514 TVACGPYPANHIASTRNGTYLLVSSDDPNIKLIDVTKSTVTELVG 558

RESULT 14  
ID O10619 PRELIMINARY; PRT; 649 AA.  
AC O10619; Q82480;  
DT 01-JUL-1997 (TReMBLrel. 04, Created)  
DT 01-JUL-1997 (TReMBLrel. 04, Last sequence update)  
DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)  
DE IMMEDIATE EARLY PROTEIN 1.  
GN IE1.  
OS Helicoverpa zea nuclear polyhedrosis virus.  
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;  
OC Nucleopolyhedrovirus.  
OX NCBI\_TaxID=10468;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ELKAR;  
RX MEDLINE=95053907; PubMed=7964631;

RA Cowan P., Bulach D., Goodge K., Robertson A., Tribe D.E.;  
RT "Nucleotide sequence of the polyhedrin gene region of Helicoverpa zea single nucleocapsid nuclear polyhedrosis virus: placement of the virus in lepidopteran nuclear polyhedrosis virus group II.";  
RL J. Gen. Virol. 75:3211-3218(1994).  
RN [2]  
RP REVISIONS.  
RC STRAIN=ELKAR (ELCAR);  
RA Le T.H., Wu T., Robertson A., Bulach D., Cowan P., Goodge K.,  
RA Tribe D.;  
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U67264; AAB54100.1; -.  
SQ SEQUENCE 649 AA; 75522 MW; B0D133AC9FEBD0E4 CRC64;

Query Match 12.8%; Score 71; DB 14; Length 649;  
Best Local Similarity 24.3%; Pred. No. 14;  
Matches 26; Conservative 18; Mismatches 33; Indels 30; Gaps 3;  
QY 1 SPVTPSP-----TLKELIEELVNITQNASLCSNGSMVSVNLTAGMYCAALES 48  
Db 97 SPIAMSPQRITPRSERSENVIESLSLQKQVTVSLRRGS-----GLYGKNIQN 147  
QY 49 LIN-----VSDCSAIQRTQMLKALCSQKPAAGISSERSRDTK 86  
Db 148 LKENYEKTMDPYEDSSSLELTPKPKRSNTEKKIAGVGEKRSKKEK 194

RESULT 15  
ID Q98780 PRELIMINARY; PRT; 150 AA.  
AC Q98780;  
DT 01-FEB-1997 (TReMBLrel. 02, Created)  
DT 01-FEB-1997 (TReMBLrel. 02, Last sequence update)  
DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)  
DE PHOSPHOPROTEIN (FRAGMENT).  
OS Vesicular stomatitis virus.  
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
OC Rhabdoviridae; Vesiculovirus.  
OX NCBI\_TaxID=11276;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=0986CRB2;  
RX MEDLINE=97075113; PubMed=8917539;  
RA Rodriguez L.L., Fitch W.M., Nichol S.T.;  
RT "Ecological factors rather than temporal factors dominate the evolution of vesicular stomatitis virus";  
RL Proc. Natl. Acad. Sci. U.S.A. 93:13030-13035(1996).  
DR EMBL; U39212; AAB50940.1; -.  
DR INTERPRO; IPR000224; -.  
DR PFAM; PF00922; Phosphoprotein; 1.  
FT NON\_TER 1 150  
FT NON\_TER 150 150  
SQ SEQUENCE 150 AA; 16611 MW; E3D1095B8E8A65FD CRC64;

Query Match 12.7%; Score 70.5; DB 14; Length 150;  
Best Local Similarity 24.2%; Pred. No. 3;  
Matches 29; Conservative 18; Mismatches 42; Indels 31; Gaps 6;  
QY 2 PVTSPPTLKELEIEL-----VNITQNSA-----SLCNGSMVSVN---LTAGMY 42  
Db 14 PSWTQPVIKENGGERSLSLFPVPVGLTVQTEQWKKTIVTVCESKYWNLSQCIVTSG-N 72  
QY 43 CAALESLINVSDCSAIQRTQMLKALCSQKPAAGISSERSR-----DTKIEVIQLV 93  
Db 73 CLILRGQVMTSDCSSSAKSN--SQSSSESPSPNSPEHASRASASPNLWDFKFTVQLI 130

Search completed: May 14, 2001, 06:01:18  
Job time: 43961 sec

